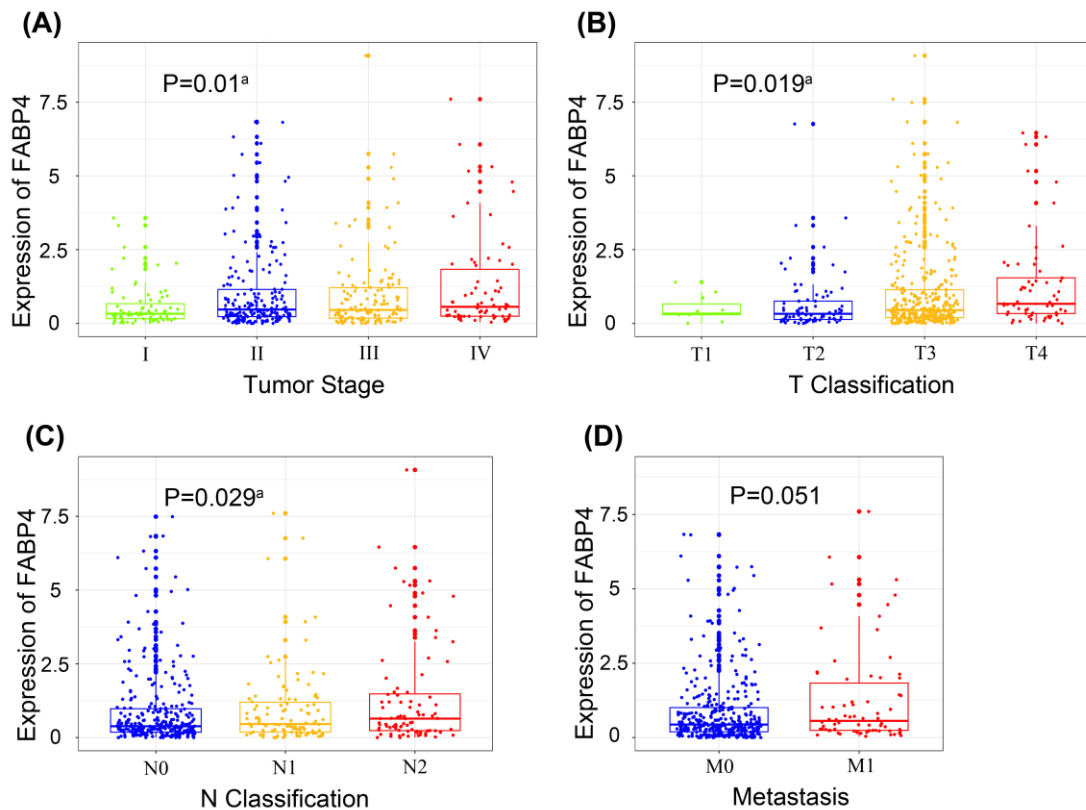
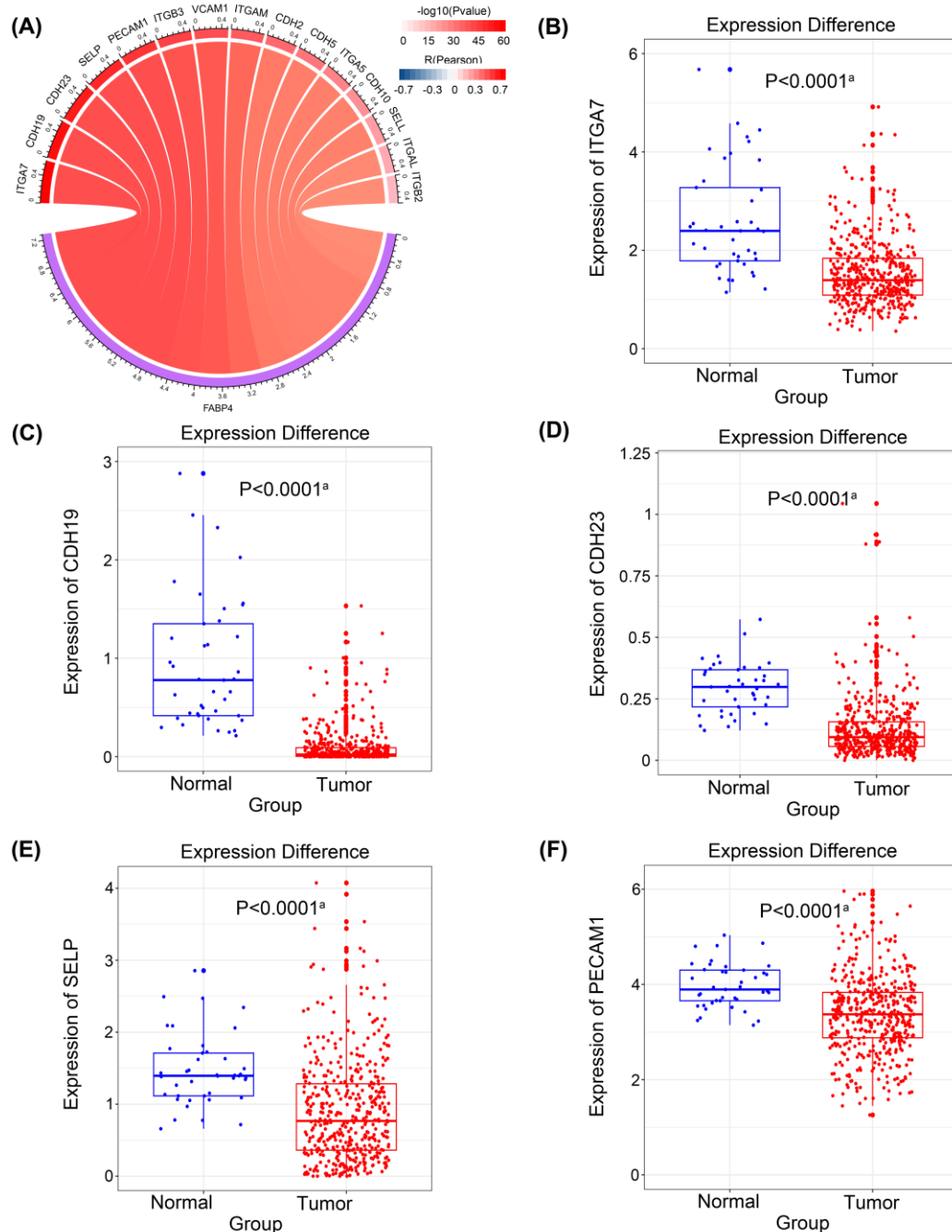


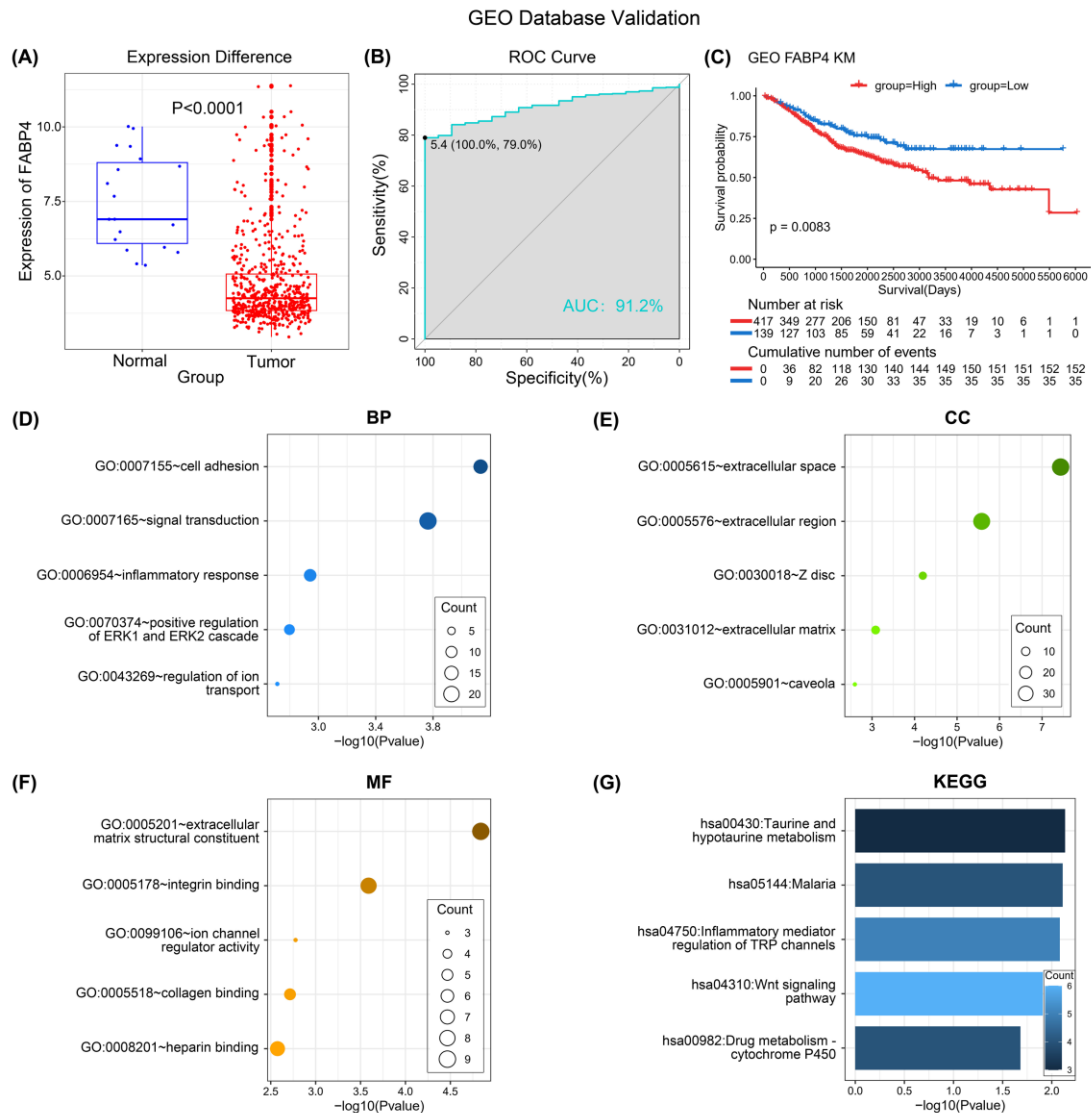
Expression Difference



Supplementary Figure 1 Relationships between *FABP4* expression and the clinicopathological features of patients with COAD. A: *FABP4* expression in high-grade COAD was significantly increased. B: *FABP4* expression was significantly increased in COAD with an advanced T stage. C: *FABP4* expression was significantly increased in COAD with an advanced N stage. D: *FABP4* expression was elevated in metastatic COAD, but this difference was not statistically significant according to TCGA database. ^a $P < 0.05$. COAD, colon adenocarcinoma; TCGA, The Cancer Genome Atlas.

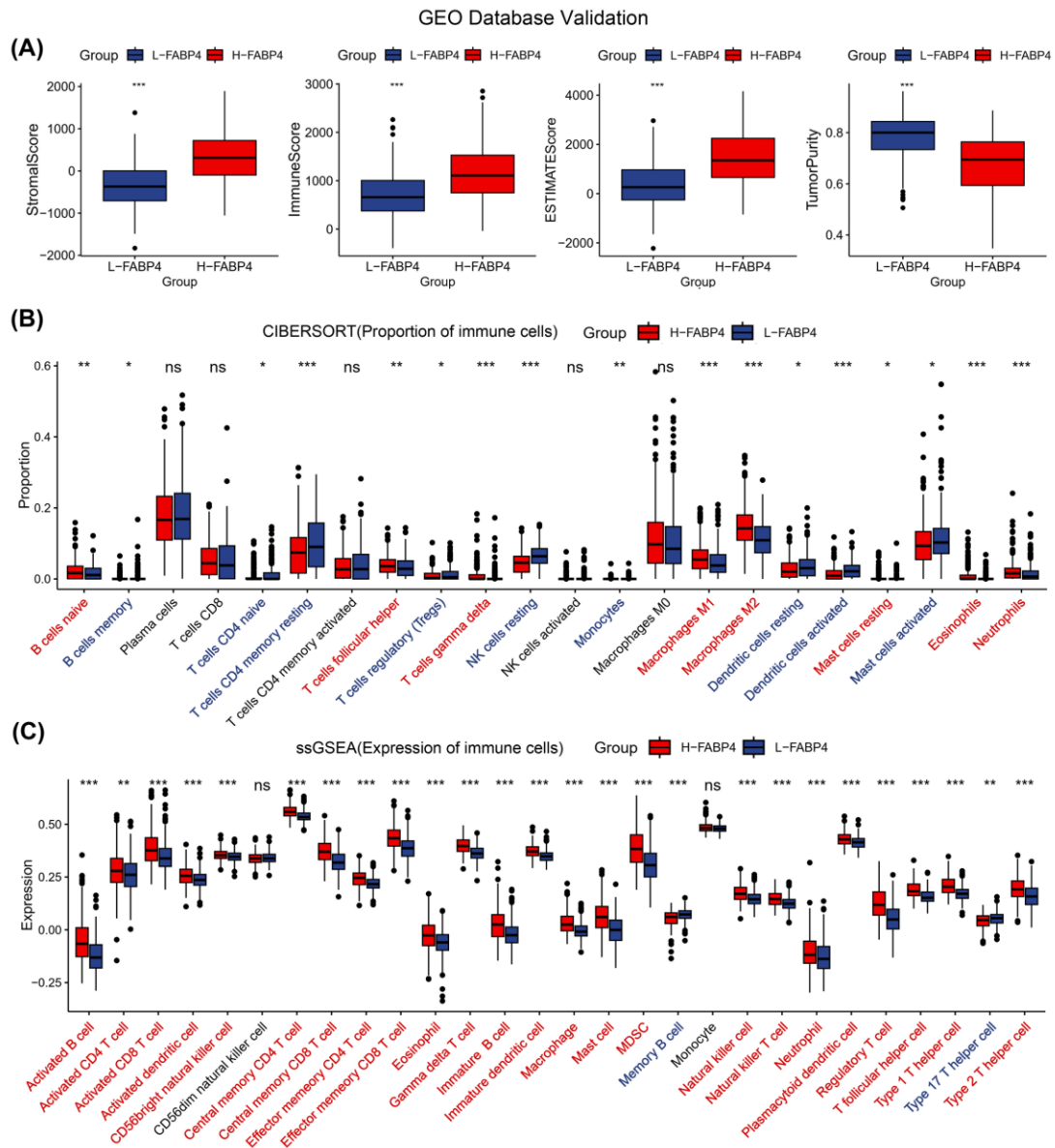


Supplementary Figure 2 Pearson's correlation coefficients between *FABP4* and CAMs and the differences in the expression of the top 5 CAMs associated with *FABP4*. A: Pearson's correlation coefficients between *FABP4* and CAMs; the width of the band represents the R value. B-F: Differences in the expression of *ITGA7*, *CDH19*, *CDH23*, *SELP*, and *PECAM1* between COAD tissues and adjacent noncancerous colon tissues. $^aP < 0.001$. CAMs, cell adhesion molecules; COAD, colon adenocarcinoma.



Supplementary Figure 3 The GEO dataset GSE39582 validated the clinical value of *FABP4* expression in COAD, and Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) functional enrichment analyses were performed. A: Differences in the expression level of the *FABP4* mRNA between tumors and normal tissues. B: A ROC curve was constructed to verify the diagnostic performance of differences in *FABP4* expression. C: Kaplan–Meier survival curves of the high *FABP4* expression group and low *FABP4* expression group in the GEO database. The cutoff for each group was the quartile of *FABP4* expression. D-F: Analysis of the biological process (BP), cellular component (CC) and molecular function (MF) terms of genes strongly associated with *FABP4*. G: KEGG analysis of genes strongly associated with

FABP4. GEO, Gene Expression Omnibus; COAD, colon adenocarcinoma; ROC, receiver operating characteristic; AUC, area under the curve.



Supplementary Figure 4 The GEO dataset GSE39582 verified the difference in immune cell infiltration between the high and low *FABP4* expression groups. A: Comparisons of the stromal score, immune score, ESTIMATE score, and tumor purity between the two groups. B: Comparison of the proportions of immune cells between the two groups. C: Differences in immune cell marker expression between the two groups. P values are marked with asterisks (ns: Not statistically significant; *: $P < 0.05$; **: $P < 0.01$; and ***: $P < 0.001$). GEO, Gene Expression Omnibus.

Supplementary Table 1 Immunohistochemical staining score

No.	tumor			normal		
	intensity of immunostaining	the percentage of positive tumor cells	weighted score	intensity of immunostaining	the percentage of positive tumor cells	weighted score
1	1	1	1 (-)	3	4	12 (+++)
2	1	1	1 (-)	3	4	12 (+++)
3	1	2	2 (-)	3	4	12 (+++)
4	1	2	2 (-)	3	4	12 (+++)
5	1	1	1 (-)	3	4	12 (+++)
6	1	1	1 (-)	3	4	12 (+++)
7	1	1	1 (-)	3	4	12 (+++)
8	1	2	2 (-)	3	4	12 (+++)
9	1	1	1 (-)	3	4	12 (+++)
10	1	1	1 (-)	3	3	9 (++)

The percentage of positive tumor cells and staining intensity were multiplied to produce a weighted score: <3 score (-), 3~5 score (+), 6~9 score (++) , >9 score (+++), which was double-blind detected by two senior diagnostic

physicians.

Supplementary Table 2 Comparison of clinical parameters between the H-FABP4 and L-FABP4 groups

Clinical Parameters	H-FABP4 (N=246)	L-FABP4 (N=246)	P value
Age (years)			0.53
>69	122 (49.6%)	114 (46.3%)	
≤69	124 (50.4%)	132 (53.7%)	
Gender			>0.99
Female	116 (47.2%)	117 (47.6%)	
Male	130 (52.8%)	129 (52.4%)	
Stage			0.01 ^a
I	26 (10.6%)	53 (21.5%)	
II	106 (43.1%)	92 (37.4%)	
III	71 (28.9%)	62 (25.2%)	
IV	39 (15.9%)	31 (12.6%)	
NA	4 (1.6%)	8 (3.3%)	
T Classification			0.02 ^a
T1	4 (1.6%)	7 (2.8%)	
T2	30 (12.2%)	52 (21.1%)	
T3	171 (69.5%)	166 (67.5%)	
T4	41 (16.7%)	20 (8.1%)	
NA	0 (0%)	1 (0.4%)	
N classification			0.03 ^a
N0	136 (55.3%)	158 (64.2%)	
N1	59 (24.0%)	51 (20.7%)	
N2	51 (20.7%)	37 (15.0%)	
Metastasis			0.05
M0	177 (72.0%)	181 (73.6%)	
M1	39 (15.9%)	31 (12.6%)	

NA	30 (12.2%)	34 (13.8%)
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^a $P < 0.05$.

NA, not available (represent missing value)