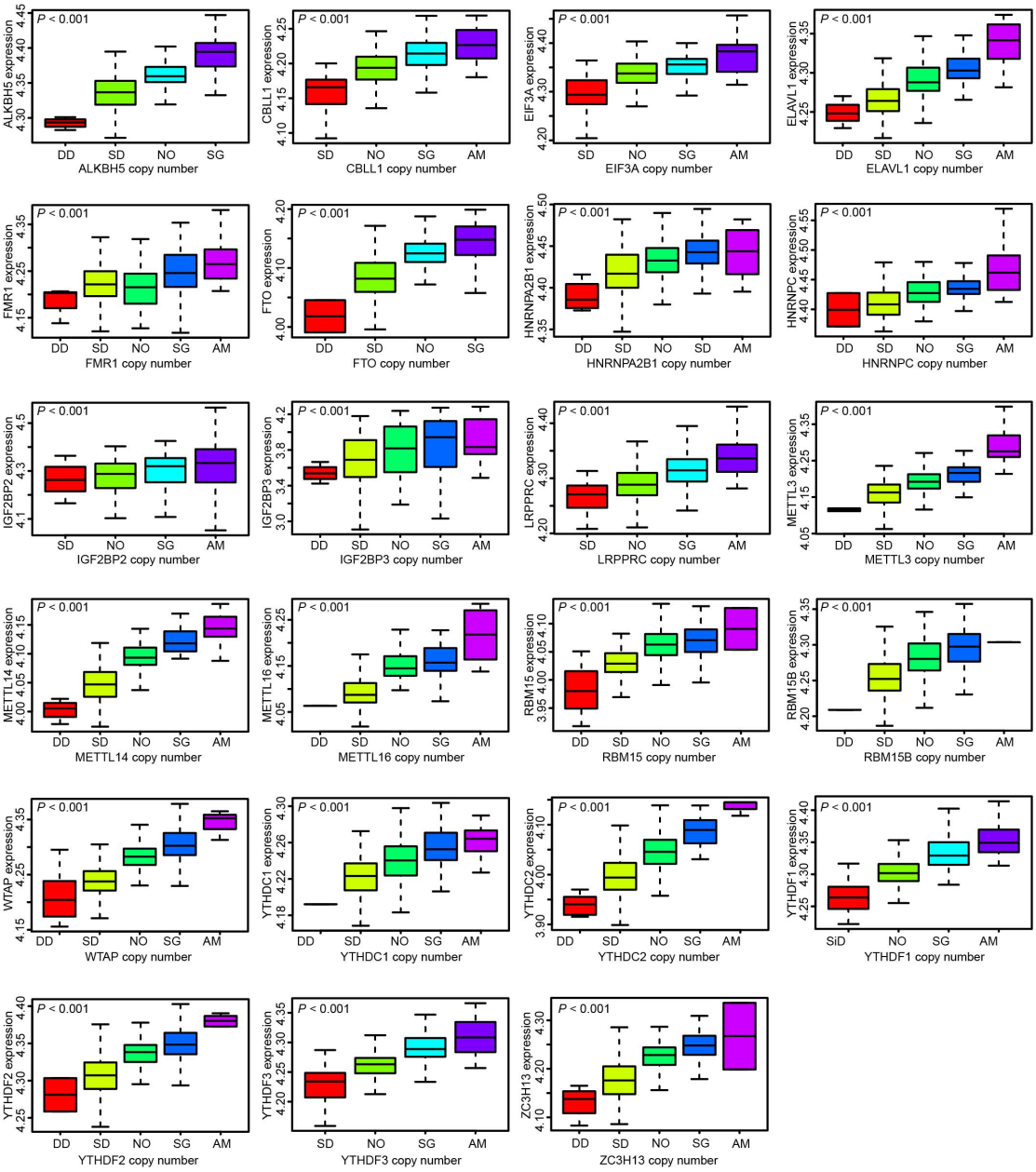


Fig. S1 DNA copy number variation of 23 m^{6}A regulators in ovarian cancer as per TCGA database. Differential mRNA levels of 23 m^{6}A regulators (ALKBH5, CBLL1, EIF3A, ELAVL1, FMR1, FTO, HNRNPA2B1, HNRNPC, IGF2BP2, IGF2BP3, LRPPRC, METTL3/14/16, RBM15/15B, WTAP, YTHDC1/2, YTHDF1/2/3, and ZC3H13) with a different type of DNA copy number variation in ovarian cancer. DD: double deletion; SD: single deletion; NO: normal; SG: single gain; AM: amplification.

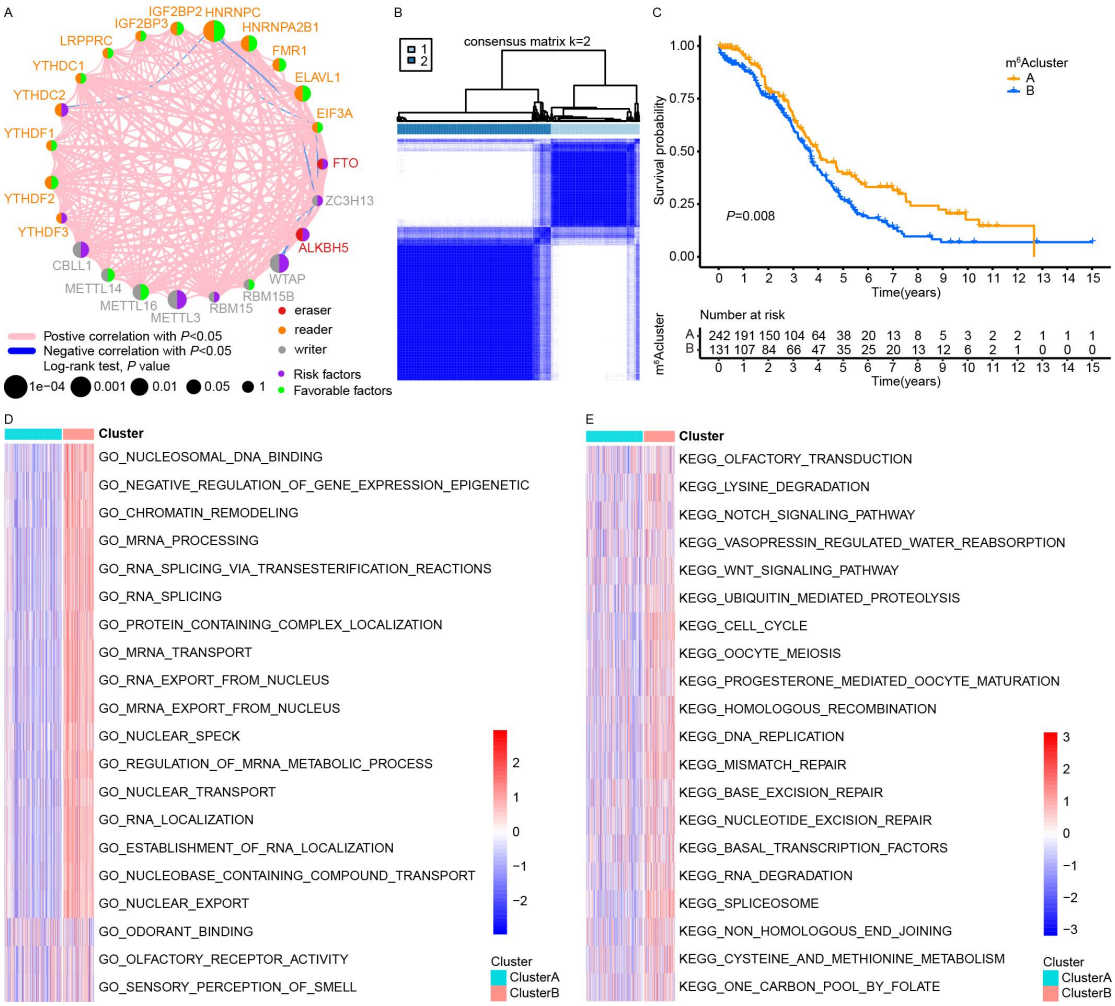


Fig. S2 Unsupervised clustering of m^{6}A regulators as per TCGA OV dataset. **(A)** The interplay between 23 m^{6}A regulators and their prognostic values detected by the Log-rank test in ovarian cancer. **(B)** Consensus matrix $k = 2$ for TCGA OV cohort. **(C)** Kaplan-Meier curves displaying the overall survival of ovarian patients identified in 2 m^{6}A modification patterns. **(D, E)** Heatmaps showing the enriched GO (D) and KEGG (E) terms between the identified 2 m^{6}A modification patterns

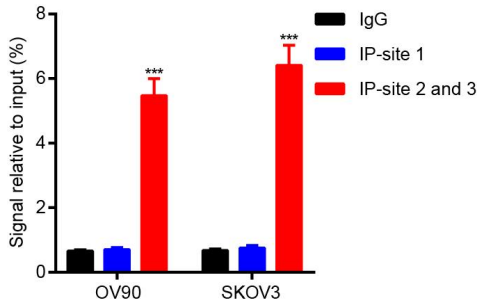


Fig. S3 m6A modification of PTGER2 mRNA. MeRIP assay measuring m6A modification of PTGER2 mRNA in OV90 and SKOV3 cells. The enriched RNAs were further subjected to RT-qPCR. $^{***}P < 0.001$

Table. S1 The relationship between the clinicopathologic characteristics and PTGER2 expression in ovarian cancer

Characteristics	n	PTGER2 expression		*P* value
		Low (n = 75)	High (n = 83)	
Age (years)				
≤51	79	39 (49.4%)	40 (50.6%)	0.633
＞51	79	36 (45.6%)	43 (54.4%)	
T stage				
T1-2	46	25 (54.3%)	21 (45.7%)	0.267
T3	112	50 (44.6%)	62 (55.4%)	
N stage				
N0	116	60 (51.7%)	56 (48.3%)	0.075
N1	42	15 (35.7%)	27 (64.3%)	
M stage				
M0	125	65 (52.0%)	60 (48.0%)	0.021
M1	33	10 (30.3%)	23 (69.7%)	

FIG.2C

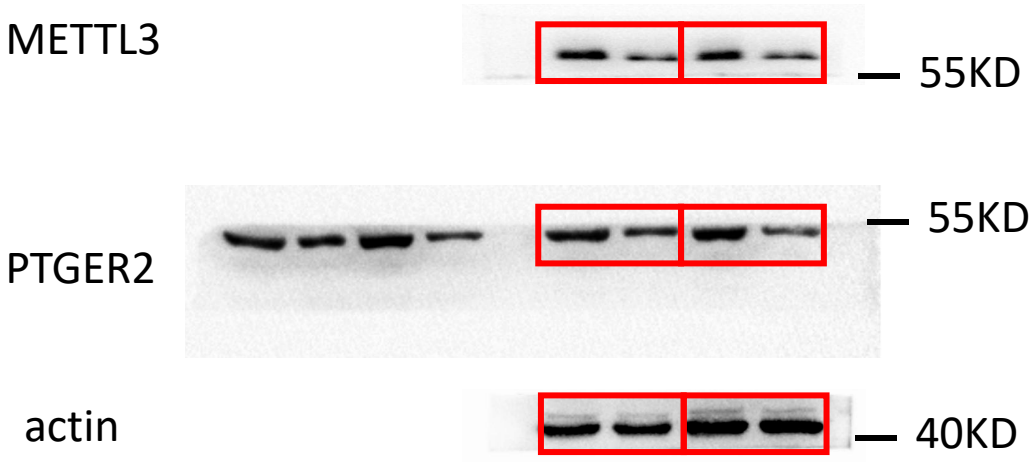
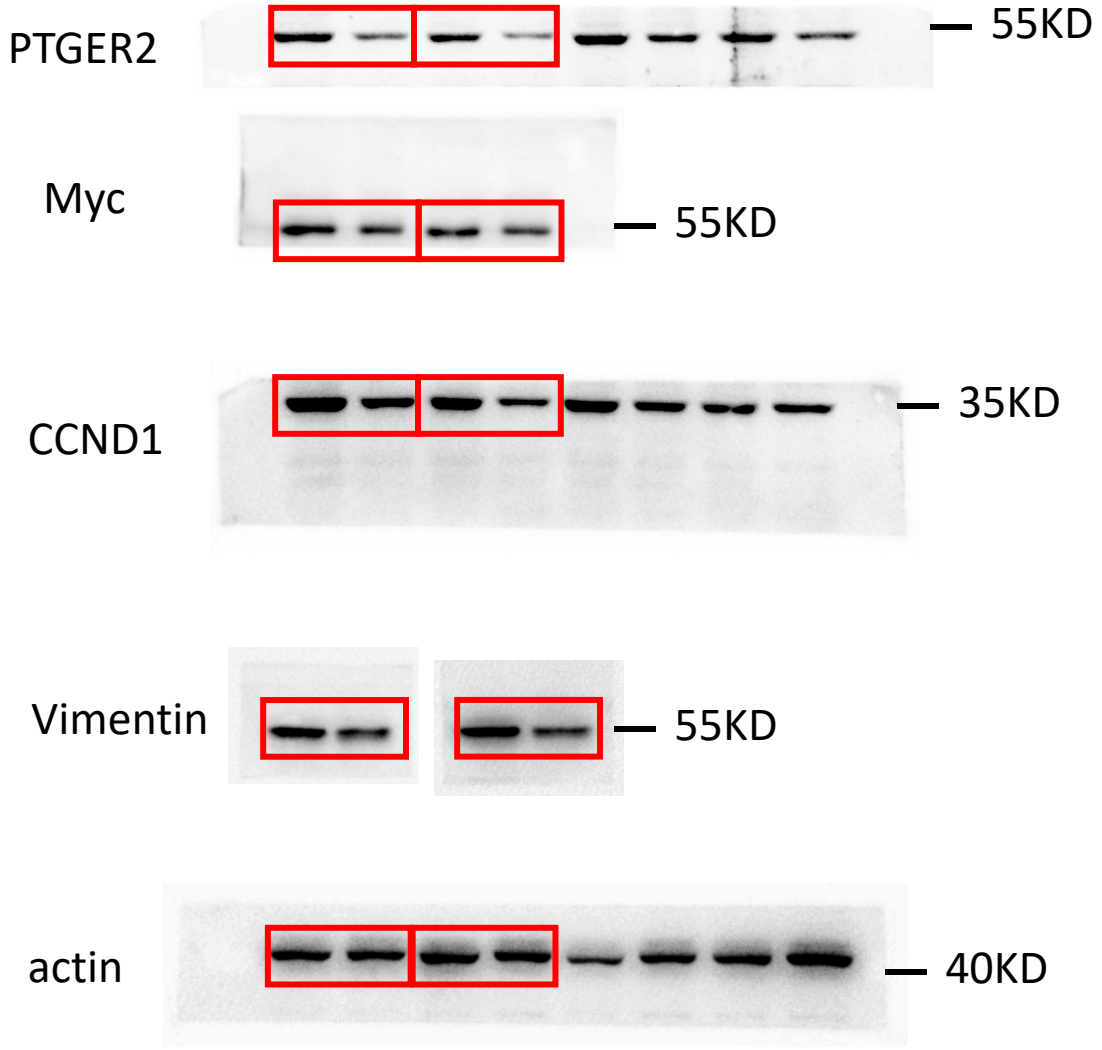

METTL3
55KD
PTGER2
55KD
actin
40KD

FIG.3I


PTGER2
55KD
Myc
55KD
CCND1
35KD
Vimentin
55KD
actin
40KD

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