

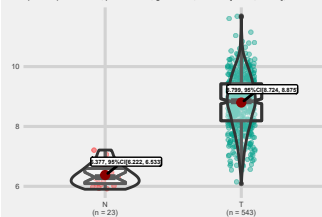
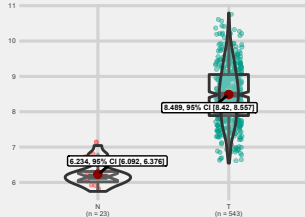
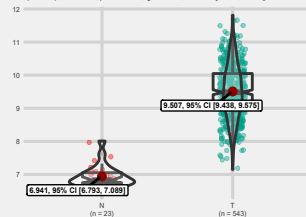
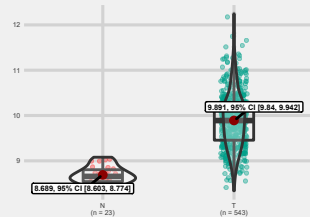
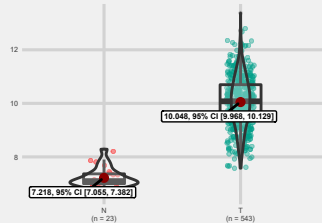
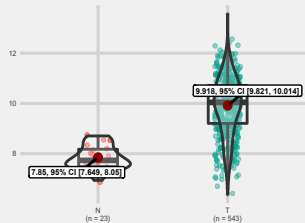
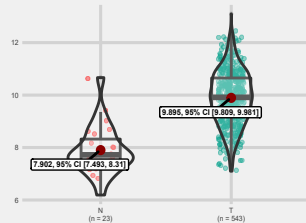
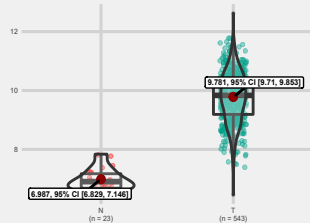
A NUF2 expression in UCEC normal & tumor group
 $t(35.132) = -28.782, p < 0.001, g = 6.141, 95\% \text{ CI } [5.590, 6.692], n = 566$ **B** CDCA2 expression in UCEC normal & tumor group
 $t(34.781) = -29.386, p < 0.001, g = 6.269, 95\% \text{ CI } [5.713, 6.825], n = 566$ **C** CDCA3 expression in UCEC normal & tumor group
 $t(33.658) = -32.389, p < 0.001, g = 6.908, 95\% \text{ CI } [6.327, 7.489], n = 566$ **D** CDCA4 expression in UCEC normal & tumor group
 $t(42.654) = -24.767, p < 0.001, g = 5.292, 95\% \text{ CI } [4.773, 5.812], n = 566$ **E** CDCA5 expression in UCEC normal & tumor group
 $t(35.391) = -31.766, p < 0.001, g = 6.778, 95\% \text{ CI } [6.202, 7.354], n = 566$ **F** CBX2 expression in UCEC normal & tumor group
 $t(34.789) = -19.061, p < 0.001, g = 4.066, 95\% \text{ CI } [3.586, 4.547], n = 566$ **G** CDCA7 expression in UCEC normal & tumor group
 $t(24.229) = -9.872, p < 0.001, g = 2.099, 95\% \text{ CI } [1.663, 2.535], n = 566$ **H** CDCA8 expression in UCEC normal & tumor group
 $t(33.097) = -33.020, p < 0.001, g = 7.041, 95\% \text{ CI } [6.455, 7.628], n = 566$ 

Table S1. clinical parameters of patients with endometrial carcinoma in TCGA cohort

Clinical parameters		Total	%
Age at diagnosis		63(33-90)	
FIGO cancer staging system	I	339	62.43%
	II	51	9.39%
	III	124	22.83%
	IV	29	5.34%
Histological grade	well	98	18.05%
	moderate	120	22.09%
	poor	325	59.86%
Histologic subtype	EEA	407	74.95%
	MSE	22	4.05%
	SEA	114	21.00%

FIGO: International Federation of Gynecology & Obstetrics; EEA: endometrioid endometrial adenocarcinoma; MSE: mix serous and endometrioid carcinoma; SEA: serous endometrial adenocarcinoma

Table S2

Function	FDR	Genes in network	Genes in genome
mitosis	1.32E-13	12	180
chromosome, centromeric region	7.34E-13	10	98
nuclear division	3.18E-12	12	256
chromosome segregation	5.80E-12	10	128
organelle fission	5.87E-12	12	281
spindle	1.04E-11	10	141
microtubule cytoskeleton organization	1.42E-11	11	220
protein-DNA complex	2.49E-11	10	158
kinetochore	1.79E-10	8	74
condensed chromosome kinetochore	6.93E-10	6	22
regulation of cell division	9.28E-10	9	153
condensed chromosome, centromeric	1.78E-09	6	26
spindle microtubule	2.50E-08	6	40
midbody	2.50E-08	7	81
condensed chromosome	3.53E-08	7	86
regulation of mitosis	6.74E-08	7	95
regulation of nuclear division	9.82E-08	7	101
spindle organization	6.46E-07	6	70
condensed chromosome outer kinetochore	1.13E-06	4	11
G2/M transition of mitotic cell cycle	1.42E-06	7	152
cell cycle G2/M phase transition	1.42E-06	7	152
establishment of chromosome localization	1.61E-05	4	21
spindle pole	1.61E-05	5	59
chromosome localization	1.61E-05	4	21
microtubule	4.51E-05	6	149
regulation of mitotic cell cycle	9.94E-05	7	290
mitotic spindle organization	0.000123	4	35
cell cycle phase	0.000228	4	41
spindle checkpoint	0.000295	4	44
cytokinesis	0.000323	5	112
mitotic sister chromatid segregation	0.000428	4	49
sister chromatid segregation	0.000616	4	54
establishment of organelle localization	0.00077	5	136
attachment of spindle microtubules to kinetochore	0.001439	3	19
organelle localization	0.001598	5	160
M phase	0.001598	3	20
positive regulation of cell cycle process	0.002507	5	177
microtubule binding	0.00253	4	80
protein localization to chromosome	0.002608	3	24
positive regulation of cell cycle	0.003208	4	86
positive regulation of mitosis	0.004831	3	30
microtubule anchoring	0.004831	3	30
positive regulation of nuclear division	0.006323	3	33
organelle assembly	0.006904	5	226
spindle assembly	0.007234	3	35
spindle assembly checkpoint	0.008385	3	37
metaphase/anaphase transition of mitotic cell cycle	0.010405	3	40
metaphase/anaphase transition of cell	0.010982	3	41
microtubule polymerization or depolymerization	0.011343	3	42
tubulin binding	0.011343	4	125
regulation of mitotic metaphase/anaphase transition	0.013706	3	45

regulation of metaphase/anaphase			
transition of cell cycle	0.014367	3	46
protein kinase binding	0.014943	5	276
centrosome organization	0.033945	3	62
regulation of microtubule cytoskeleton			
organization	0.039453	3	66
microtubule organizing center organization	0.039453	3	66
spindle assembly involved in mitosis	0.052329	2	13
regulation of microtubule-based process	0.070012	3	81
cell cycle checkpoint	0.070114	4	209
maintenance of protein location in cell	0.073818	3	84
regulation of centrosome cycle	0.073818	2	16
metaphase plate congression	0.073818	2	16
maintenance of location in cell	0.090903	3	91
mitotic cytokinesis	0.090989	2	18
maintenance of protein location	0.090989	3	92