Prognostic and biological relevance of collagen-related genes in prostate cancer

Methods, figures and tables for the transcriptome part

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# Methods

Analyses of collagen-related transcriptome and survival in transcriptomic cohorts were done with R version 4.2.3 (R foundation). Their details are provided in **Supplementary Methods**.

## Transcriptome data sets

Seven publicly available transcriptome data sets of primary prostate cancer samples, the [TCGA](https://www.cbioportal.org/study/summary?id=prad_tcga_pan_can_atlas_2018) prostate cancer cohort (1,2) (n = 493 cancer samples, RNA sequencing), [GSE16560](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16560) (3) (n = 281, microarray) [GSE54460](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE54460) (4) (n = 106, RNA sequencing), [GSE70768](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE70768) (5) (n = 125, microarray), [GSE70769](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE70769) (5) (n = 94, microarray), [GSE220095](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE220095) (6) (n = 176, RNA sequencing), and [DKFZ](https://www.cbioportal.org/study/summary?id=prostate_dkfz_2018) (7) (n = 118, RNA sequencing) were re-analyzed. Selection criteria for the transcriptomic cohorts were: information of biochemical relapse and relapse-free survival or death and overall survival, and availability of expression data for collagen-related transcript investigated in our previous collagen project (8).

Normalized gene expression data and clinical information were fetched from the cBioportal repository (DKFZ, TCGA) or Gene Expression Omnibus (GEO). The microarray signals of RNA sequencing counts were analyzed as -transformed counts adjusted for differences in distribution between the cohorts with ComBat algorithm (9). ComBat-adjusted expression and clinical information for the GSE54460, GSE70768, GSE70769, and GSE220095 studies was merged into a ‘pooled GEO cohort’. In machine learning models of BCR-free survival, the pooled GEO cohort was used for training, and TCGA and DKFZ served as validation cohorts. The GSE16560 cohort split into a training and test subset in a 2:1 ratio was used for modeling of overall survival. Characteristic of the cohorts and a list of the collagen-related genes of interest are are provided in **Supplementary Tables S1 - S4**.

## Co-expression network analyses

Co-expression networks of the collagen-related transcripts were constructed in the poled GEO, DKFZ, and TCGA cohorts. The networks’ edges were defined by pairwise correlations of the ComBat-adjusted expression levels with Spearman’s 0.5; transcripts without any network neighbors were removed. Importance of the network’s vertices, i.e. the collagen-related transcripts, was assessed by degree as a measure of connectivity (number of neighbors), hub score as a metric of overall correlation strength (eigenvector of the affinity matrix), betweenness as a measure of connectivity and centrality (minimum/maximum-scaled number of the shortest paths between all pairs of vertices that pass through the vertex of interest), and transitivity (fraction of neighbor vertices that are connected with each other) (10) (**Supplementary Table S5**).

## Univariable modeling of BCR-free survival

For univariable analysis of BCR-free survival, PCA patients in the pooled GEO, TCGA, and DKFZ cohort were classified as high and low expressors of each collagen-related gene with a cutoffs corresponding to the largest difference in survival between the expression strata. BCR risk of the high as compared with low expressors was assessed by unavailable Cox proportional hazard regression. Inference of the Cox proportional hazard models was assessed by hazard ratio (HR) with 95% confidence intervals, and p values corrected for multiple testing with the false discovery rate method (FDR). Harrell’s concordance index (11) and Integrated Brier Score (12) were used as statistics of, respectively, model accuracy and calibration (**Supplementary Table S6**).

## Multi-parameter modeling of BCR-free survival

Machine learning models of BCR-free survival were constructed for the following sets of explanatory variables: (1) first- and second-order terms of ComBat-adjusted expression levels of the collagen-related transcripts, (2) pathological tumor stage, ISUP grade, and ComBat-adjusted mRNA levels of the PSA-coding gene *KLK3* (13,14) as clinical predictors of BCR, and (3) pathological tumor stage, ISUP grade, ComBat-adjusted *KLK3* mRNA levels, as well as the first- and second-order terms of ComBat-adjusted expression levels of the collagen-related transcripts. The models were trained in the pooled GEO cohort with six algorithms (RIDGE regularized Cox proportional hazard regression, Elastic Net regularized Cox proportional hazard regression, LASSO regularized Cox proportional hazard regression, Support Vector Machines [SVM], Random Forest, and Gradient Boosted Machines [GBM]) (15–25). Performance of the models was evaluated by comparison of the predicted and actual BCR-free survival in the pooled GEO training cohort, and TCGA and DKFZ validation collectives with Harrell’s concordance index and Integrated Brier Scores (**Supplementary Tables S7** - **S8**). Additionally, BCR-free survival in patients stratified by tertiles of predictor scores returned by the machine learning models was explored with Kaplan-Meier plots and Peto-Peto tests. Finally, confidence and calibration of the models was assessed by plots of Brier Scores for unique follow-up times.

## Multi-parameter modeling of overall survival

Overall survival of PCA patients was modeled in the GSE16560 watchful waiting cohort (3). First- and second-order terms of ComBat-adjusted -transformed expression levels of the collagen-related genes served as explanatory factors. Machine learning models using the algorithms outlined above for the BCR-free survival were trained in a training subset of the GSE16560 cohort, and validated in the test subset. Performance of the models of overall survival was evaluated in the training and test subsets of the GSE16560 cohort as described above for BCR-free survival (**Supplementary Tables S9** - **S10**).

## Data and code availability

Publicly available data sets were analyzed: the links are provided in **Methods/Transcriptome data sets**. Formatted data sets used for analyses will be made available upon request to the corresponding author. The R analysis pipeline for the transcriptome data is available from GitHub (<https://github.com/PiotrTymoszuk/BCR_collagen>).

# Figures

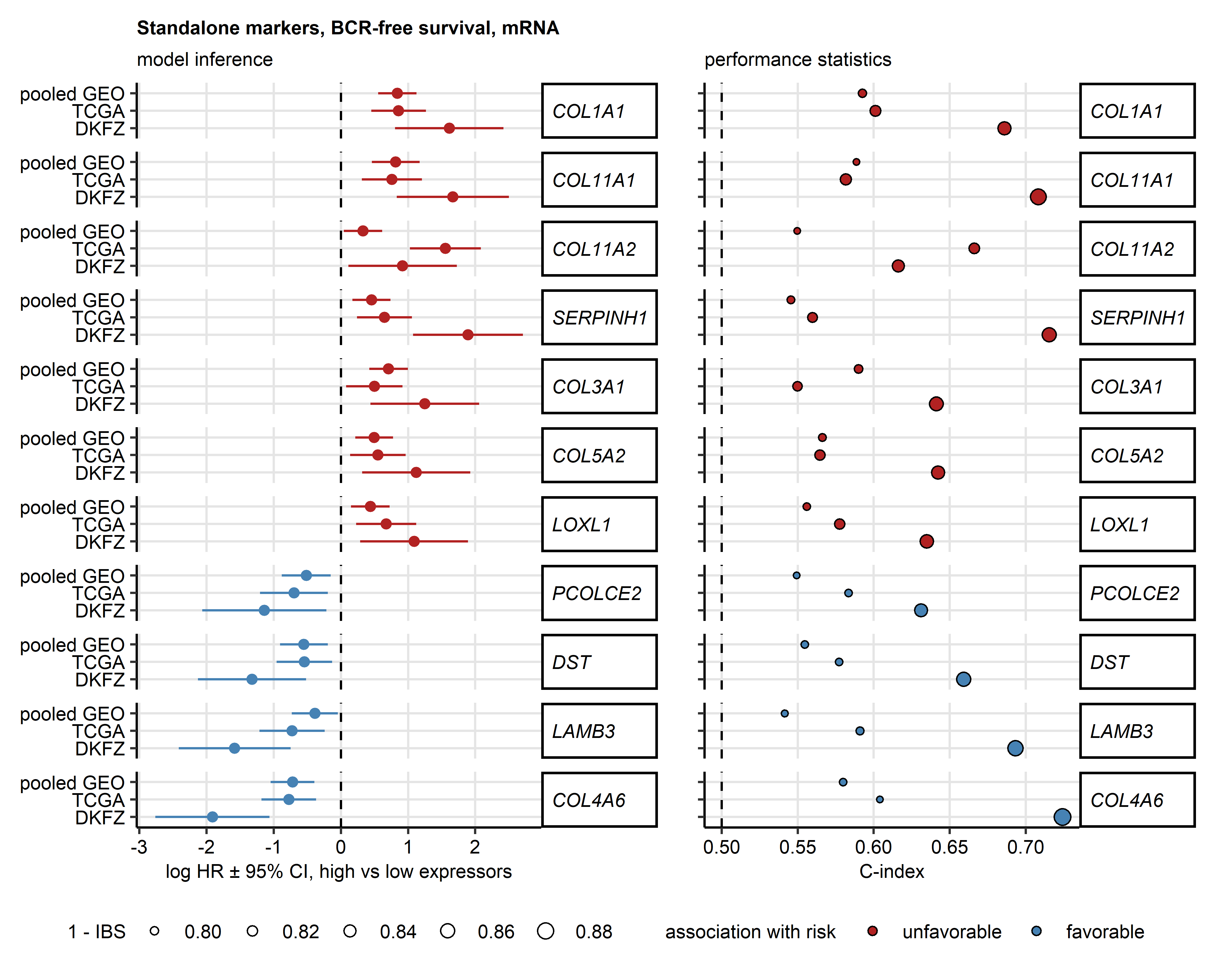


Figure 1: Univariable analysis of BCR-free survival with collagen-related transcripts as candidate standalone prognostic factors.

**Figure 1. Univariable analysis of BCR-free survival with collagen-related transcripts as candidate standalone prognostic factors.**

*Prostate cancer (PCA) patients in the pooled GEO (total: n = 485, biochemical relapse [BCR]: n = 194), TCGA (total: n = 493, BCR: n = 93), and DKFZ cohort (total: n = 105, BCR: n = 24) were classified as high and low expressors for each of the rlength(globals$genes)` collagen-related transcripts with the expression cutoffs corresponding to the largest differences in survival between the high and low expressors.* *BCR risk was compared between the high and low expressors for each transcript by univariable Cox proportional hazard regression. P values were corrected for multiple testing with the false discovery rate (FDR) method.* *Standalone BCR risk markers were defined as transcripts associated with unfavorable prognosis (high versus low expressors, hazard ratio [HR] > 1, pFDR < 0.05) or favorable prognosis (HR < 1, pFDR < 0.05) in all three cohorts.*

*HR with 95% confidence intervals for BCR risk in the high versus low expression strata are presented in a Forest plot (left). The model performance statistics, Harrell’s concordance index (C-index, measure of model accuracy), and Integrated Brier Scores (IBS, measure of model calibration, low values indicative of good calibration) are presented in a dot plot (right).*

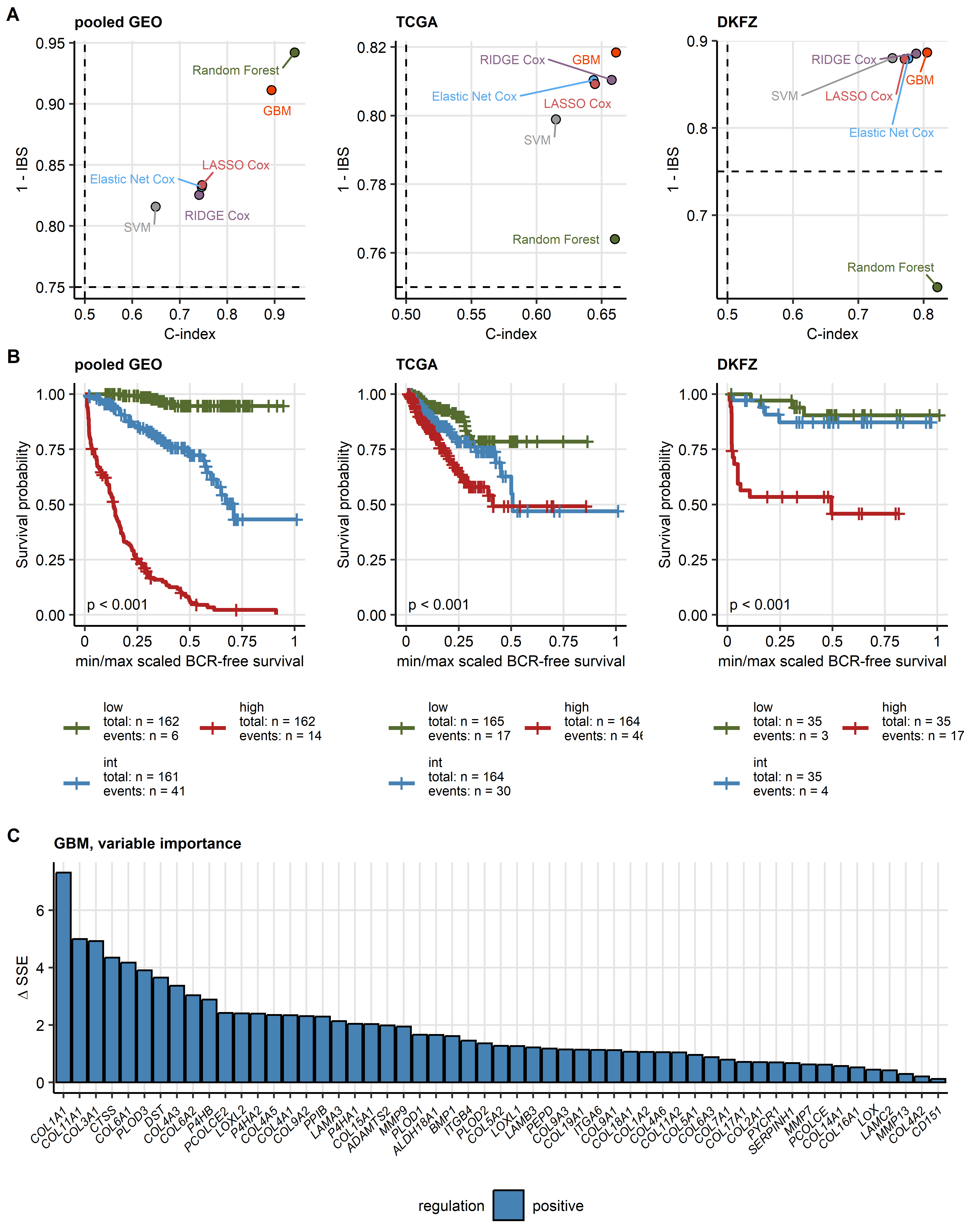


Figure 2: Machine learning modeling of BCR-free survival with expression levels of the collagen-related transcripts as explanatory factors.

**Figure 2. Machine learning modeling of BCR-free survival with expression levels of the collagen-related transcripts as explanatory factors.**

*Risk of biochemical relapse (BCR) in prostate cancer (PCA) was modeled by multi-parameter machine learning models with ComBat-processed -transformed expression levels of 55 collagen-related transcripts as explanatory factors.* *The models were trained in the pooled GEO cohort with six machine learning algorithms (RIDGE Cox regression, Elastic Net Cox regression, LASSO Cox regression, survival Support Vector Machines [SVM], survival Random Forest, and survival Gradient Boosted Machines [GBM]).* *Performance of the models was evaluated in the pooled GEO training cohort (total: n = 485, BCR: n = 194), and the TCGA (total: n = 493, BCR: n = 93) and DKFZ (total: n = 105, BCR: n = 24) validation collectives.*

*(A) Metrics of performance of the survival models, Harrell’s concordance index (C-index, measure of model accuracy) and Integrated Brier Score (IBS, measure of model calibration, low values are characteristic for good calibration), are presented in dot plots. Dashed lines represent C-index and IBS values expected for random BCR risk prediction. Note the superior accuracy and calibration of the GBM model in the validation collectives.*

*(B) BCR-free survival of PCA patients stratified by tertiles of the predictor scores of the best performing GBM model. Statistical significance of differences between the predictor score tertiles was determined by Peto-Peto test corrected for multiple testing wit the false discovery rate method. Fractions of BCR-free patients and minimum/maximum scaled time after diagnosis are visualized in Kaplan-Meier plots. Numbers of patients and BCR in the predictor score tertiles are indicated in the legends. P values are displayed in the plots.*

*(C) Importance of the explanatory variables for BCR-risk prediction by the GBM model was gauged by difference in sum of squared error () attributed to inclusion of a particular collagen-related transcript in the GBM learner ensemble. High values are characteristic for highly influential variables. values for the variables that contributed substantially to the BCR risk prediction ( > 0) are presented in a bar plot.*

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