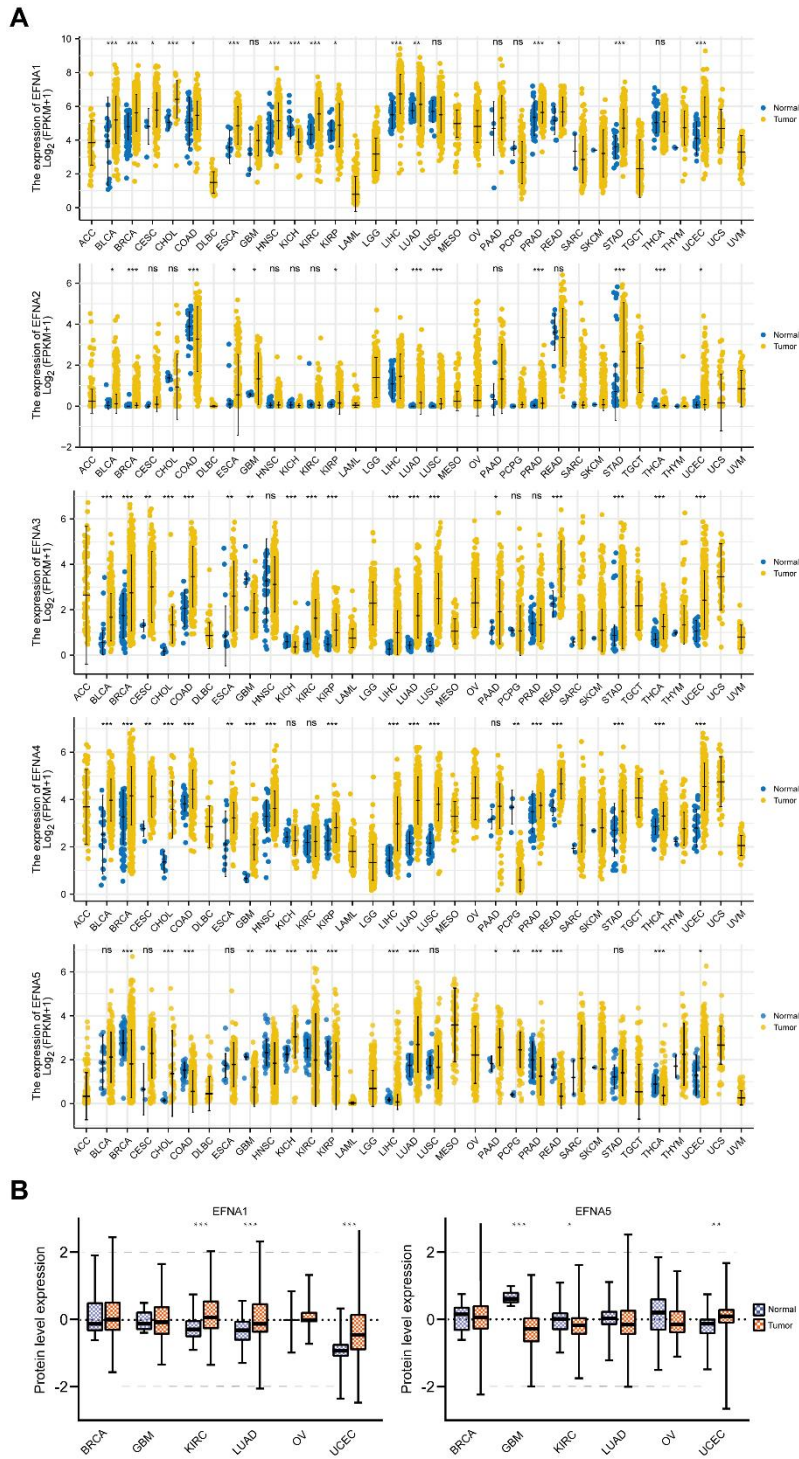
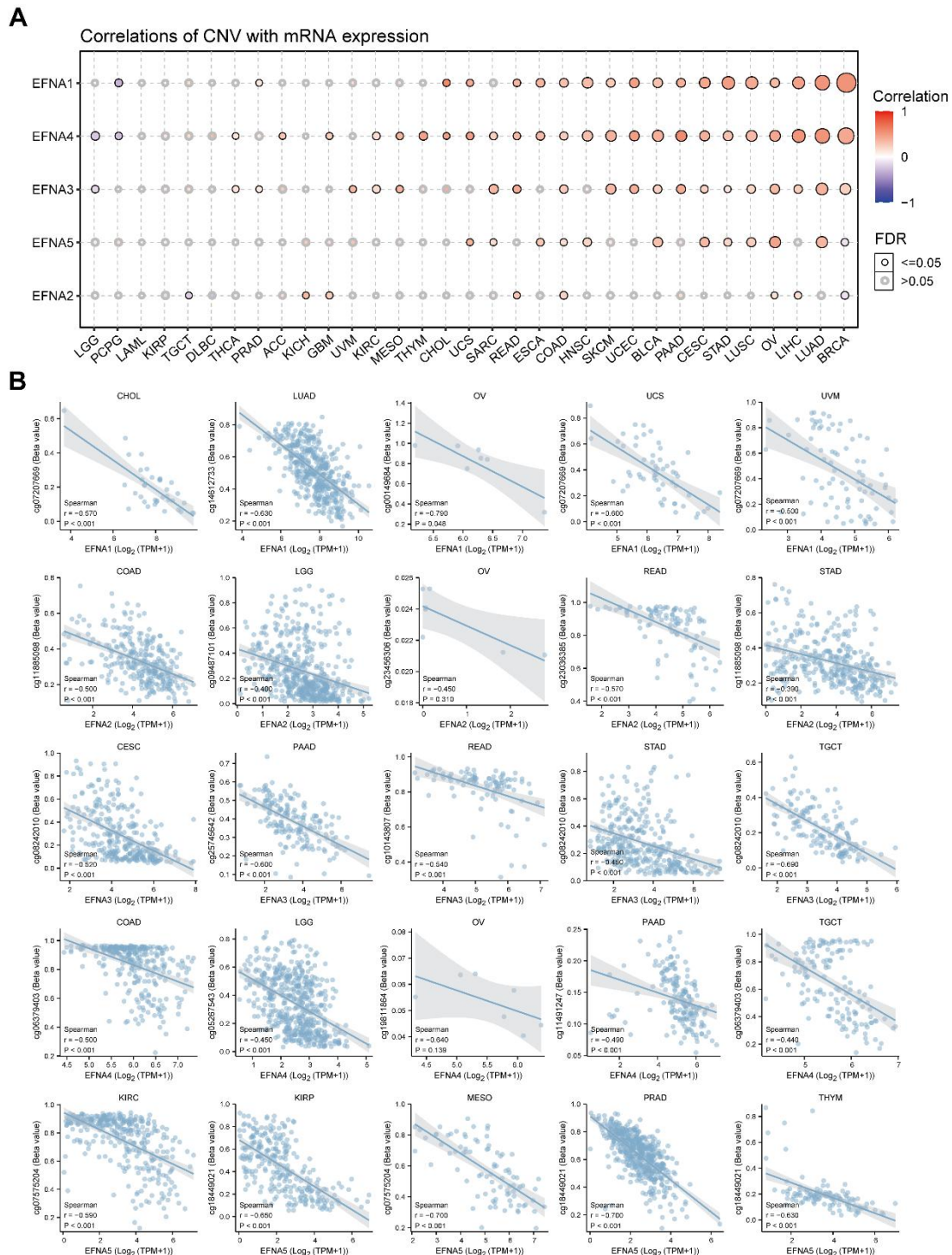


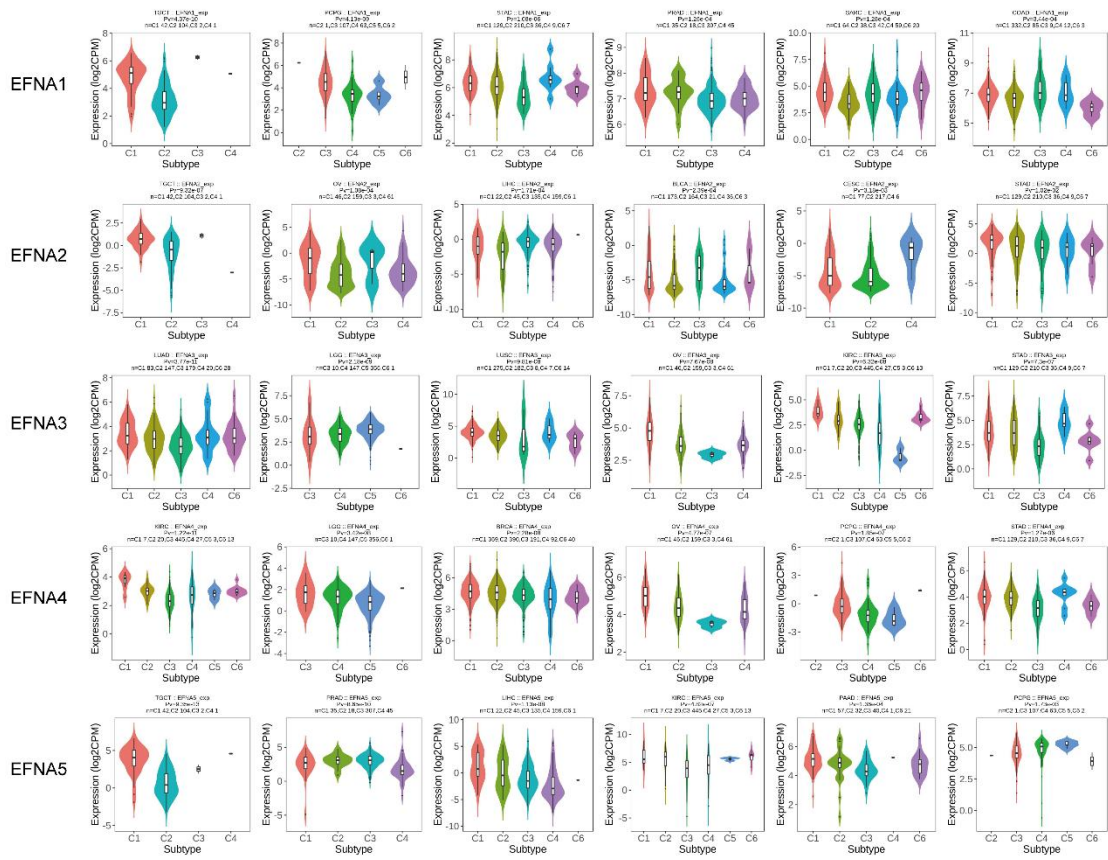
Supplementary Files



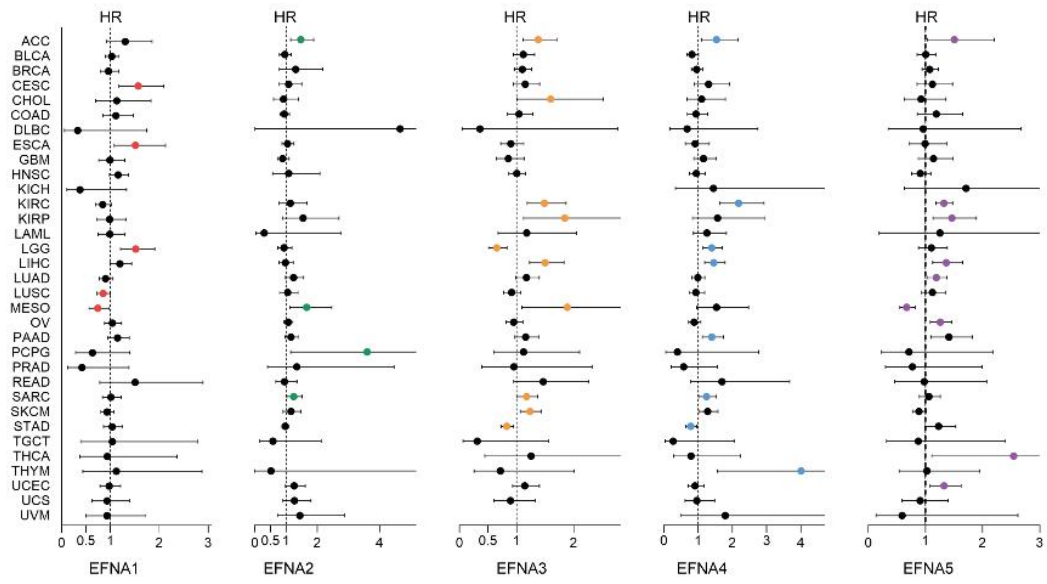
**Fig. S1** Expression of EFNA family in tumor and normal tissues **(A)** The mRNA expression of EFNAs was evaluated across 33 cancers from TCGA. **(B)** The protein expression of EFNA1 and EFNA5 was evaluated from CPTAC. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ .



**Fig. S2** CNA and DNA methylation of EFNA family in human cancers. **(A)** The correlation between EFNAs mRNA expression and CNV from TCGA. **(B)** The top 5 negative correlation between EFNAs mRNA expression and DNA methylation was demonstrated by TCGA.



**Fig. S3** EFNA mRNA expression in different immune subtypes through TISIDB. Showing the five most statistically significant cancer types for each gene.



**Fig. S4** Overall survival prognosis forest map of EFNA family genes in TCGA. The prominently colored labels indicated  $p < 0.05$ .

**Table S1.** The relation between EFNA5 expression and clinical characteristics in LUAD in TMA

Characteristics	EFNA5-High	EFNA5-Low	P
n	53	39	
T stage, n (%)			0.309
T1-T2	31 (39.2%)	29 (36.7%)	
T3-T4	13 (16.5%)	6 (7.6%)	
N stage, n (%)			0.841
N0	19 (27.1%)	15 (21.4%)	
N1-N3	22 (31.4%)	14 (20%)	
Pathologic stage, n (%)			1.000
I-II	24 (38.7%)	17 (27.4%)	
III-IV	12 (19.4%)	9 (14.5%)	
Gender, n (%)			0.635
Female	22 (23.9%)	19 (20.7%)	
Male	31 (33.7%)	20 (21.7%)	
Age, n (%)			0.218
≤ 65	30 (32.6%)	27 (29.3%)	
> 65	23 (25.0%)	12 (13.0%)	
Anatomic neoplasm subdivision, n (%)			0.334
Left	21 (23.6%)	11 (12.4%)	
Right	30 (33.7%)	27 (30.3%)	

**Table S2.** Univariate and multivariate analyses of overall survival in patients with LUAD in TMA

Characteristics	Total(N)	Univariate analysis		Multivariate analysis	
		Hazard ratio (95% CI)	P value	Hazard ratio (95% CI)	P value
Pathologic stage (Stage III&IV vs. Stage I&II)	62	3.096 (1.500-5.991)	<b>0.001</b>	3.044 (1.578-5.874)	<b>0.001</b>
Gender (Male vs. Female)	92	1.030 (0.782-1.356)	0.836		
Age (>65 vs. ≤ 65)	92	1.541 (0.884-2.687)	0.127		
Anatomic neoplasm subdivision (Right vs. Left)	89	1.018 (0.565-1.833)	0.953		
EFNA5 (High vs. Low)	92	2.399 (1.317-4.369)	<b>0.004</b>	1.408 (1.006-1.971)	<b>0.046</b>

Primer sequences of EFNA5 are as follows:

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GAPDH-F	CACCCACTCCACCTTTGA
GAPDH-R	ACCACCCTGTTGCTGTAGCCA
EFNA5-F	GAGGACTCCGTCCCAGAAGAT
EFNA5-R	TTGGAGAGTGAGGCCGGTTA

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Figure 8B. The full blots with membrane edges. (Multiple exposure images)

