Supplementary

Table S1 Patient characteristics of LUAD

Variables	Total (n=320)	Low (n=142)	High (n=178)	P
Age				0.30
<66 years	153 [48]	73 [51]	80 [45]	
≥66 years	167 [52]	69 [49]	98 [55]	
Gender				0.02
Female	172 [54]	65 [46]	107 [60]	
Male	148 [46]	77 [54]	71 [40]	
Residual tumor				0.70
R0	306 [96]	137 [96]	169 [95]	
R1/R2	14 [4]	5 [4]	9 [5]	
Smoking status				0.007
Nonsmoker	45 [14]	11 [8]	34 [19]	
Current	83 [26]	44 [31]	39 [22]	
Former	192 [60]	87 [61]	105 [59]	
T stage				0.22
T1	108 [34]	41 [29]	67 [38]	
T2	173 [54]	84 [59]	89 [50]	
T3/T4	39 [12]	17 [12]	22 [12]	
N stage				0.09
N0	211 [66]	86 [61]	125 [70]	
N1/N2/N3	109 [34]	56 [39]	53 [30]	
M stage				0.41
M0	228 [71]	105 [74]	123 [69]	
M1/MX	92 [29]	37 [26]	55 [31]	
Radiotherapy				0.047
No	288 [90]	122 [86]	166 [93]	
Yes	32 [10]	20 [14]	12 [7]	
Chemotherapy				0.99
No	213 [67]	94 [66]	119 [67]	
Yes	107 [33]	48 [34]	59 [33]	

Data are presented as n [%]. LUAD, lung adenocarcinoma.

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Table S2 Regression coefficient of feature in LR model

Features	Estimate	Std. error	z value	Pr(>|z|)
(Intercept)	−0.160642518	0.334625359	−0.480066777	0.631179911
Original_shape_Flatness	−1.076946783	0.410015712	−2.626598815	0.008624295
Original_glszm_SizeZoneNonUniformity	−1.915813063	0.74581873	−2.568738201	0.010206954
Original_firstorder_Minimum	−0.894156152	0.781893626	−1.143577748	0.252798794
Original_gldm_LargeDependenceHighGrayLevelEmphasis	1.328802785	0.660241068	2.012602443	0.04415647
Original_glcm_ClusterProminence	0.266224178	0.587584581	0.453082308	0.650489474
Original_glszm_LowGrayLevelZoneEmphasis	−0.218082501	0.503235684	−0.433360566	0.664752844
Original_ngtdm_Strength	0.150126087	0.371671128	0.403921844	0.686270193
Original_glrlm_RunVariance	0.43439711	0.831935245	0.522152551	0.60156412

LR, logistic regression; Std. error, standard error.

Table S3 Characteristics of clinical intersection samples of TCIA-GEO

Variables	Total (n=63)	Low (n=27)	High (n=36)	P
Age				0.21
<66 years	18 [29]	5 [19]	13 [36]	
≥66 years	45 [71]	22 [81]	23 [64]	
Gender				0.84
Female	16 [25]	6 [22]	10 [28]	
Male	47 [75]	21 [78]	26 [72]	
Histology				0.76
Adenocarcinoma	49 [78]	20 [74]	29 [81]	
Squamous cell carcinoma	14 [22]	7 [26]	7 [19]	
Smoking status				0.23
Nonsmoker	9 [14]	6 [22]	3 [8]	
Current	18 [29]	8 [30]	10 [28]	
Former	36 [57]	13 [48]	23 [64]	
T stage				1.00
Tis/T1	31 [49]	13 [48]	18 [50]	
T2/T3/T4	32 [51]	14 [52]	18 [50]	
N stage				0.03
N0	51 [81]	18 [67]	33 [92]	
N1/N2	12 [19]	9 [33]	3 [8]	
M stage				1.00
M0	60 [95]	26 [96]	34 [94]	
M1	3 [5]	1 [4]	2 [6]	
KRAS mutation status				0.40
Mutant	12 [19]	3 [11]	9 [25]	
Unknown	10 [16]	5 [19]	5 [14]	
Wildtype	41 [65]	19 [70]	22 [61]	
EGFR mutation status				0.66
Mutant	13 [21]	4 [15]	9 [25]	
Unknown	10 [16]	5 [19]	5 [14]	
Wildtype	40 [63]	18 [67]	22 [61]	
Radiotherapy				0.08
No	57 [90]	22 [81]	35 [97]	
Yes	6 [10]	5 [19]	1 [3]	
Chemotherapy				0.20
No	46 [73]	17 [63]	29 [81]	
Yes	17 [27]	10 [37]	7 [19]	
OS				0.09
0	39 [62]	13 [48]	26 [72]	
1	24 [38]	14 [52]	10 [28]	
OS time, mean ± SD	39.63 ±22.03	33.79±22.73	44±20.73	0.07

Data are presented as n [%] or mean ± standard deviation. OS, overall survival; TCIA-GEO, The Cancer Imaging Archive-Gene Expression Omnibus.

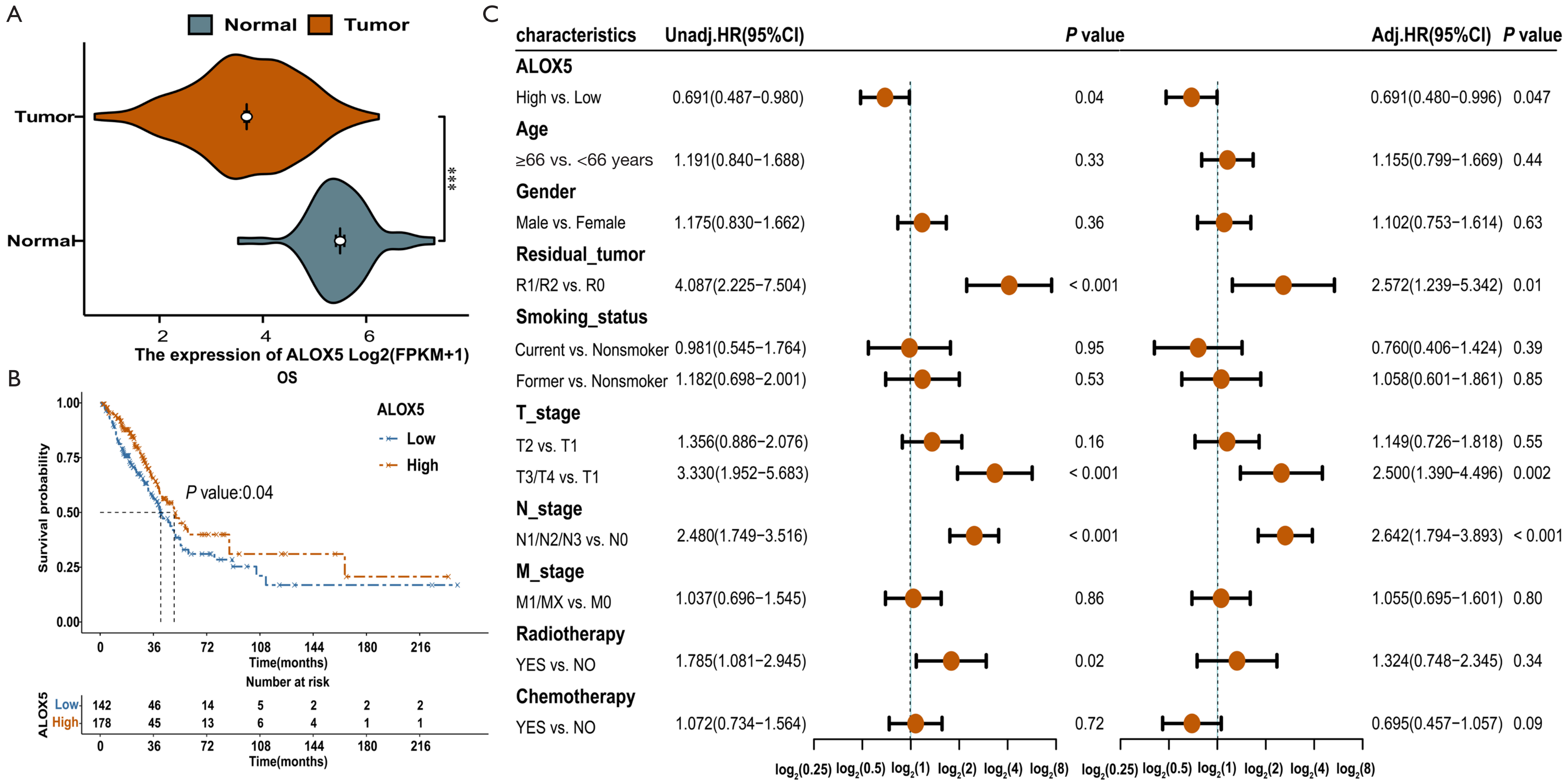

Figure S1 Clinical Characteristics and the Level of Gene Expression in LUAD. (A) ALOX5 expression in normal and tumor tissues. (B) Kaplan-Meier curve for ALOX5 expression and Overall Survival (OS) in LUAD. (C) Univariate Cox and Multivariate Cox regression analyses in LUAD. ***, P<0.001. ALOX5, arachidonic acid 5-lipoxygenase; CI, confidence interval; FPKM, fragments per kilobase of transcript per million mapped reads; HR, hazard ratio; LUAD, lung adenocarcinoma; OS, overall survival.

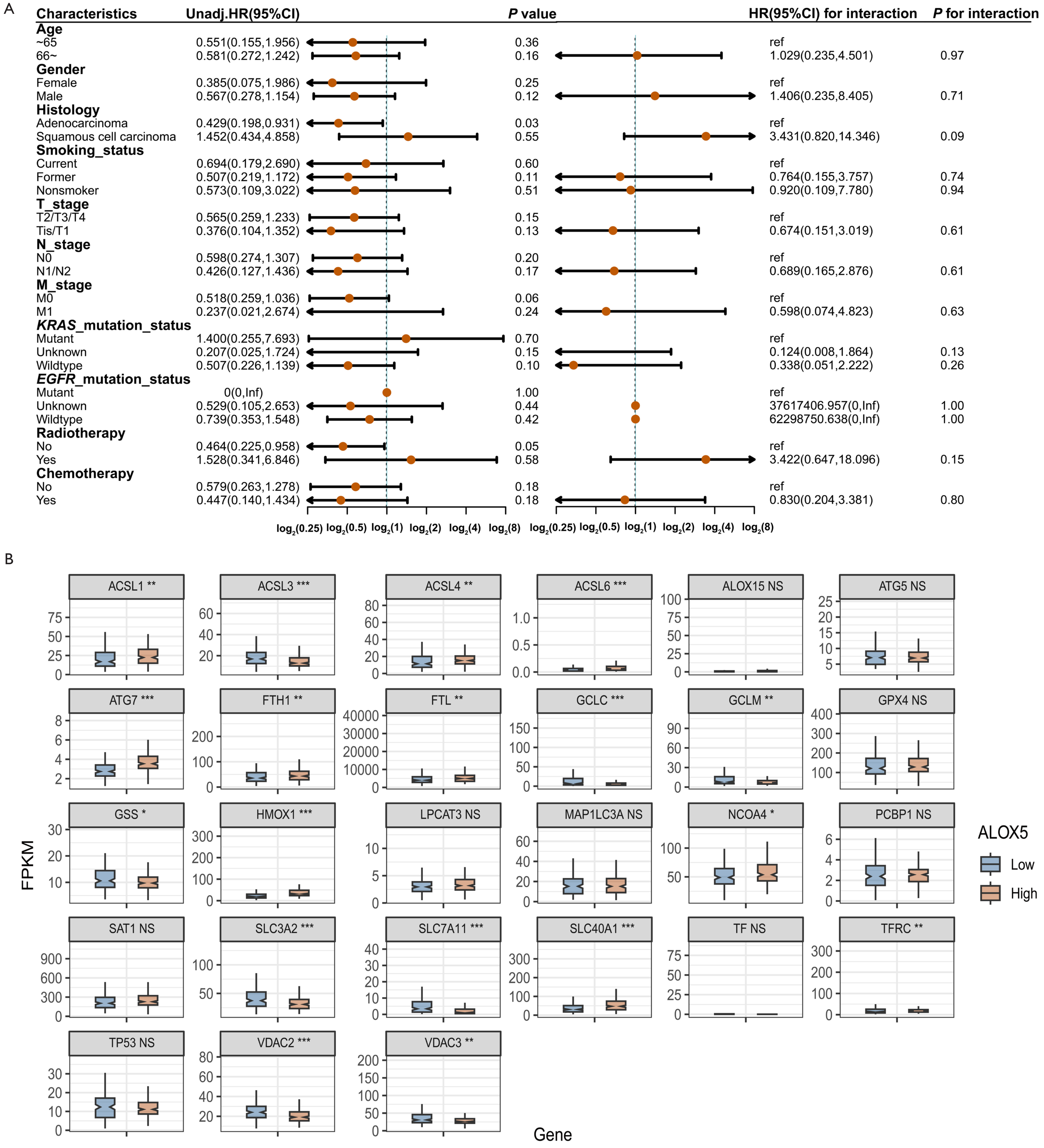

Figure S2 Subgroup analysis and differential gene analysis of iron death-related gene set. (A) Subgroup analysis in NSCLC. (B) Differential analysis of the iron death-related gene set between high and low ALOX5 groups in LUAD. *, P<0.05; **, P<0.01; ***, P<0.001. NS, no significance; ALOX5, arachidonic acid 5-lipoxygenase; CI, confidence interval; FPKM, fragments per kilobase of transcript per million mapped reads; HR, hazard ratio; NSCLC, non-small cell lung cancer.

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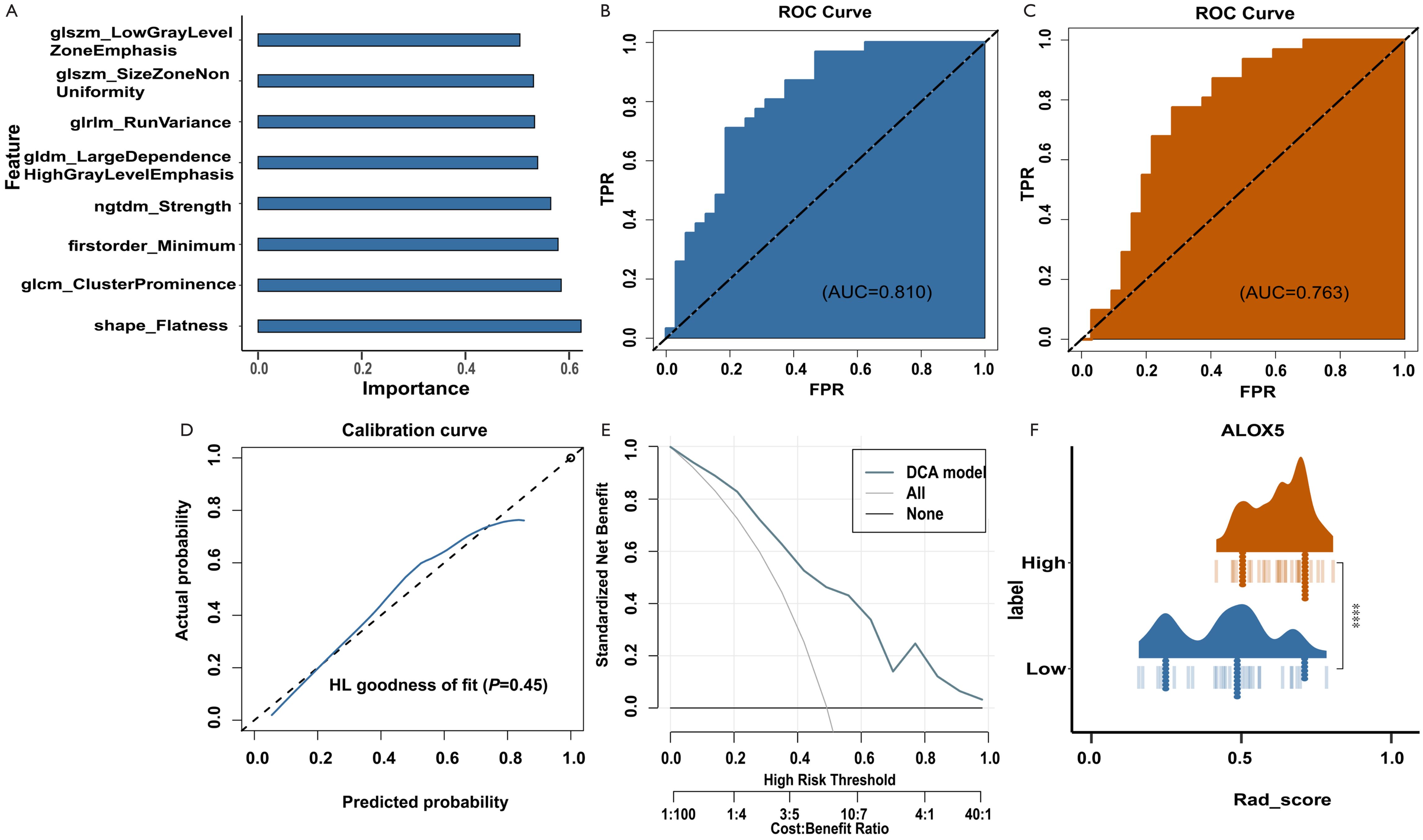

Figure S3 SVM model development and assessment. (A) The importance of the selected features in the SVM model. (B) ROC curve analysis of the SVM model. (C) Cross-validation ROC curve of the SVM model. (D) SVM model calibration curve evaluation. (E) DCA of the SVM model. (F) Analysis of differences between model groups. ****, P<0.0001. ALOX5, arachidonic acid 5-lipoxygenase; AUC, area under the curve; DCA, decision curve analysis; FPR, false positive rate; HL, Hosmer-Lemeshow; ROC, receiver operating characteristic; SVM, Support Vector Machine; TPR, true positive rate.

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