A multi-step classifier addressing cohort heterogeneity improves performance of prognostic biomarkers in three cancer types

SUPPLEMENTARY TABLES

Supplementary Table S1: Details of the patients and variables used in analysis for the three cancer cohorts.

See Supplementary File 1

Supplementary Table S2: Sensitivity and specificity for predicting good prognosis for melanoma cohort

Melanoma	***Gene expression***	***Clinical***	***Prevalidation***	***Random forest***	***Two stage***
Sensitivity	0.69	0.75	0.79	0.7	0.71
Specificity	0.73	0.57	0.60	0.56	0.76

Supplementary Table S3: Sensitivity and specificity for predicting good prognosis for breast cancer cohort

Breast	***Gene expression***	***Clinical***	***Prevalidation***	***Random forest***	***Two stage***
Sensitivity	0.42	0.95	0.82	0.76	0.80
Specificity	0.48	0.00	0.03	0.27	0.71

Supplementary Table S4: Sensitivity and specificity for predicting good prognosis for colon cancer cohort

Colon	***Gene expression***	***Clinical***	***Prevalidation***	***Random forest***	***Two stage***
Sensitivity	0.63	0.67	0.60	0.67	0.76
Specificity	0.54	0.53	0.51	0.62	0.68