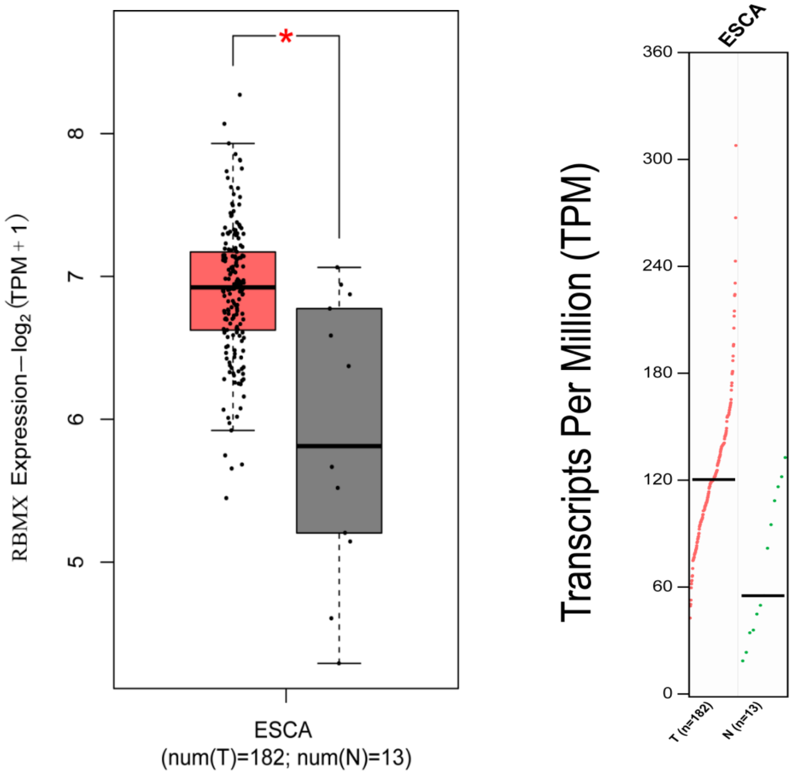


Figure S1 mRNA expression of RBMX in esophageal carcinoma. (A) The red box diagram and the gray box diagram respectively represent the expression of RBMX in esophageal cancer tissue and normal tissue, and each black dot represents a sample. (B) Each red dot represents a sample of esophageal cancer, and each green dot represents a normal sample. The horizontal lines in the two figures represent the normalized mean expression of RBMX in esophageal cancer. P value significant codes: *, P<0.05.

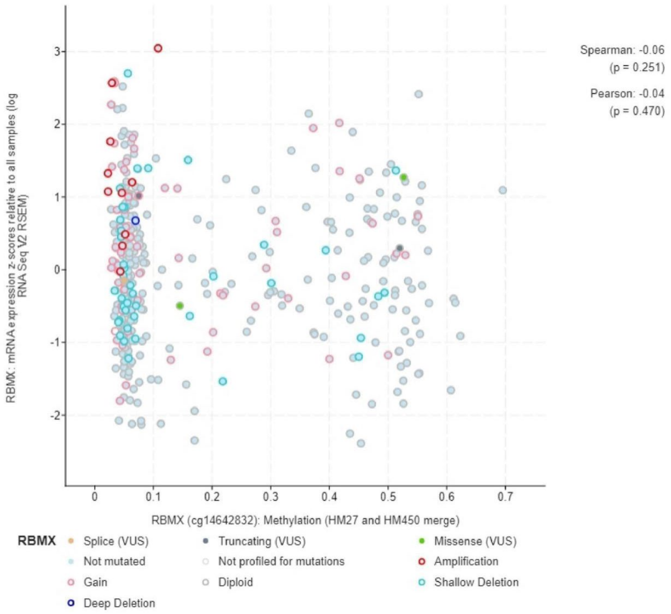


Figure S2 Analysis of correlation between RBMX expression and DNA methylation.

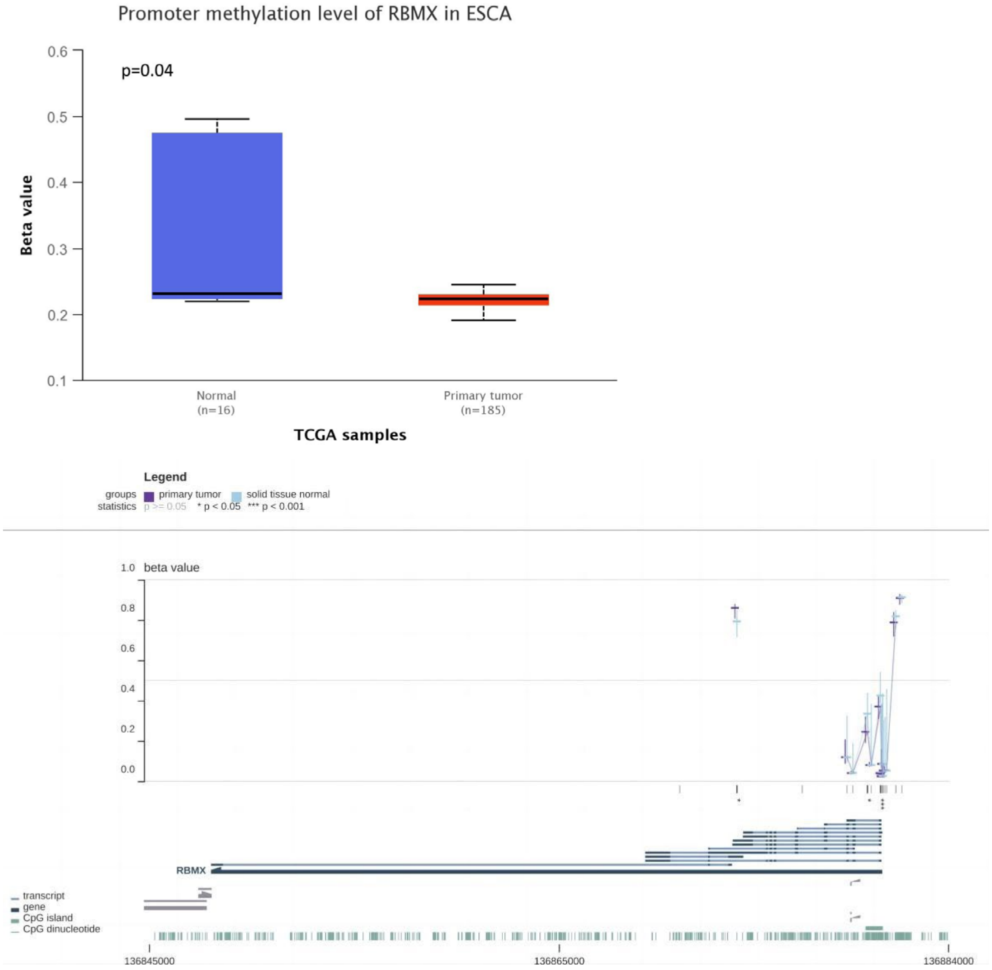


Figure S3 Promoter methylation levels.

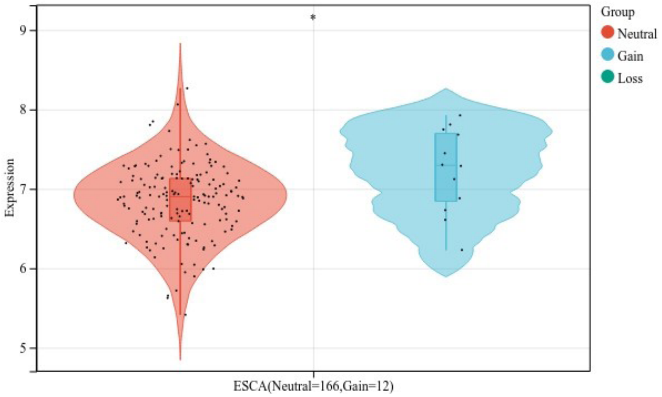


Figure S4 Gene mutation and expression analysis. In the figure, the red violin figure and the blue violin figure show the expression level of RBMX in esophageal cancer and the expression level of RBMX in esophageal cancer after mutation. The red box diagram and the blue box diagram respectively represent the expression of RBMX in esophageal cancer and the expression of RBMX in esophageal cancer after mutation. Each black dot represents a sample; the horizontal lines in the two figures represent the normalized mean expression of RBMX in esophageal cancer. P value significant codes: *, P<0.05, represent the RBMX had higher expression in esophageal cancer after mutation.

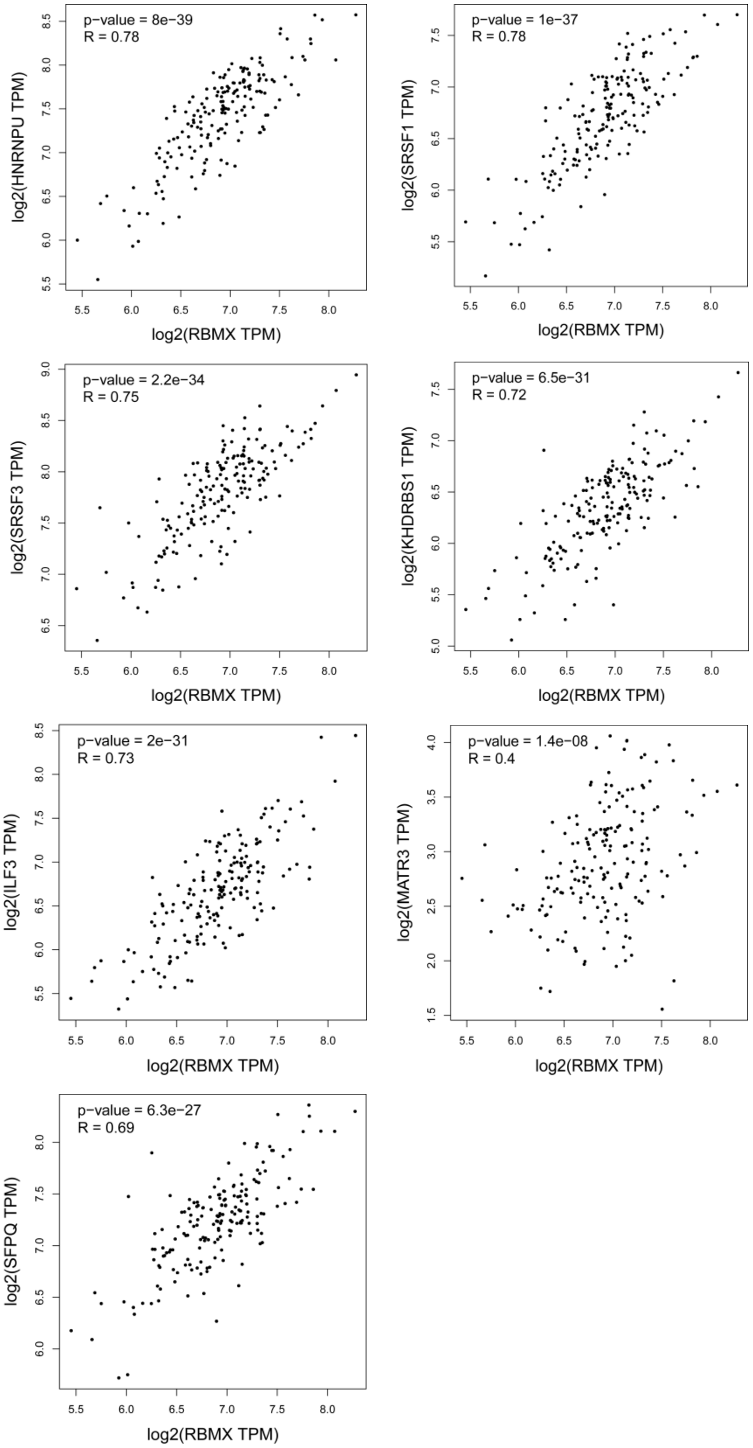
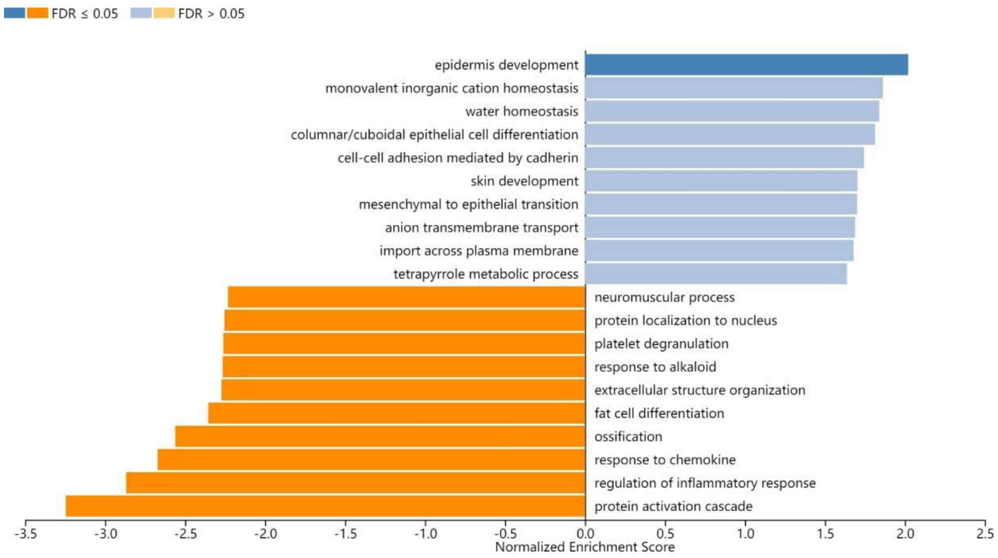
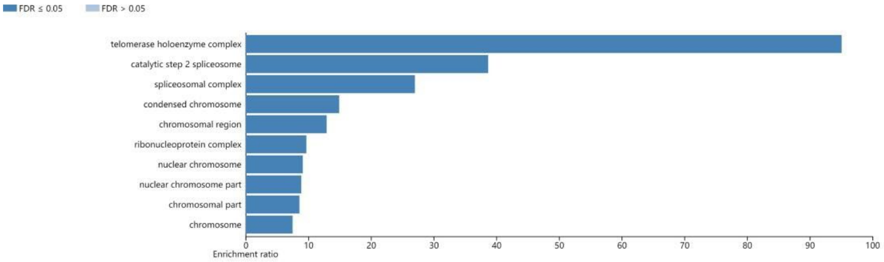


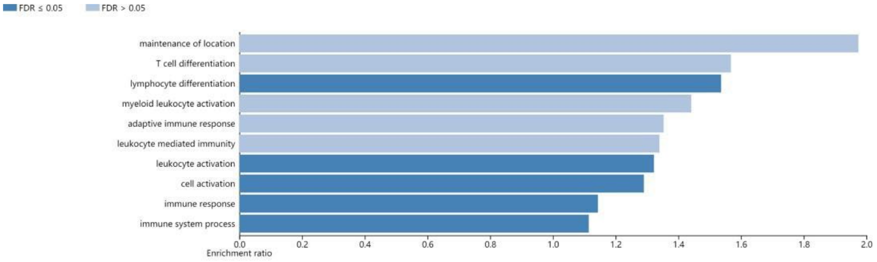
Figure S5 PPI network construction and related protein interaction analysis of RBMX.



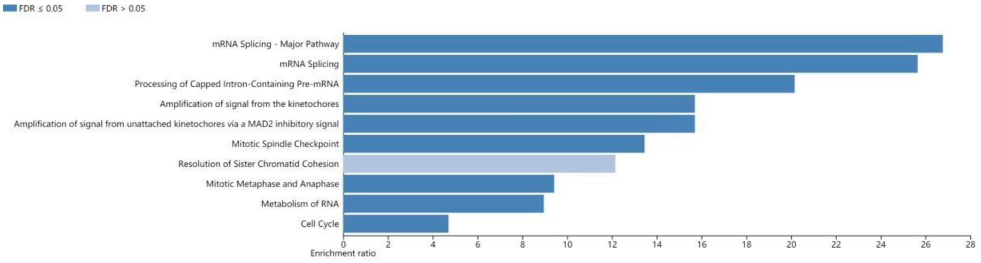
GO-BP



GO-CC



GO-MF



KEGG

Figure S6 Differential co-expression gene screening and functional enrichment analysis of RBMX in esophageal cancer.

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