**Supplementary Figure S1:** Model performance measured by additional metrics. **A.** Box plots of test set normalized root mean square error (NRMSE) between the transcript-predicted and actual protein level for each protein are shown across five feature sets (column: single/self transcript, CORUM interactors, STRING high-confidence associated proteins; STRING low-confidence associated proteins, and all transcripts) and three algorithms (multiple linear regression, elastic net, and random forest). In each plot, x axis denotes the number of CPTAC data set used to train the models box: interquartile range; whiskers: +/- 1.5 IQR. **B.** As above, but for test set goodness-of-fit ($R^2$).