ELECTRONIC SUPPLEMENTARY MATERIAL

Enhanced CT-based radiomics predicts pathological complete response after neoadjuvant chemotherapy for advanced adenocarcinoma of the esophagogastric junction: A two-center study

Table S1. AUC values and 95% confidence intervals for selected arterial radiomics features in predicting the pCR of AEG in the trainingand external validation groups

	Training group		External va	lidation group
Variable	AUC values	95%CI	AUC values	95%CI
wavelet.HHL_glszm_SizeZoneNonUniformity	0.606	0.453~0.759	0.728	0.352~1.000
log.sigma.1.0.mm.3D_firstorder_RootMeanSquared	0.583	0.431~0.736	0.634	0.382~0.886
log.sigma.3.0.mm.3D_gldm_LargeDependenceEmphasis	0.629	0.486~0.772	0.580	0.374~0.787
log.sigma.5.0.mm.3D_firstorder_InterquartileRange	0.615	0.472~0.758	0.616	0.307~0.925
wavelet.LLH_glcm_ClusterProminence	0.579	0.415~0.743	0.598	0.384~0.813
wavelet.LHH_glszm_GrayLevelNonUniformity	0.603	0.448~0.758	0.482	0.166~0.799

Note: CI: confidential interval; pCR: pathological complete response; AEG: adenocarcinoma of the esophagogastric junction

Training group						
Variable	Sample	pCR	Non-pCR	Statistics	P value	
wavelet.HHL_glszm_SizeZoneNonUniformity	60	-0.43(-0.51, -0.11)	-0.48(-0.52, -0.37)	1.311	0.190	
log.sigma.1.0.mm.3D_firstorder_RootMeanSquared	60	-0.19(-0.64, 0.43)	-0.27(-0.71, -0.18)	1.033	0.302	
log.sigma.3.0.mm.3D_gldm_LargeDependenceEmphasis	60	-0.14±1.09	0.31±0.69	-1.915	0.061	
log.sigma.5.0.mm.3D_firstorder_InterquartileRange	60	-0.18(-0.67, 1.12)	-0.47(-0.68, -0.09)	1.422	0.155	
wavelet.LLH_glcm_ClusterProminence	60	-0.35(-0.37, -0.25)	-0.37(-0.37, -0.30)	0.977	0.328	
wavelet.LHH_glszm_GrayLevelNonUniformity	60	-0.25(-0.75, 0.05)	0.01(-0.54, 0.50)	-1.279	0.201	
Rad-score_AP_pCR	60	0.35(0.00, 0.66)	0.68(0.53, 0.76)	-2.916	0.004	
E>	kternal vali	dation group				
Variable	Sample	pCR	Non-pCR	Statistics	P value	
wavelet.HHL_glszm_SizeZoneNonUniformity	32	-0.37(-0.48, -0.16)	-0.51(-0.57, -0.17)	1.453	0.146	
log.sigma.1.0.mm.3D_firstorder_RootMeanSquared	32	-0.74(-1.20, 0.13)	-1.18(-1.23, -0.68)	0.855	0.393	

 Table S2. Statistical differences of the selected arterial radiomics features and Rad-score_AP_pCR between pCR and non-pCR groups in the training and external validation groups

log.sigma.3.0.mm.3D_gldm_LargeDependenceEmphasis	32	0.62(-0.75, 1.28)	0.82(0.43, 0.98)	-0.513	0.608
log.sigma.5.0.mm.3D_firstorder_InterquartileRange	32	-0.56(-0.90, 0.69)	-0.65(-1.05, -0.41)	0.741	0.459
wavelet.LLH_glcm_ClusterProminence	32	-0.37(-0.37, -0.34)	-0.37(-0.37, -0.35)	-0.627	0.531
wavelet.LHH_glszm_GrayLevelNonUniformity	32	-0.26(-0.65, 0.22)	-0.10(-0.67, 0.11)	0.114	0.909
Rad-score_AP_pCR	32	0.48(0.06, 0.70)	0.74(0.59, 0.77)	-1.595	0.111

Note: pCR: pathological complete response; The variables without normal distribution were depicted by median (interquartile range, IQR); The variables with normal distribution were depicted by mean \pm SD; Statistically significant level: P < 0.05

 Table S3. AUC values and 95% confidence intervals for selected venous radiomics features in predicting the pCR of AEG in the training and external validation groups

	Training group		External v	alidation group
Variable	AUC values	95%CI	Variable	AUC values
log.sigma.5.0.mm.3D_ngtdm_Complexity	0.674	0.521~0.827	0.643	0.400~0.886
wavelet.LHH_gldm_LargeDependenceEmphasis	0.634	0.480~0.788	0.545	0.267~0.823
log.sigma.3.0.mm.3D_firstorder_InterquartileRange	0.648	0.499~0.797	0.563	0.335~0.790
wavelet.HHL_gldm_LargeDependenceEmphasis	0.588	0.419~0.757	0.679	0.370~0.988

log.sigma.3.0.mm.3D_glszm_SizeZoneNonUniformity	0.638	0.492~0.784	0.638	0.437~0.840
log.sigma.5.0.mm.3D_firstorder_Mean	0.562	0.418~0.706	0.696	0.471~0.922
log.sigma.1.0.mm.3D_glcm_ClusterProminence	0.640	0.484~0.796	0.741	0.436~1.000

Note: CI: confidential interval; pCR: pathological complete response; AEG: adenocarcinoma of the esophagogastric junction

Table S4. Statistical differences of the selected venous radiomics features and Rad-score_VP_pCR between pCR and non-pCR groups in the training and external validation groups

Training group					
Variable	Sample	pCR	Non-pCR	Statistics	<i>P</i> value
log.sigma.5.0.mm.3D_ngtdm_Complexity	60	-0.32(-0.70, 0.76)	-0.67(-0.83, -0.36)	2.153	0.031
wavelet.LHH_gldm_LargeDependenceEmphasis	60	0.38(-0.48, 0.75)	-0.12(-1.04, 0.53)	1.661	0.097
log.sigma.3.0.mm.3D_firstorder_InterquartileRange	60	-0.01(-0.48, 0.79)	-0.47(-1.02, 0.24)	1.835	0.066
wavelet.HHL_gldm_LargeDependenceEmphasis	60	0.19(-0.21, 0.52)	0.55(-0.09, 0.64)	-1.089	0.276
log.sigma.3.0.mm.3D_glszm_SizeZoneNonUniformity	60	-0.45(-0.68, 0.76)	-0.53(-0.75, -0.35)	1.708	0.088
log.sigma.5.0.mm.3D_firstorder_Mean	60	0.21(-0.64, 0.81)	0.47(-0.14, 0.65)	-0.771	0.441

log.sigma.1.0.mm.3D_glcm_ClusterProminence	60	-0.46(-0.54, 0.07)	-0.54(-0.55, -0.32)	1.732	0.083
Rad-score_VP_pCR	60	0.60(0.00, 0.82)	0.87(0.62, 0.93)	-3.107	0.002
Ext	ernal validat	ion group			
Variable	Sample	pCR	Non-pCR	Statistics	<i>P</i> value
log.sigma.5.0.mm.3D_ngtdm_Complexity	32	-0.59(-0.82, 0.40)	-0.80(-0.84, -0.45)	0.912	0.362
wavelet.LHH_gldm_LargeDependenceEmphasis	32	-0.44±0.73	-0.63±0.59	0.489	0.628
log.sigma.3.0.mm.3D_firstorder_InterquartileRange	32	-0.66(-1.15, 0.04)	-0.96(-1.04, -0.54)	0.399	0.690
wavelet.HHL_gldm_LargeDependenceEmphasis	32	-0.19(-0.53, 0.04)	-0.41(-0.92, -0.13)	1.140	0.254
log.sigma.3.0.mm.3D_glszm_SizeZoneNonUniformity	32	-0.64(-0.75, -0.12)	-0.41(-0.62, -0.19)	-0.883	0.377
log.sigma.5.0.mm.3D_firstorder_Mean	32	-0.02±1.11	0.71±0.56	-2.076	0.077
log.sigma.1.0.mm.3D_glcm_ClusterProminence	32	-0.55(-0.56, -0.41)	-0.57(-0.57, -0.53)	1.538	0.124
Rad-score_VP_pCR	32	0.70(0.16, 0.88)	0.92(0.65, 0.94)	-1.709	0.087

Note: pCR: pathological complete response; The variables without normal distribution were depicted by median (interquartile range, IQR); The variables with normal distribution were depicted by mean \pm SD; Statistically significant level: P < 0.05

Table S5. The results of univariate logistic regression analysis of clinical characteristics in predicting pCR of AEG patients

VariableBWaldOdds ratio95% CIP va	ue
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Gender	-18.109	0	0	NA~9.303×10 ⁵⁴	0.993
Age	-0.583	0.910	0.558	0.156~1.778	0.340
T-staging before NAC	-0.884	2.391	0.413	0.129~1.242	0.122
N-staging before NAC	-0.327	0.309	0.721	0.216~2.232	0.578
Borrmann typing	-1.667	6.658	0.189	0.047~0.624	0.010
CEA	-1.124	2.522	0.325	0.068~1.179	0.112
CA199	0.903	1.373	2.467	0.523~11.718	0.241
CA125	-1.088	1.076	0.337	0.018~1.757	0.300
Serum albumin	0.564	1.008	1.757	0.589~5.427	0.315
Tumor thickness	1.275	4.386	3.578	1.137~12.812	0.036
Degree of tumor differentiation	0.975	2.932	2.652	0.879~8.361	0.087

Note: B logistic regression coefficient; CI confidence interval; Statistically significant level: P < 0.05

 Table S6. The results of Delong test for AUC values of all models

	Training group		External validation gro	
Models	Ζ	<i>P</i> value	Ζ	<i>P</i> value
Arterial model.vs. Venous model	-0.180	0.857	-0.088	0.930
Arterial model.vs. Clinical model	-0.175	0.861	-0.668	0.504
Arterial model.vs. Arterial-Venous combined model	-0.694	0.488	-0.418	0.676
Arterial model.vs. Arterial-Clinical combined model	-1.481	0.139	-1.294	0.196
Arterial model.vs. Venous-Clinical combined model	-0.959	0.338	-1.037	0.300
Arterial model.vs. Arterial-Venous-Clinical combined model	-1.657	0.097	-1.300	0.193
Venous model.vs. Clinical model	-0.019	0.985	-0.517	0.605
Venous model.vs. Arterial-Venous combined model	-0.303	0.762	-0.202	0.840
Venous model.vs. Arterial-Clinical combined model	-0.964	0.335	-0.797	0.426
venous model.vs.Venous-Clinical combined model	-0.955	0.340	-0.981	0.327
venous model.vs. Arterial-Venous-Clinical combined model	-1.305	0.192	-0.925	0.355
Clinical model.vs. Arterial-Venous combined model	-0.150	0.881	0.347	0.729
Clinical model.vs. Arterial-Clinical combined model	-1.957	0.050	-0.963	0.336

Clinical model.vs. Venous-Clinical combined model	-1.593	0.111	-0.561	0.575
Clinical model.vs. Arterial-Venous-Clinical combined model	-1.436	0.151	-1.093	0.275
Arterial-Venous combined model.vs. Arterial-Clinical combined model	-0.965	0.335	-0.771	0.441
Arterial-Venous combined model.vs. Venous-Clinical combined model	-0.680	0.496	-0.819	0.413
Arterial-Venous combined model.vs. Arterial-Venous-Clinical combined model	-1.348	0.178	-0.897	0.370
Arterial-Clinical combined model.vs. Venous-Clinical combined model	0.450	0.652	0.169	0.866
Arterial-Clinical combined model.vs. Arterial-Venous-Clinical combined model	-0.084	0.933	-0.337	0.736
Venous-Clinical combined model.vs. Arterial-Venous-Clinical combined model	-0.593	0.553	-0.500	0.617

Table S7. The results of the Hosmer-Lemeshow test for different models in the training and external validation groups

	Training	group	External va	lidation group
Model	Statistics	P value	Models	Statistics
Arterial model	4.997	0.758	7.949	0.438

Venous model	8.427	0.393	8.467	0.389
Clinical model	0.732	0.392	1.189	0.276
Arterial-Venous combined model	12.152	0.145	5.326	0.722
Arterial-Clinical combined model	6.900	0.547	1.831	0.986
Venous-Clinical combined model	11.885	0.156	2.038	0.980
Arterial-Venous-Clinical combined model	14.879	0.062	10.478	0.233

Note: *P*>0.05: no significant difference between the predicted and actual value.

	Model	AUC	95%CI	Threshold	Specificity	Sensitivity	Accuracy	NPV	PPV
	Naïve Bayes	0.736	0.607~0.865	0.510	0.610	0.789	0.667	0.862	0.484
Training group	Logistic regression	0.720	0.592~0.848	0.341	0.634	0.789	0.683	0.867	0.500
	Support vector machines	0.707	0.564~0.850	1.000	0.732	0.632	0.700	0.811	0.522
	Decision tree	0.856	0.768~0.945	0.588	0.756	0.895	0.800	0.939	0.630
	AdaBoost	1.000	1.000~1.000	0.493	1.000	1.000	1.000	1.000	1.000

Table S8. Performance of arterial models based on other classifiers in the training and external validation groups

	Naïve Bayes	0.750	0.535~0.965	0.510	0.536	0.750	0.563	0.938	0.188
External validation	Logistic regression	0.679	0.417~0.940	0.341	0.536	0.750	0.563	0.938	0.188
group	Support vector machines	0.554	0.315~0.792	1.000	0.643	0.250	0.594	0.857	0.091
	Decision tree	0.652	0.426~0.870	0.588	0.500	0.750	0.531	0.933	0.176
	AdaBoost	0.607	0.372~0.842	0.493	0.821	0.250	0.750	0.885	0.167

Table S9. Performance of venous models based on other classifiers in the training and external validation groups

	Model	AUC	95%CI	Threshold	Specificity	Sensitivity	Accuracy	NPV	PPV
	Naïve Bayes	0.751	0.614~0.888	0.856	0.829	0.632	0.767	0.829	0.632
Training group	Logistic regression	0.728	0.581~0.875	0.396	0.854	0.579	0.767	0.814	0.647
	Support vector machines	1.000	1.000~1.000	0.042	1.000	1.000	1.000	1.000	1.000
	Decision tree	0.367	0.254~0.479	/	0	1.000	0.317	/	0.317
	AdaBoost	1.000	1.000~1.000	0.493	1.000	1.000	1.000	1.000	1.000

	Naïve Bayes	0.768	0.489~1.000	0.856	0.750	0.750	0.750	0.955	0.300
External validation	Logistic regression	0.491	0.212~0.770	0.396	0.429	0.500	0.438	0.857	0.111
group	Support vector machines	0.527	0.179~0.874	0.042	0	1.000	0.125	/	0.125
	Decision tree	0.589	0.293~0.886	/	1.000	0	0.875	0.875	/
	AdaBoost	0.759	0.414~1.000	0.493	0.821	0.750	0.813	0.958	0.375

 Table S10.
 Performance of clinical models based on other classifiers in the training and external validation groups

	Model	AUC	95%CI	Threshold	Specificity	Sensitivity	Accuracy	NPV	PPV
	Naïve Bayes	0.753	0.622~0.884	0.351	0.683	0.789	0.717	0.875	0.536
Training group	Logistic regression	0.753	0.622~0.884	0.364	0.683	0.789	0.717	0.875	0.536
	Support vector machines	0.750	0.619~0.881	0.999	0.756	0.684	0.733	0.838	0.565
	Decision tree	0.733	0.603~0.863	0.606	0.756	0.684	0.733	0.838	0.565
	AdaBoost	0.791	0.680~0.903	0.340	0.610	0.895	0.700	0.926	0.515

	Naïve Bayes	0.848	0.710~0.987	0.351	0.857	0.750	0.844	0.960 0.429
External validation	Logistic regression	0.848	0.710~0.987	0.364	0.857	0.750	0.844	0.960 0.429
group	Support vector machines	0.304	0.187~0.420	0.999	0.071	1.000	0.188	1.000 0.133
	Decision tree	0.723	0.473~0.973	0.606	0.929	0	0.813	0.867 0
	AdaBoost	0.670	0.490~0.849	0.340	0.679	0.750	0.688	0.950 0.250

Figure:



Fig.S1 ROC curves of individual features in different models to predict pathological complete response (pCR). 1A: ROC curves of individual features of arterial model predicting pCR in the training group; 1B: ROC curves of individual features of arterial model predicting pCR in the external validation group; 1C: ROC curves of individual features of venous model predicting pCR in the training group; 1D: ROC curves of individual features of venous model predicting pCR in the external validation group; 1C: ROC curves of individual features of venous model predicting pCR in the external validation group; 1D: ROC curves of individual features of venous model predicting pCR in the external validation group.