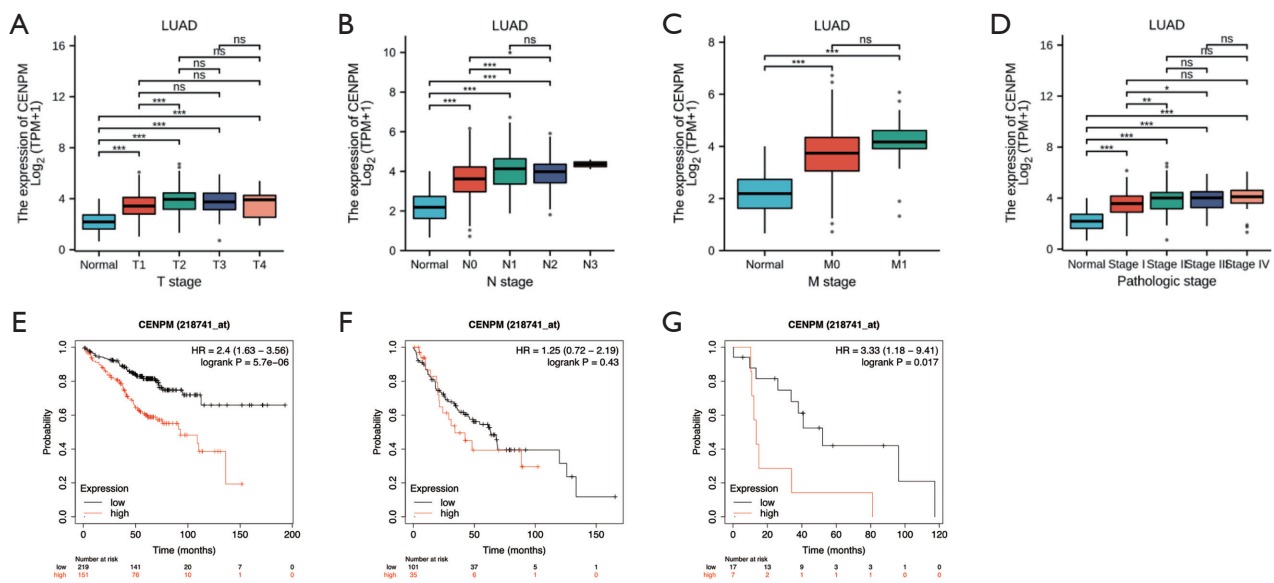


**Figure S1** *CENPM* is upregulated but is not relevant with the survival rate in LUSC. (A) *CENPM*, *CENPA*, *CENPF*, *CENPU*, *CENPO* and *CENPH* gene expression upregulated in LUSC tissues compared with normal tissues. (B) *CENPM* gene expression upregulated in LUSC (TCGA, n=515) compared with normal tissues (GTEx, n=347). (C) *CENPM* expression in paired samples (n=57) in TCGA database. (D) ROC curve of *CENPM* expression for LUSC with AUC of 0.968. (E) Kaplan-Meier survival curves for OS and DSS of LUSC patients from TCGA database. \*\*\*,  $P < 0.001$ . *CENP*, centromere protein; TPM, transcript per million; LUSC, lung squamous cell carcinoma; TPR, true positive rate; FPR, false positive rate; AUC, area under the curve; CI, confidence interval; HR, hazard ratio; TCGA, The Cancer Genome Atlas; GTEx, Genotype-Tissue Expression; ROC, receiver operative characteristic; AUC, area under the curve; OS, overall survival; DSS, disease specific survival.



**Figure S2** Upregulation of *CENPM* in LUAD was associated with TNM stages, pathologic stages and poor overall survival rate. *CENPM* gene expression upregulated in LUAD patients with different T stages (A), N stages (B) and M stages (C) compared with normal tissues from TCGA database. (D) *CENPM* gene expression upregulated in LUAD patients with different pathological stages from TCGA database. Kaplan-Meier survival curves for OS of LUAD patients with pathologic stage I (E), stage II (F) and stage III (G) from Kaplan-Meier Plotter database. Bars indicate the means  $\pm$  SD. \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ . *CENPM*, centromere protein M; HR, hazard ratio; LUAD, lung adenocarcinoma; ns, not significant; TPM, transcript per million; TNM, tumor-node-metastasis; TCGA, The Cancer Genome Atlas; OS, overall survival; SD, standard deviation.