Overexpression of MYBL2 predicts poor prognosis and promotes oncogenesis in endometrial carcinoma

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Table S1. 10 DEGs copy number p-value data.

| Gene  | Spearman | p       | Pearson | p       |
|-------|----------|---------|---------|---------|
| MYBL2 | 0.34     | 4.08E-15| 0.54    | 1.43E-39|
| CCNB2 | 0.13     | 4.72E-03| 0.11    | 0.01    |
| ZNF695| 0.26     | 1.99E-09| 0.29    | 2.89E-11|
| TCF23 | 0.01     | 0.92    | -0.06   | 0.42    |
| ASPA  | -0.02    | 0.64    | -0.03   | 0.44    |
| TROAP | 0.22     | 5.21E-07| 0.24    | 2.78E-08|
| CLEC4M| -0.08    | 0.29    | 0.03    | 0.68    |
| CDC25C| 0.01     | 0.86    | 0.15    | 6.17E-04|
| SKA3  | 0.07     | 0.12    | 0.20    | 8.45E-06|
| FGF10 | -0.03    | 0.73    | -0.03   | 0.67    |

Download the copy number of 10 DEGs, compare the Spearman and Pearson of each gene, and the p-value for each gene. The p-value of MYBL2 is the lowest, so the CNAs of MYBL2 gene is the most obvious.

Table S2. 5 DEGs Survival analysis.

| Gene | p-value | 0S | DFS |
|------|---------|----|-----|
| ASPS | 0.46    | 0.172|
| MYBL2| 0.020   | 0.014|
| TROAP| 0.685   | 0.255|
| CCNB2| 0.030   | 0.856|
| CDC25C| 0.416  | 0.295|

The five most significant genes in EC were verified by GEO data set. Both overall survival (OS) and disease-free survival (DFS) of MYBL2 gene are meaningful (p<0.05).
**Figure S1.**
**IHC of MYBL2 expression in EC tissue.** A) the IHC scores of EC and adjacent tissues. B) IHC and HE staining results of EC and adjacent tissues. In IHC, MYBL2 stained positively in the nucleus and cytoplasm.

**Figure S2.**
Flow chart of the study.