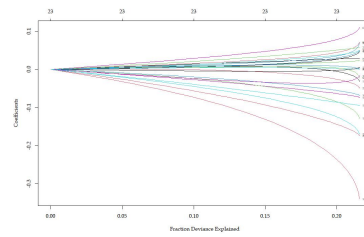
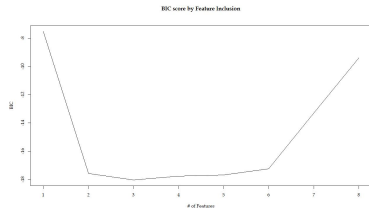


(A)

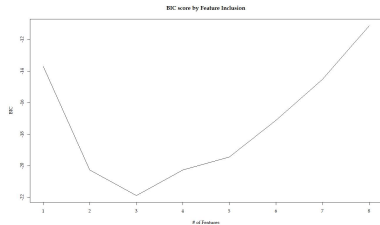


(B)

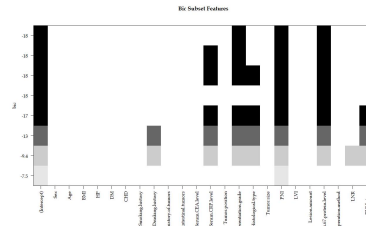
**Supplementary Figure 1 Experimental results of ridge regression on the overall survival predictive models.**



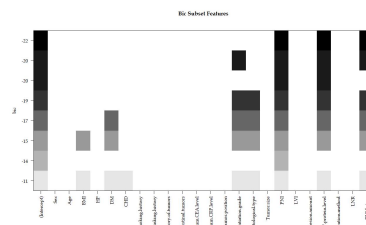
(A)



(C)



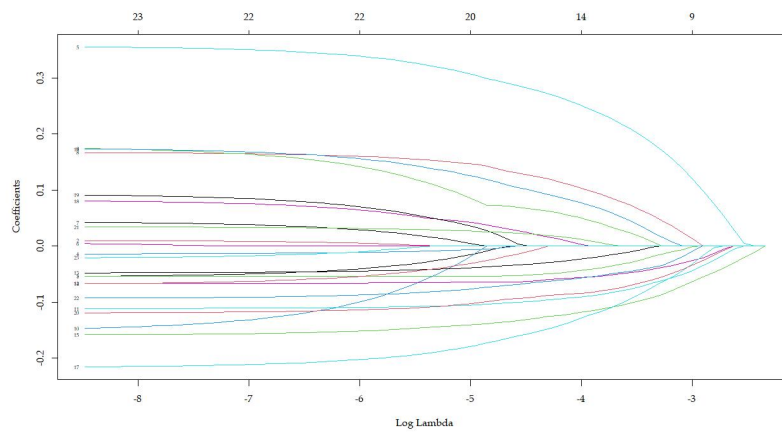
(B)



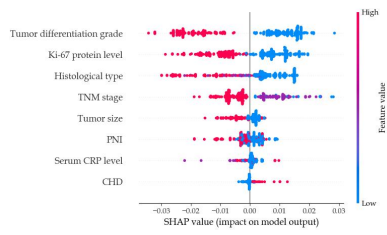
(D)

**Supplementary Figure 2 Experimental results of subset regression on the disease-free survival and distant metastasis-free survival predictive models.**

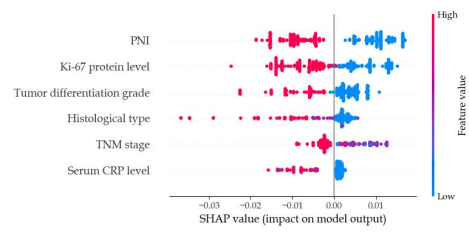
A: Number of characteristic variables obtained according to the Bayesian information criterion for the disease-free survival predictive model (6); B: The important variables (PNI, Ki-67 protein level, tumor differentiation grade, serum CRP level, histological type, and TNM stage) from the disease-free survival predictive model; the most important variable was PNI; C: Number of characteristic variables obtained according to the Bayesian information criterion for the distant metastasis-free survival predictive model (5); D: The important variables (PNI, Ki-67 protein level, TNM stage, tumor differentiation grade, and histological type) from the distant metastasis-free survival predictive model; PNI was the most important variable



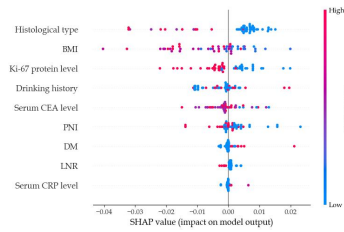
**Supplementary Figure 3 Experimental results of LASSO regression on the recurrence-free survival models**



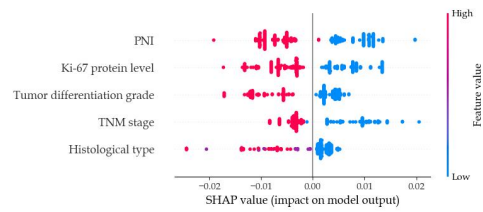
(A)



(B)

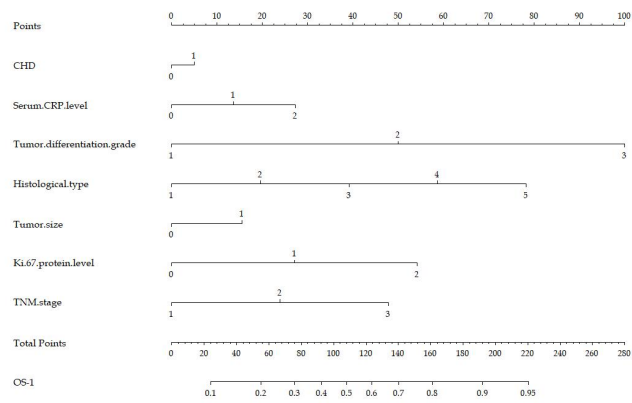


(C)

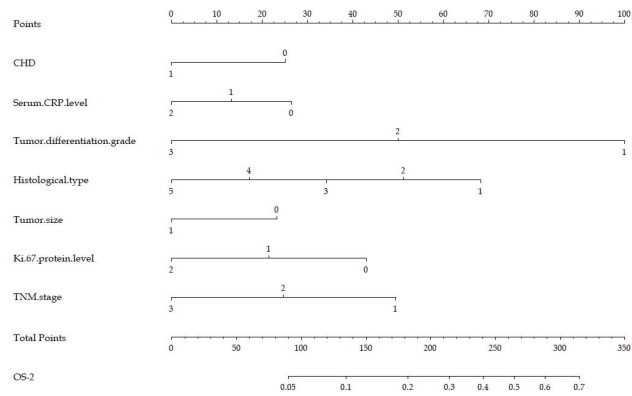


(D)

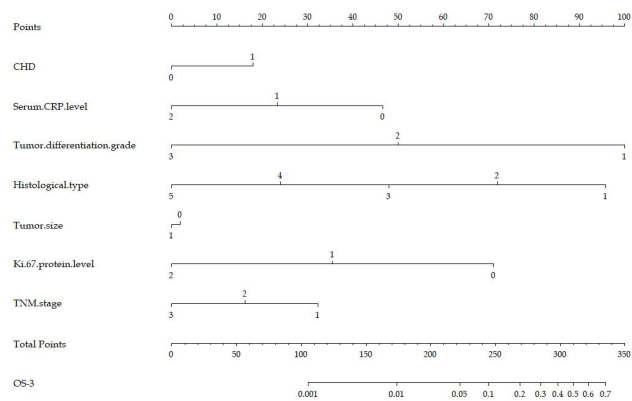
**Supplementary Figure 4 SHapley Additive exPlanations plots of the 4 machine learning models. A: Overall survival model; B: Disease-free survival model; C: Recurrence-free survival model; D: Distant metastasis-free survival model**



(A)

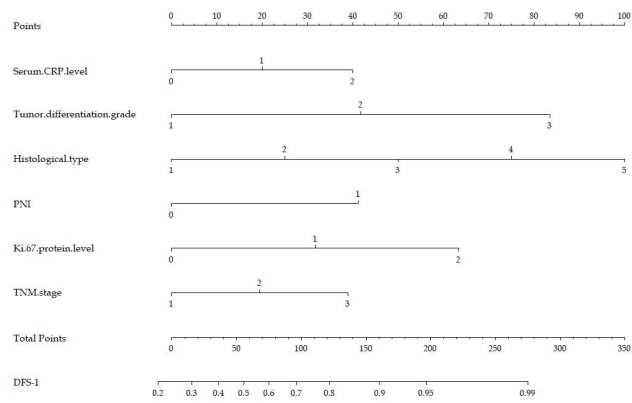


(B)

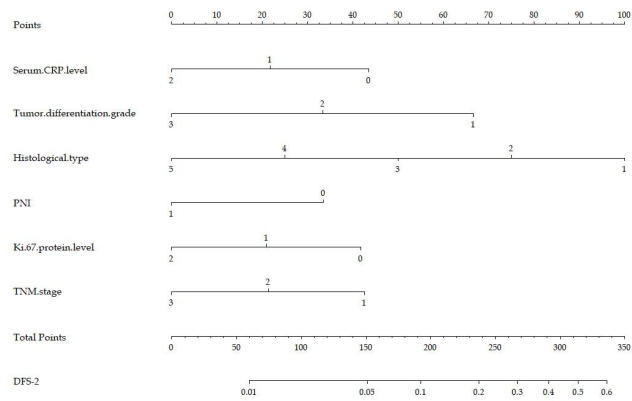


(C)

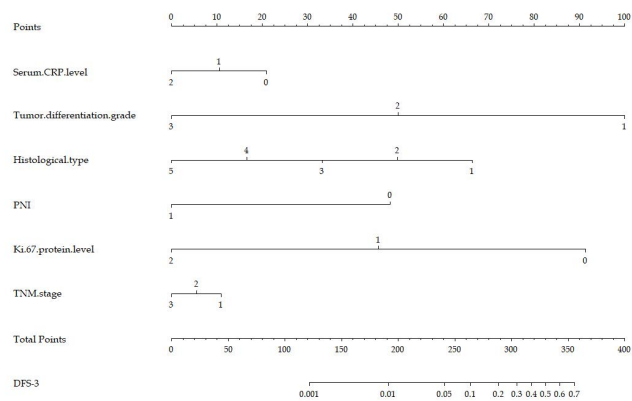
**Supplementary Figure 5 Nomograms of the overall survival predictive models (classes 1 to 3). A: cl 1; B: cl 2; C: cl 3.**



(A)

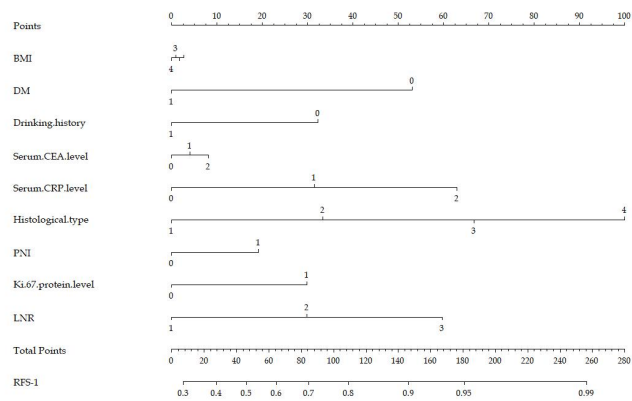


(B)

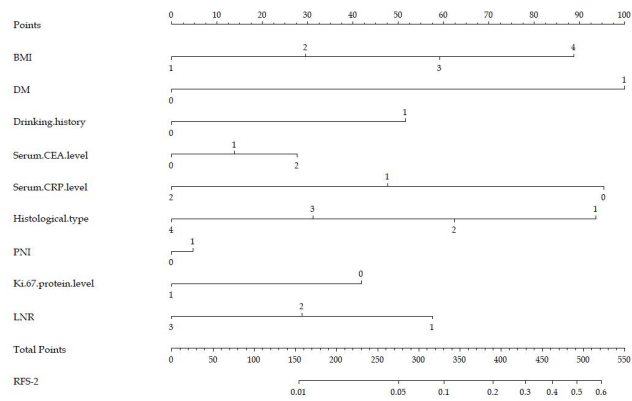


(C)

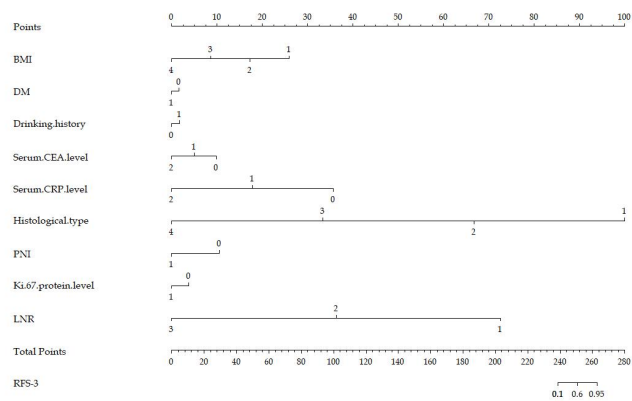
**Supplementary Figure 6 Nomograms of the disease-free survival predictive models (classes 1 to 3). A: cl 1; B: cl 2; C: cl 3**



(A)

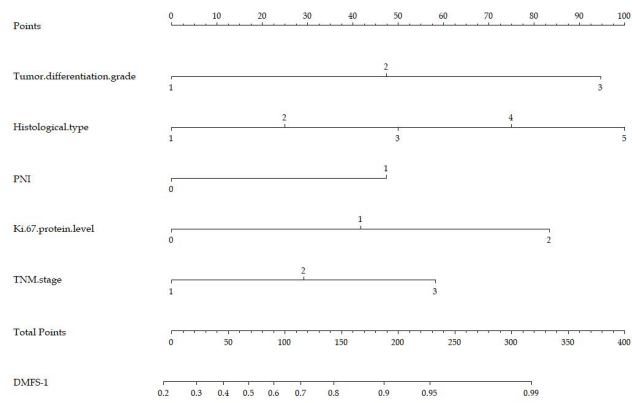


(B)

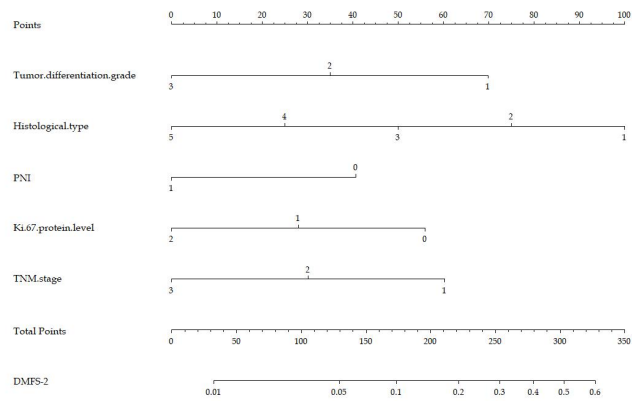


(C)

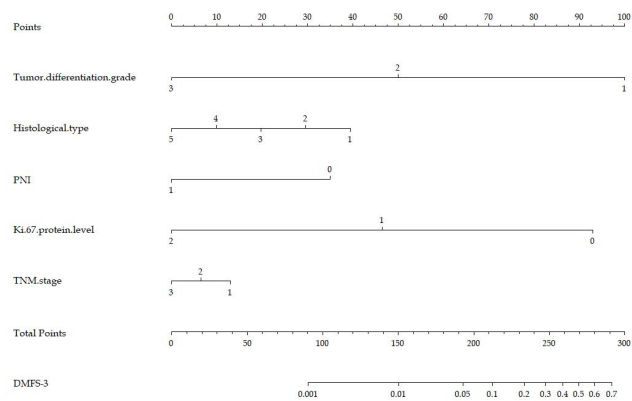
**Supplementary Figure 7 Nomograms of the recurrence-free survival predictive models (classes 1 to 3). A: cl 1; B: cl 2; C: cl 3**



(A)



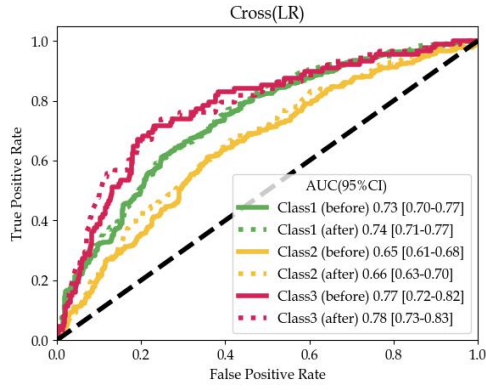
(B)



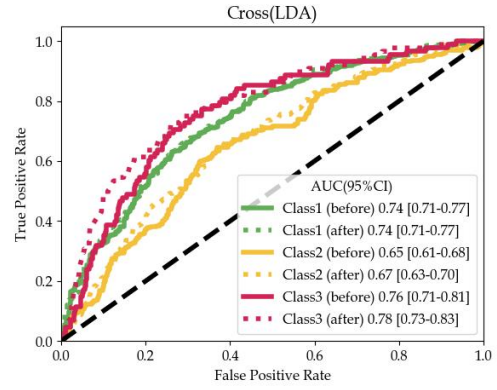
(C)

**Supplementary Figure 8 Nomograms of the distant metastasis-free survival predictive models (classes 1 to 3). A: cl 1; B: cl 2; C: cl 3**

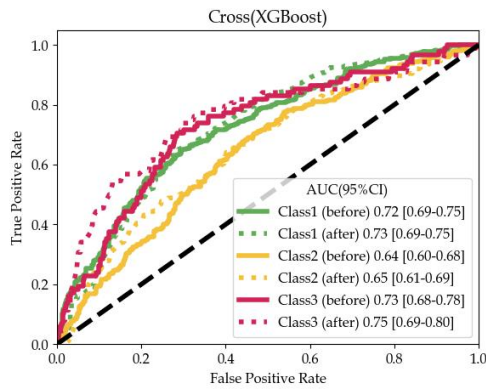




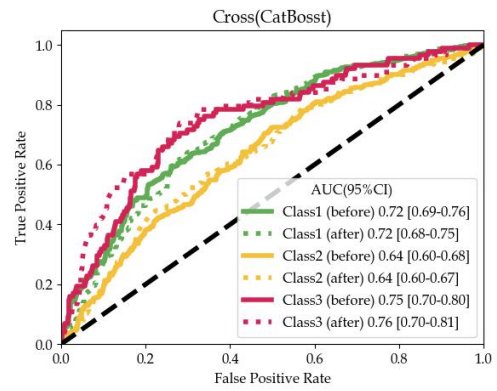
(A)



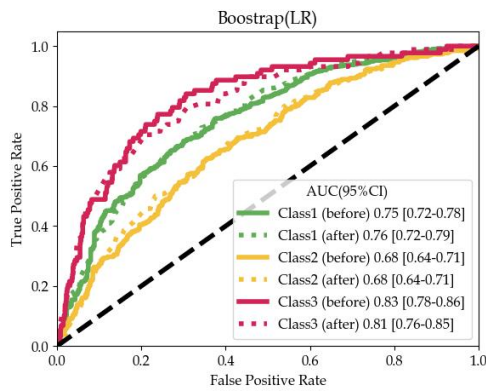
(B)



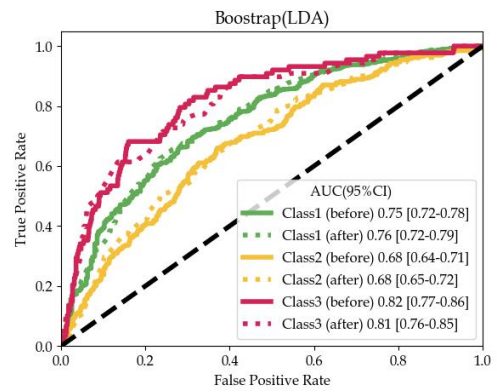
(C)



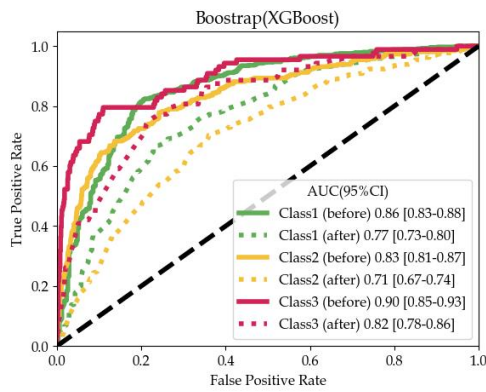
(D)



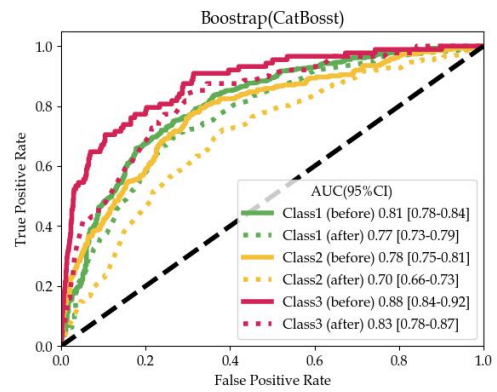
(E)



(F)

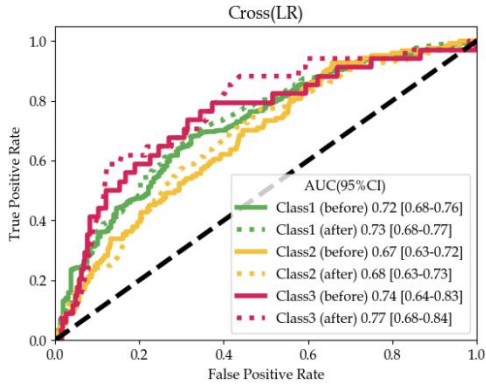


(G)

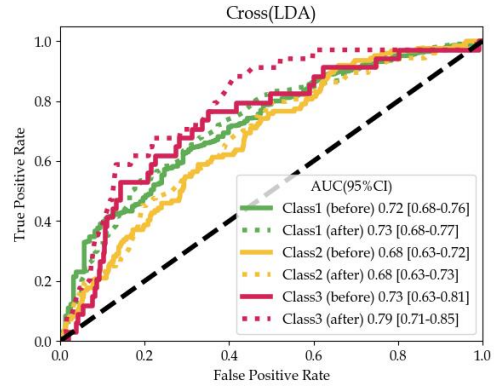


(H)

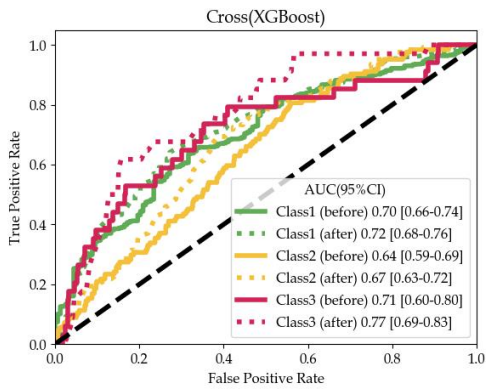
**Supplementary Figure 9 ROC curves of the four overall survival prediction models generated following cross-validation and bootstrap resampling for cl 1, cl 2, and cl 3 before and after filtering the variables.** A, B, C, D: ROC curves generated for the different overall survival models following 5-fold cross-validation in the training dataset before and after screening the variables; E, F, G, H: ROC curves generated for the different overall survival models following bootstrap validation with 300 iterations of resampling in the validation dataset before and after screening the variables



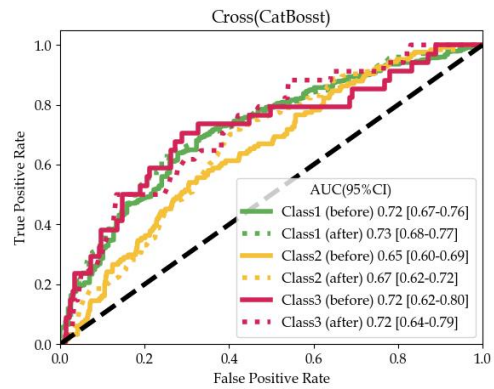
(A)



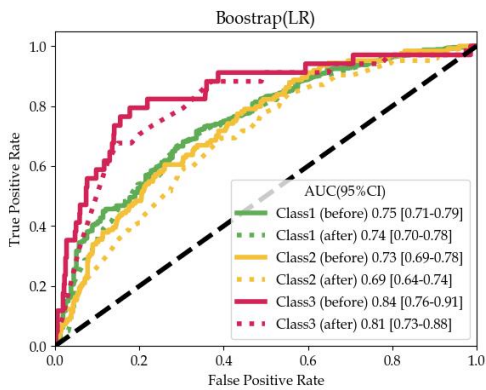
(B)



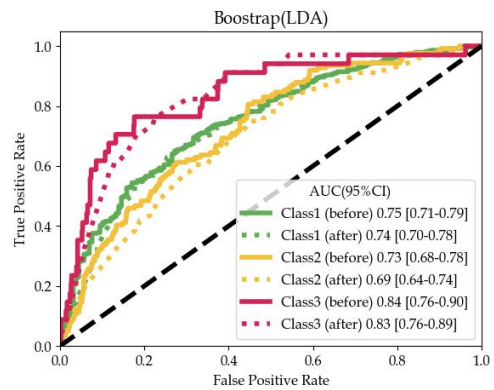
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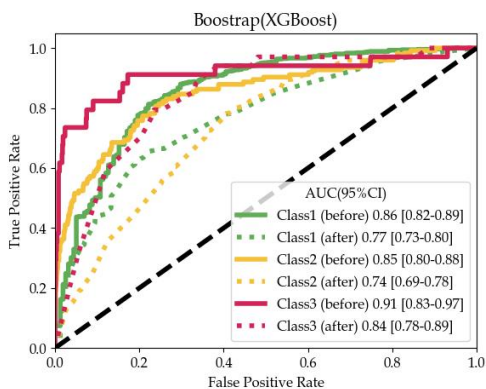
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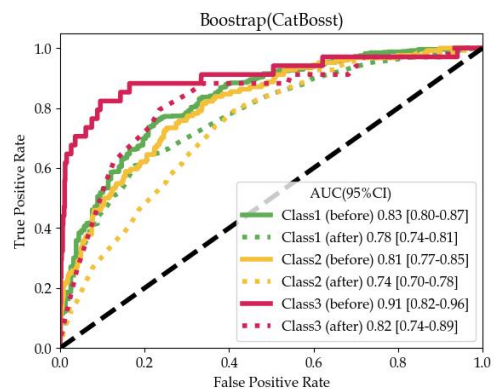
(E)



(F)

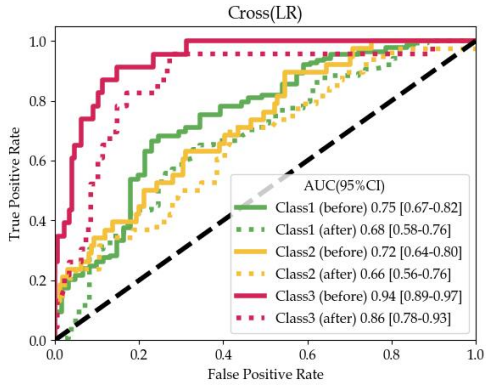


(G)

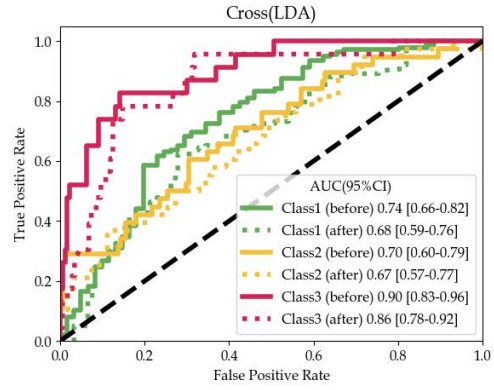


(H)

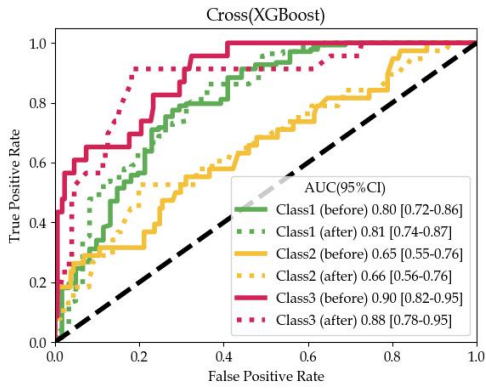
**Supplementary Figure 10 ROC curves of the four disease-free survival prediction models following cross-validation and bootstrap resampling for cl 1, cl 2, and cl 3 before and after filtering the variables.** A, B, C, D: ROC curves generated for the different disease-free survival models following 5-fold cross-validation in the training dataset before and after screening the variables; E, F, G, H: ROC curves generated for the different disease-free survival models following bootstrap validation with 300 iterations of resampling in the testing dataset before and after screening the variables



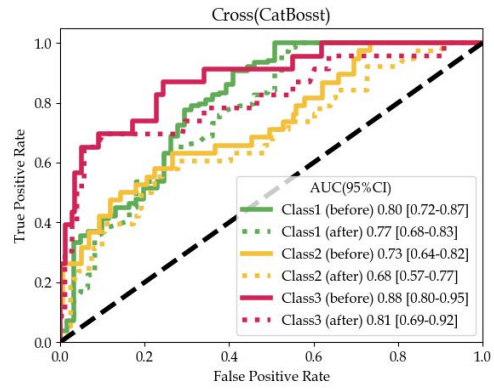
(A)



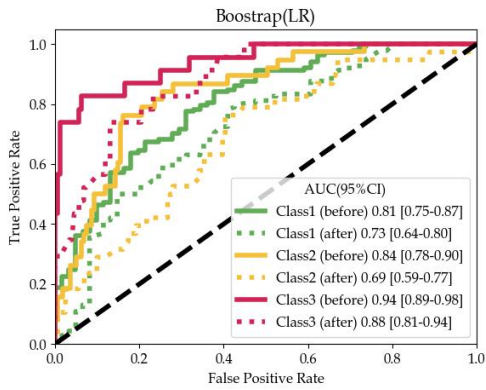
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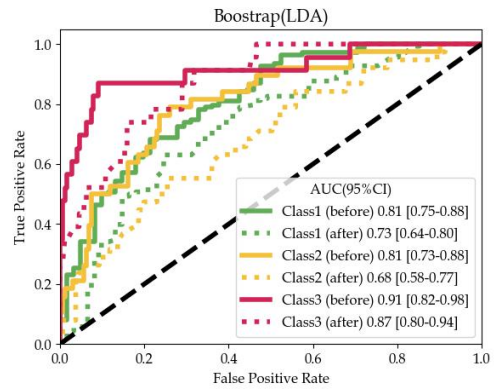
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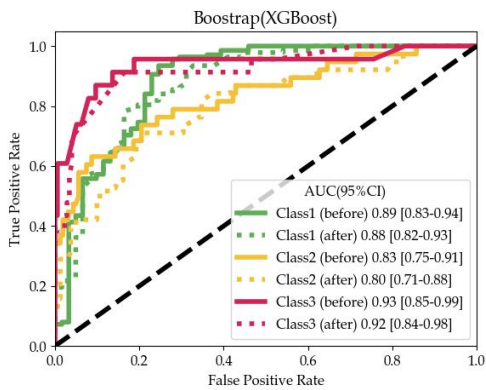
(D)



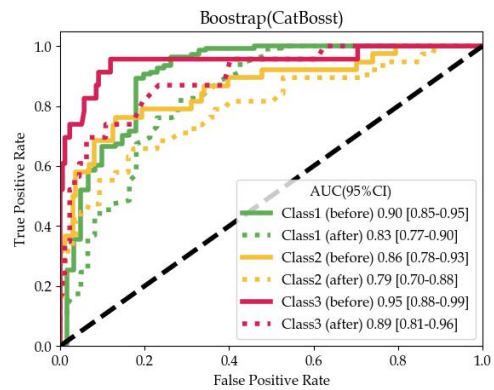
(E)



(F)

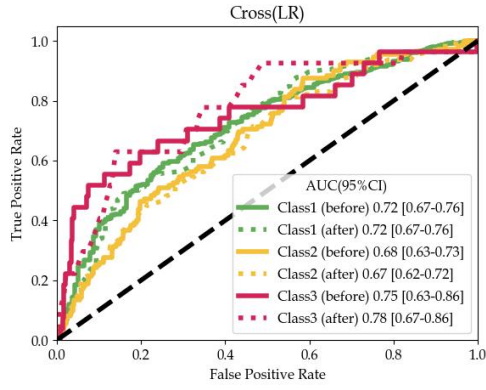


(G)

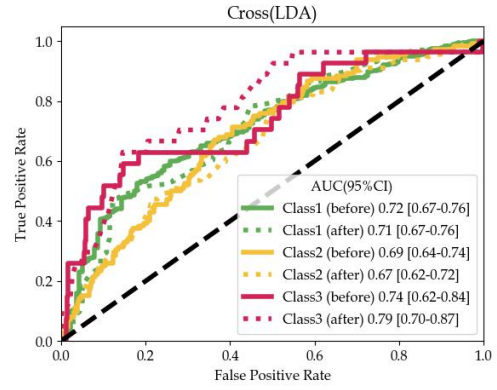


(H)

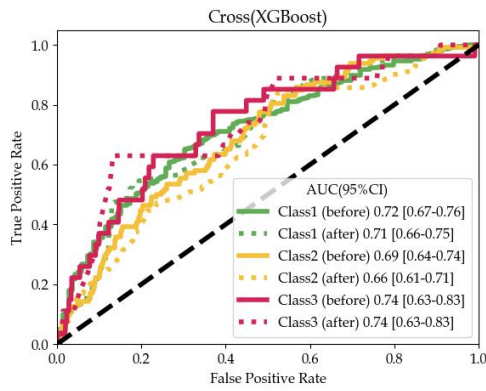
**Supplementary Figure 11 ROC curves of the four recurrence-free survival prediction models following cross-validation and bootstrap resampling for cl 1, cl 2, and cl 3 before and after filtering the variables.** A, B, C, D: ROC curves generated for the different recurrence-free survival models following 5-fold cross-validation in the training dataset before and after screening the variables; E, F, G, H: ROC curves generated for the different recurrence-free survival models following 300 iterations of bootstrap resampling in the testing dataset before and after screening the variables



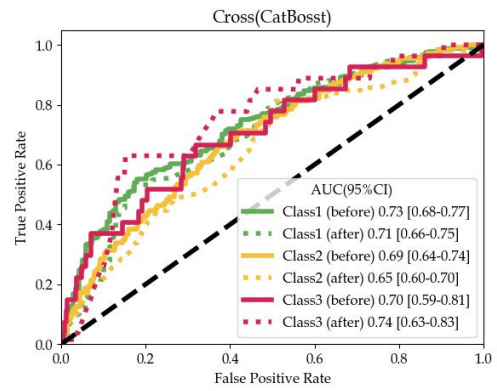
(A)



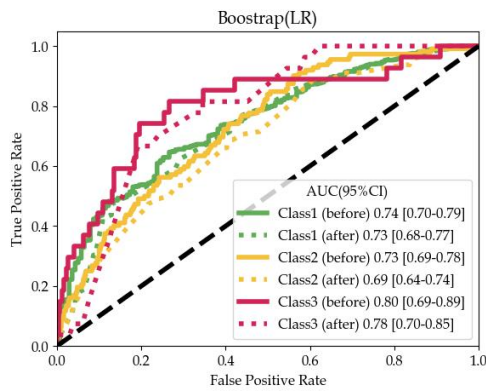
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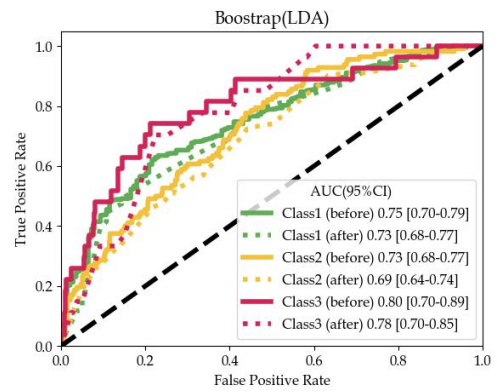
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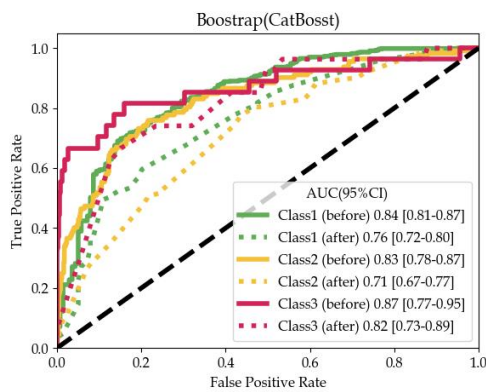
(D)



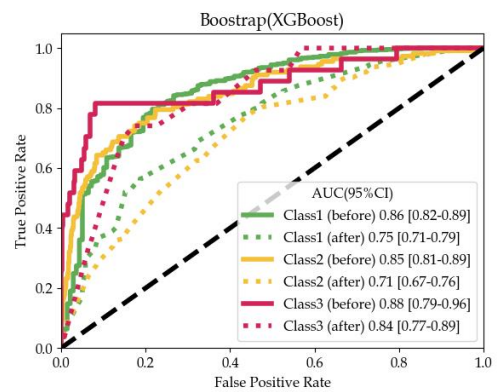
(E)



(F)



(G)



(H)

**Supplementary Figure 12 ROC curves of the four distant metastasis-free survival prediction models following cross-validation and bootstrap resampling for cl 1, cl 2, and cl 3 before and after filtering the variables. A, B, C, D: ROC curves generated for the different distant metastasis-free survival models following 5-fold cross-validation in the training dataset before and after screening the variables; E, F, G, H: ROC curves generated for the different distant metastasis-free models following 300 iterations of bootstrap resampling in the testing dataset before and after screening the variables.**





Presence	241	92	198	84	41	16	179	75
Absence	486	220	413	179	77	35	382	166
Drinking history								
Presence	205	90	176	81	37	17	164	71
Absence	522	222	435	182	81	34	397	170
Family history of tumors								
Presence	113	35	86	44	22	7	81	32
Absence	614	277	525	219	96	44	480	209
Family history of gastroenterology tumors								
Presence	80	23	59	29	16	5	53	20
Absence	647	289	552	234	102	46	508	221
Serum CEA level								
High	394	174	356	143	61	26	316	147
Normal	278	115	206	96	48	21	195	74
Missing	55	23	49	24	9	4	50	20
Serum CRP level								
High	32	13	31	7	4	1	23	12
Normal	637	29	83	38	15	6	81	31
Missing	58	270	497	218	99	44	457	198
Tumor position								
Ascending colon	105	36	70	32	13	5	59	34
Transverse colon	28	19	20	10	9	3	17	9
Descending colon	20	6	12	6	2	1	11	5

Sigmoid colon	134	45	117	50	24	11	98	55
Rectum	440	206	392	165	70	31	376	138
Tumor differentiation grade								
High	8	2	0	3	0	1	1	1
Moderate	421	184	414	182	81	37	379	163
Low	298	126	197	78	37	13	181	77
Histological type								
AC	501	208	471	200	82	36	423	199
AMC	63	31	44	20	12	7	39	17
MA	146	64	81	41	23	8	84	24
SRCC	10	8	8	1	1	0	7	1
The others	7	1	7	1	0	0	8	0
Tumor size								
>20mm	199	96	193	67	53	19	157	73
≤20mm	528	216	418	196	65	32	404	168
PNI								
Presence	355	154	325	129	60	21	293	126
Absence	372	158	286	134	58	30	268	115
LVI								
Presence	328	135	279	115	44	15	267	113
Absence	399	177	332	148	74	36	294	128
Lesion number								
Unifocal	695	299	585	243	111	47	539	225
Multifocal	32	13	26	20	7	4	22	16

Ki-67 protein level										
High	333	147	335	127	65	29	292	130		
Normal	15	1	2	3	0	0	3	2		
Missing	379	164	274	133	53	22	266	109		
Operation method										
Laparotomy	509	231	409	183	80	33	386	159		
Laparoscopy	218	81	202	80	38	18	175	82		
LNR										
≤0.25	615	266	512	218	99	44	465	205		
0.26-0.5	103	43	91	38	18	7	86	32		
0.51-0.75	7	3	7	7	1	0	9	4		
>0.75	2	0	1	0	0	0	1	0		
TNM stage										
I	52	18	34	14	9	5	28	10		
II	203	100	171	71	41	23	133	71		
III	472	194	406	178	68	23	400	160		

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OS overall survival, DFS disease-free survival, RFS recurrence-free survival, DMFS distant metastasis-free survival, BMI body mass index, HP hypertension, DM diabetes mellitus, CHD chronic heart disease, CEA carcinoembryonic antigen, CRP C-reactive protein, AC adenocarcinoma, AMC adenocarcinoma with mucus composition, MA mucinous adenocarcinoma, SRCC signet ring cell carcinoma, PNI perineural invasion, LVI lymphovascular invasion, LNR lymph node ratio, TNM stage tumor node metastasis stage