Integrated muti-omics analyses and experimental validation reveal the clinical and biological Significances of APBB1IP in Colon Cancer

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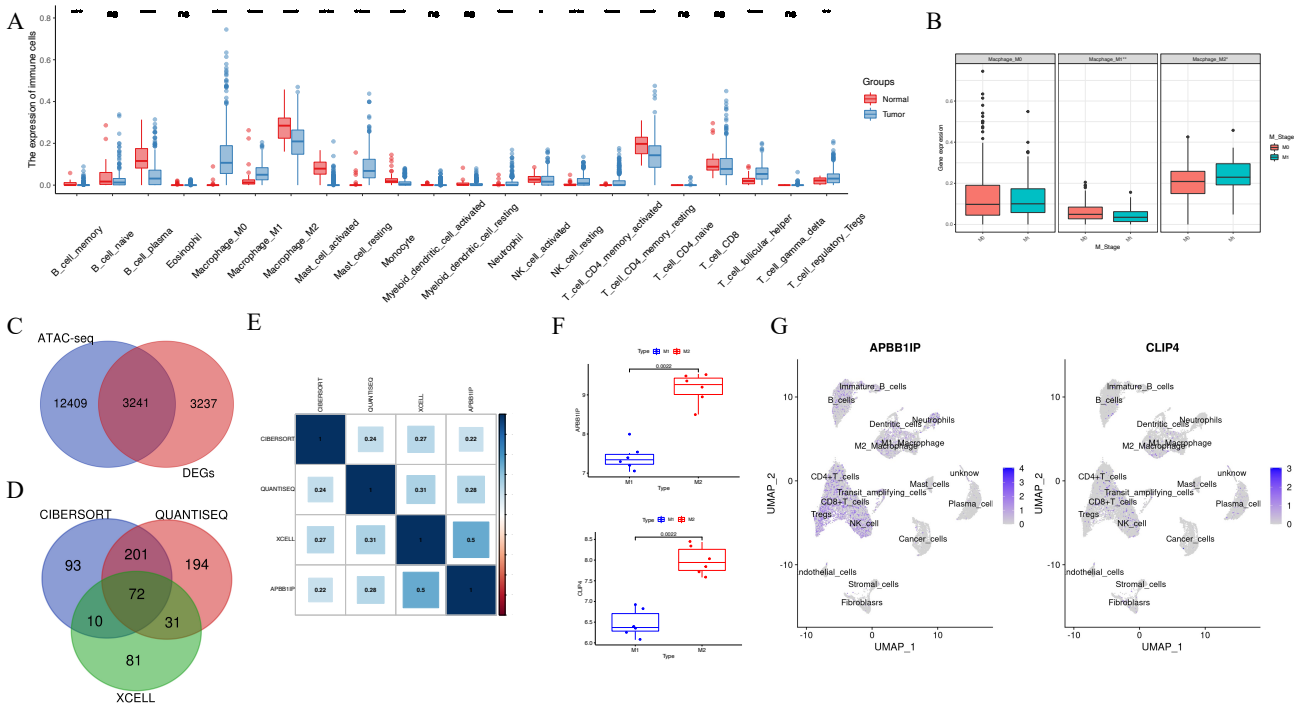
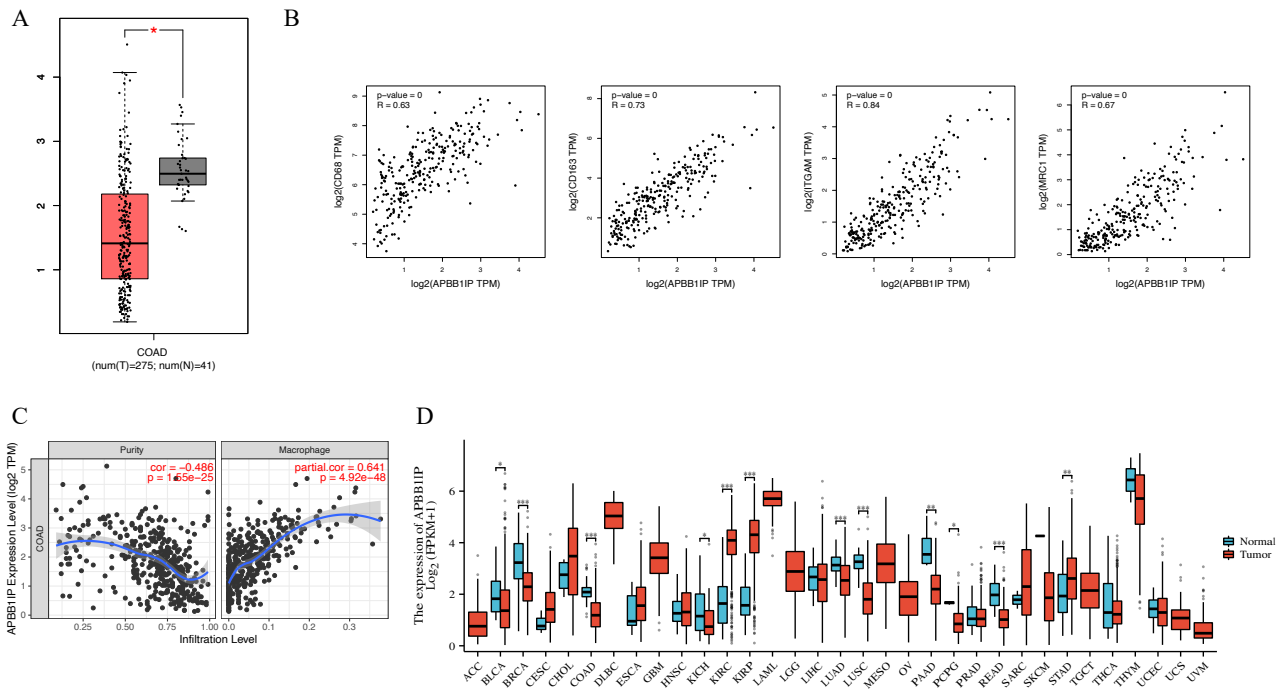


Supplementary Figure 1. The expression of the immune cells, CLIP4 and APBB1IP in RNAseq and scRNA-seq as well as corelationship. (A) The relative fraction of tumor-infiltrating immune cells in COAD quantified by CIBERSORT. (B) Different phenotypes were differential expressed in M0 stage patients and M1 stage patients. M2 macrophages high expressed in M1 stage patients. (C) Venn diagram depicting hub gene identified by the ATAC-seq and RNA-seq, 3,241 genes were identified. (D) Venn diagram depicting only 72 genes shown correlation with M2 macrophages after co-analyzing 3 methods. (E) The correlation between M2 macrophages and *APBB1IP* expression. (F) *APBB1IP* and *CLIP4* high expressed in M2 macrophage. (G) The *APBB1IP* and *CLIP4* expression in different cell types was performed in UMAP.



Supplementary Figure 2. The validation results based on online database. (A) Based on GEPIA database, *APBB1IP* was significantly downregulated in COAD samples(red) ($p < 0.05$). (B) Correlation between *APBB1IP* and macrophage surface antigens *CD68* ($r = 0.63$, $p < 0.01$), *CD163* ($r = 0.73$, $p < 0.01$), *ITGAM* ($r = 0.84$, $p < 0.01$) and MRC1 ($r = 0.67$, $p < 0.01$) in the GEPIA database. (C) Correlation between macrophage and *APBB1IP* ($r = 0.64$, $p < 0.01$) in TIMER database. (D) Expression levels of FBLN5 in various cancers. Expression levels of FBLN5 in various cancers. Expression levels of *APBB1IP* in various cancers.

Table S1 RNAi target sequences and the primer sequences used for qPCR.

RNAi target sequences

Target	**Vector**	**Sequence (5’ – 3’)**
Scrambled	PLKO.1-Scrambled	CCTAAGGTTAAGTCGCCCTCG
APBB1IP	pLKO.1 - TRC cloning vector	GCCAAAGCAAAGGCTGATAAA

RT-qPCR Primers

Gene Name	**Forward Primer**	**Reverse Primer**
APBB1IP	ATTCCGGTGCACTTAGGCTC	AAACTCTTCTCGGGGTGGGT
CD206	CATGAGGCTTCTCCTGCTTCTG	TTGCCGTCTGAACTGAGATGG
CD163	GGCCGCCACACGGAG	CAGTTGTTTTCACCACCCGC
ARG1	GGGACCTGGCCTTTGTTGAT	AGTGATGCTTCCAACTGCCA
Fizz1	GTGCTGTGAGTGTTTCCACC	TCGATGTGCTTACAGGGAACC

Supplementary Table S1: RNAi target sequences and the primer sequences used for qPCR.

Supplementary Table S2: The result of 23,211 genes with chromatin accessibility.

Supplementary Table S3: The result of 15,650 genes with chromatin accessibility in promoter.

regions.

Supplementary Table S4: The result of 3,241 DEGs with chromatin accessibility in promoter regions.

Supplementary Table S5: The result of DEGs between the low and high group of *APBB1IP*.

Supplementary Table S6: The result of transcription factors that may regulate *APBB1IP*.