Supplementary Data

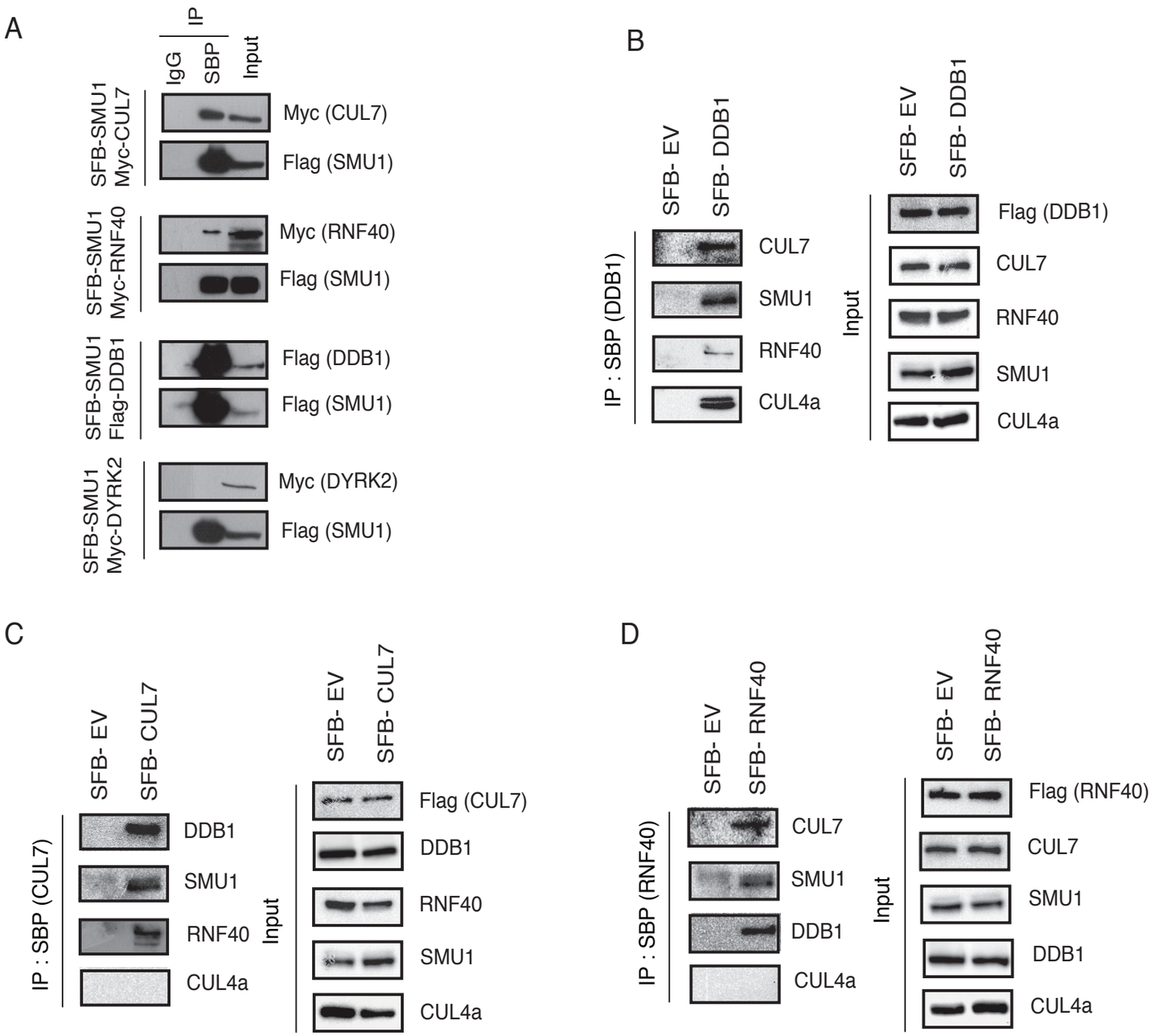
Supplementary table 1: List of primers used in this study for ChIP experiments were shown.

Gene name	Primer sequence	Location
ANAPC5 For:	GGAGATGTGGTGGTGGATCT	chr12:121756213-121756365, strand= reverse
ANAPC5 Rev:	ACCGGTACTCCTTGGAGAGG	
SMC1A For:	CGGTGAACCTCTGAAATGGT	chrX: 53449441-53449547, strand= forward
SMC1A Rev:	TGGGGTTCCTGAAACTGATT	
MUS81 For:	TCTCCAAACCCTCTCTGCTC	chr11:65632546-65632715, strand= forward
MUS81 Rev:	AAACACTTCTCGCACCGACT	
CDCA2 For:	CCTGAAACCAAGGAGTCTGC	chr8:25317784-25317933, strand= forward
CDCA2 Rev:	TCTTCCCAGTTCCCAAAATG	
ANAPC12 For:	GACCCGTAAGAAACAGAAGGAA	chr9:116029543-116029694, strand= reverse
ANAPC12 Rev:	TGAACGATTATTGGGCTTGG	
AURKA For:	CAGGCCAATCGGCTTTCTA	chr20:54967248-54967345, strand= reverse
AURKA Rev:	TTCCAAGAGCTCAGCCGTTA	

Supplementary table 2: List of primers used in this study for qRT-PCR analysis were shown.

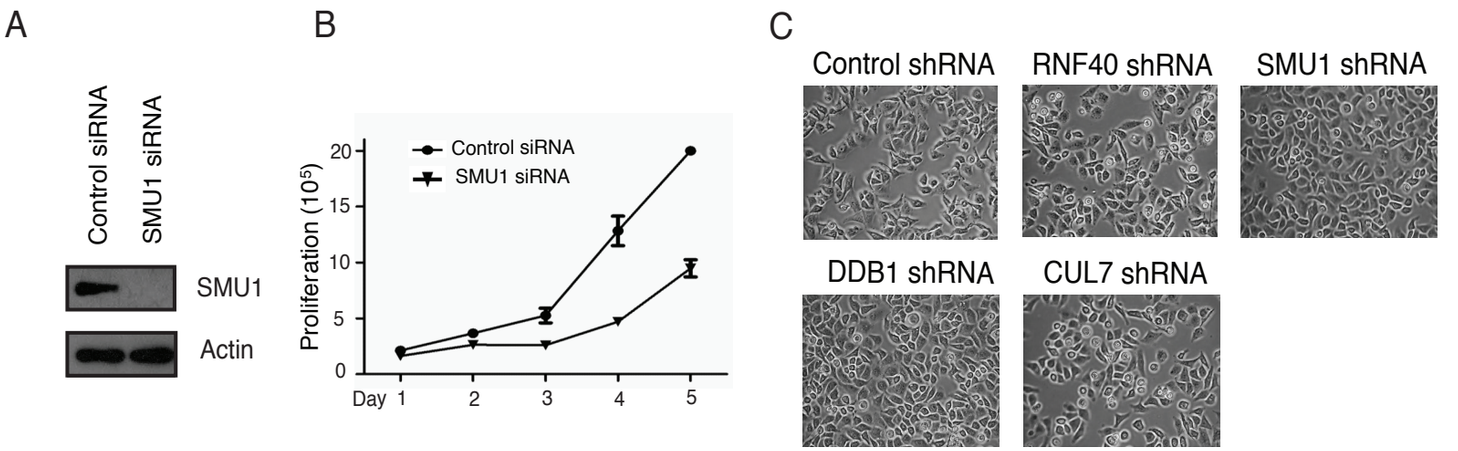
Gene name	Primer sequence
DDB1 For:	TGCCTACAAGCCCATGGAAG
DDB1 Rev:	TGGCAGCGCTATCCTTTTGA
RNF40 For:	AAGAGGGCTCAGGAGGACAT
RNF40 Rev:	CATCTGCGTAGACCTCCACC
DDB1 For:	ATCATTGACCCTGAGTGCCG
DDB1 Rev:	CCTGAGGGTCCTGGTAGACA
CUL7 For:	TACCAGGAGGGGTCCTCAAG
CUL7 Rev:	TTCTCCAAGTTCTGGCCGTC
SMU1 For:	TGGCACTGTAAAGATCTGGAA
SMU1 Rev:	CTGTTGCACACCACAAAGTG
SMC1a_For:	TACCTCAGTTCTCGGGCGTA
SMC1a_Rev:	TGACTTACCAGAGCCATTGGG
MUS81_For:	GGCCCAGGAGACCAATCCT
MUS81_Rev:	TTCAGCCGGAACTTCTGCTC
AURKA_For:	GTCAAGTCCCCTGTCGGTTC
AURKA_Rev:	GCAATGGAGTGAGACCCTCT
ANAPC5_For:	CGGTCACTATCAACAGGCAGA
ANAPC5_Rev:	GCGAGGTACGGTAACCCAAA
ANAPC12_For:	AGGCCGGCTTGAAAAGAGATTA
ANAPC12_Rev:	GGGCCAAACCCAGTGAACTA
CDCA2_For:	CCGAAGACTGGGTTCAGGTTA
CDCA2_Rev:	TGCCAAGCGATGAGGAACTT

Figure S1



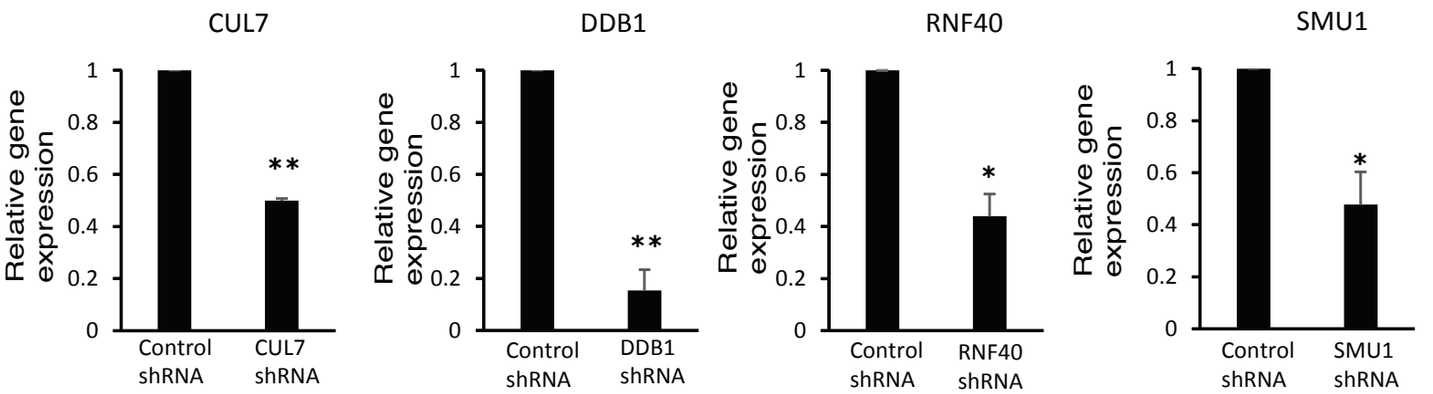
Supplementary Figure S1: (A) 293T cells were transfected with SFB tagged SMU1 along with Myc- CUL7, MYC-RNF40, Flag-DDB1 and Myc-DYRK2. The presence of RNF40, DDB1, CUL7 and DYRK2 in SMU1 complex proteins was evaluated by immunoblotting with the indicated antibodies. **(B)** Cells were transfected with either SFB-Empty vector (EV) or SFB-DDB1 **(C)** SFB-CUL7 **(D)** and SFB-RNF40. Interaction of SMU1-DDB1-CUL7-RNF40 was assessed by immunoblotting with respective antibodies after pulling down with streptavidin sepharose.

Figure S2



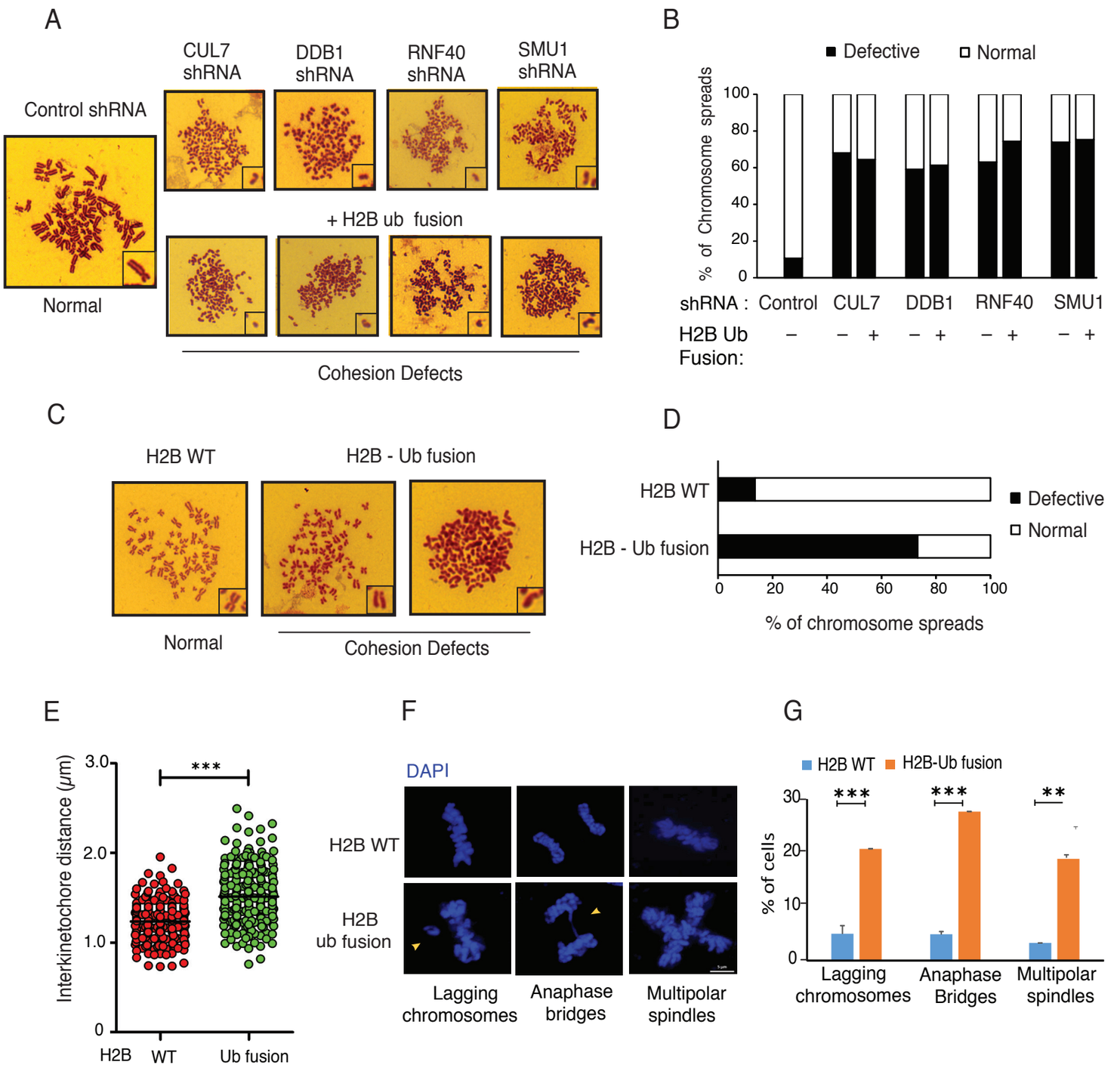
Supplementary Figure S2: (A) HeLa cells transfected with control or SMU1 siRNA. Cell lysates were checked for knockdown of SMU1 using SMU1 specific antibody and actin was used as loading control. **(B)** HeLa cells were transfected with control and SMU1 siRNA separately. 48 hr post transduction 1*10^5 cells were seeded in five different plates and rate of cell proliferation was measured by cell counting after staining with trypan blue dye. **(C)** Cells were transduced with control shRNA, RNF40 shRNA, SMU1 shRNA, DDB1 shRNA or CUL7 shRNA. 72 hours post transduction, mitotic cells (rounded off cells) were imaged in phase contrast microscope and representative images were shown.

Figure S3



Supplementary Figure S3: Total RNA was extracted from HeLa cells transfected with control or SMU1 siRNA or CUL7 shRNA or DDB1 shRNA and RNF40 shRNA, and expression levels of various genes measured by qRT-PCR was shown. Statistical analysis: error bars- standard deviation, ***P<0.001 **P<0.01; *P<0.05, Student's t-test.

Figure S4



Supplementary Figure S4: (A) Cells expressing control shRNA, CUL7 shRNA, DDB1 shRNA, RNF40 shRNA and SMU1 shRNA alone or together with H2B-Ub fusion were analysed for chromatid cohesion (n= 75). **(B)** Percentage of chromosome spreads showing normal and defective cohesion was plotted. P value is less than 0.001 for knockdown of complex proteins compared to control and non-significant between shRNA alone and along with H2B-Ub fusion (**C)** Chromosome spreads were prepared form HeLa cells transfected with either H2B wild type or H2B-Ub fusion. Representative images of chromosome spreads are shown. **(D)** Quantification of data from figure S3C is shown. (n= 90), $p < 0.001$. **(E)** The distance between paired kinetochores was measured for cells transfected with either H2B WT or H2B-Ub fusion. **(F)** Cells were transfected with H2B Wild type (WT) or H2B-Ub fusion protein. Mitotic defects were detected using immunofluorescence after staining with DAPI (Scale bar, 10μm). **(G**) Quantification of the data from figure S5F is shown (n=25 cells each). Statistical analysis: error bars- standard deviation, ***P<0.001 **P<0.01; *P<0.05, Student's t-test. (Scale bar, 5μm).