Time to Recurrence and Survival in Serous Ovarian Tumors Predicted from Integrated Genomic Profiles

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microRNA expression

microRNA data was available for 527 samples. These intensities were $\log_2$ transformed and normalized using Robust Multiarray Averaging (RMA, AgiMicroRNA package in R).

Progression Free Survival: At λ=.858, we selected 81 microRNA features (Table ST8 [1]), cv.CPE = 0.704. Tertile stratification based on training data led to a p-value of 0.09 for the test data (Figures 3SA, 3SB).

Survival: At λ=.869, we selected 87 features (Table ST9 [2]), cv.CPE = 0.71. Tertile stratification based on training data led to a p-value of 0.09 for the test data (Figures 3SA, 3SB).

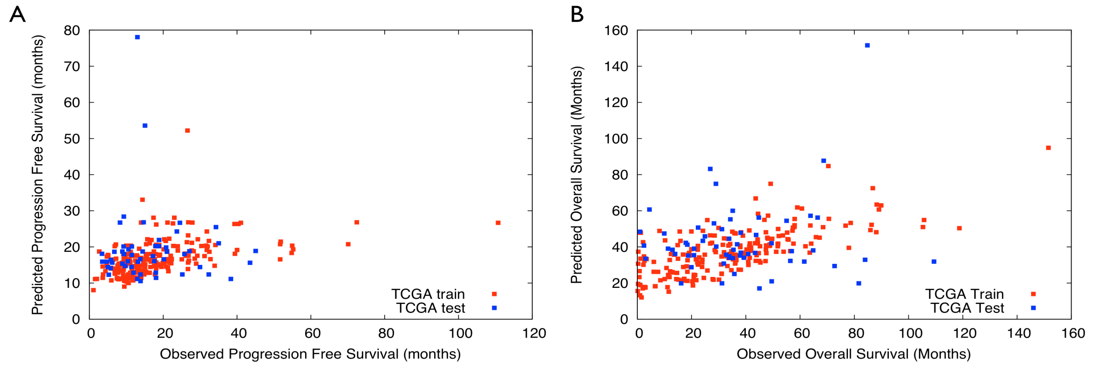

Figure 3SA: Predictions of median *time-to-event* using microRNA signatures: (A) Progression Free Survival and (B) Overall Survival; both for censored data.

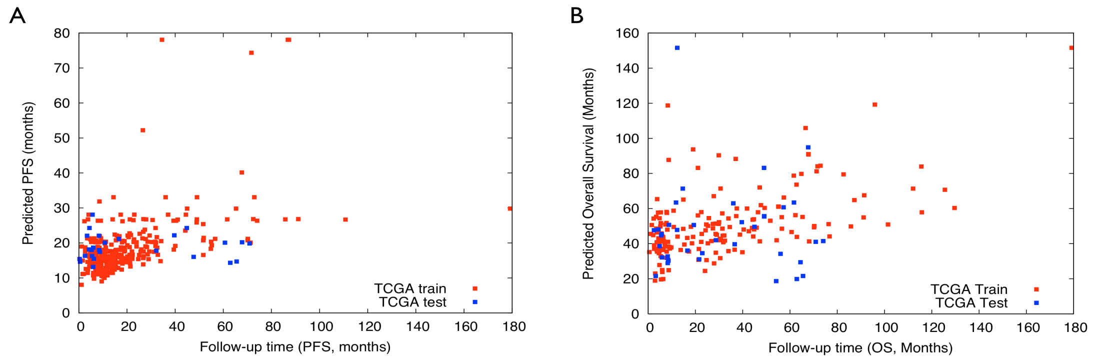

Figure 3SB: Median *time-to-event* predictions for censored data using microRNA signatures: (A) Progression Free Survival and (B) Overall Survival.

References:

[1] http://cbio.mskcc.org/~mankoo/ST8.txt

[2] http://cbio.mskcc.org/~mankoo/ST9.txt