Conclusions The MIRACLE score performed best in both effect size and frequency of studies where its association with outcome was statistically significant. No features gave substantial predictive rather than prognostic information. We expect that integration of transcriptomic features with clinical features and DNA alterations will be required to provide predictive (rather than just prognostic) information. Methods that train models on prioritization of predictive information and generalizability across studies may be required for optimal biomarker development.

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REFERENCES


Abstract 508 Figure 1  Overall survival associations of selected immunogenomics features. Rows represent selected immunogenomics features and columns represent individual datasets. Results from ICI trials are shown in the left panel, and results from TCGA datasets are shown in the right panel. Row/column intersections represent effect size (triangle direction and color) and statistical significance (triangle size) of associations with overall survival. Column-side colorbars show various dataset features for comparison.

Abstract 508 Figure 2  Predictive versus prognostic information content of selected immunogenomics features. X-axis represents the log10 hazard ratio with 95% confidence interval derived from TCGA data, and Y-axis represents log10 hazard ratio with 95% confidence interval derived from ICI data.

Abstract 508 Figure 3  Predictive versus prognostic information content of selected immunogenomics features, melanoma trials only. X-axis represents the log10 hazard ratio with 95% confidence interval derived from TCGA data, and Y-axis represents log10 hazard ratio with 95% confidence interval derived from ICI data.