Acetylation Drives Nonhistone Chromatin Protein PC4-mediated Nucleolar Organization and Function

Stephanie Kaypee^{1,4}, Kyoko Ochiai¹, Hiroki Shima¹, Mitsuyo Matsumoto¹, Mahabub Alam^{1,5}, Tsuyoshi Ikura², Tapas K. Kundu^{1,3*}, Kazuhiko Igarashi^{1*}

- ¹ Department of Biochemistry, Tohoku University Graduate School of Medicine, Seiryomachi 2-1, Sendai 980-8575, Japan
- ² Laboratory of Chromatin Regulatory Network, Department of Genome Biology, Radiation Biology Center, Graduate School of Biostudies, Kyoto University, Yoshida Konoe-cho, Sakyo-ku, Kyoto, Japan.
- ³ Transcription and Disease Laboratory, Molecular Biology and Genetics Unit, Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore-560064, India
- *Corresponding author, igarashi@med.tohoku.ac.jp (KI) or tapas@jncasr.ac.in (TKK)

Current address:

- ⁴ Ubiquitin Biology Laboratory, Graduate School of Frontier Biosciences, Osaka University, 1-3 Yamadaoka, Suita, Osaka 565-0871, Japan
- ⁵ Department of Animal Science and Nutrition, Chattogram Veterinary and Animal Sciences University, Khulshi, Chattogram-4225, Bangladesh

Supplemental Information

Table S1

Name	Forward primer (5'-3')	Reverse primer (5'-3')	Purpos
			е
EGFP-	GAAAAAAAGTTAGCGGCGAA	CGCTTGCTTTTTCGCCGCTA	Cloning
N1-PC4	A	ACTTTTTTC	Primers
K26A-	AAGCAAGCG		
R27A			
EGFP-	CAGTGATTCGGACAGCGAAG	AACCGCTTGCTTTTTCCTCT	Cloning
N1-PC4	Т	Т	Primers
K23A-	TGAAGCAGCGTTAAAGAGGA	TAACGCTGCTTCAACTTCGC	
K24A	A	Т	
	AAAGCAAGCGGTT	GTCCGAATCACTG	
EGFP-	AAGCAAGCGGTTCCAGAGA	CTTCACGGGCCTCTCTGGA	Cloning
N1-PC4	G	A	Primers
K35R	GCCCGTGAAG	CCGCTTGCTT	
mouse	CGTTGACATCCGTAAAGACC	AGCCACCGATCCACACAGA	RT-
actin	TC		qPCR
mouse	GCTGTTTTGCTTGTCCAGCC	CTCTCCGGAATCGAACCCT	RT-
47S		GA	qPCR
human	ATTTGCGGTGGACGATGGAG	AGAGATGGCCACGGCTGCT	RT-
actin		Т	qPCR
human	TGTCAGGCGTTCTCGTCTC	AGCACGACGTCACCACATC	RT-
47S			qPCR
Promote	GGTATATCTTTCGCTCCGAG	AGCGACAGGTCGCCAGAG	ChIP-
r		GA	qPCR
18S	CGACGACCCATTCGAACGTC	CTCTCCGGAATCGAACCCT	ChIP-
	Т	GA	qPCR
5.8S	AGTCGGGTTGCTTGGGAATG	CCCTTACGGTACTTGTTGAC	ChIP-
	С	Т	qPCR
I	1	1	1

28S	GAGCTCAGGGAGGACAGAA	AGGTCAGAAGGATCGTGAG	ChIP-
	A	G	qPCR
IGS	GTTGACGTACAGGGTGGACT	GGAAGTTGTCTTCACGCCT	ChIP-
	G	GA	qPCR

Table S1: List of primers used in this study.

Table S2:

	Nucleolar proteins	Nucleolar	Function
	interacting with PC4	localization	
1	Tcof1	FC	RNA polymerase I
2	Smarca5	FC	transcription
3	Supt16h	FC	
4	Mybbp1a	Nucleoli	
5	Top1	FC	rDNA topology, rDNA
6	Top2a	Nucleoli	transcription
7	Fbl	FC, DFC	rRNA processing
8	Nop56	FC	
9	Nop58	FC, Nucleoli	
10	Ftsj3	Nucleoli rim, Nucleoli	
11	Rrp5	Nucleoli rim	
12	Hmgb2	Nucleoli	Chromatin organization
13	Lbr	Nucleoli rim	
14	Ddx21	Nucleoli rim, Nucleoli	rDNA transcription, rRNA
15	Ddx5	Nucleoli	processing
16	Ddx18	Nucleoli rim, Nucleoli	rRNA processing,
17	Npm1	Nucleoli rim, Nucleoli	ribosome biogenesis
18	Ncl	Nucleoli rim, Nucleoli	
19	Rpl13	Nucleoli	Nucleolar structure,
20	Rpl13a	Nucleoli	ribosome biogenesis
21	Rpl4	Nucleoli	
22	Rpl40	Nucleoli	
23	Rpl7	Nucleoli	
24	Rpl7a	Nucleoli	
25	Rpl18a	Nucleoli	
26	Rpl26	Nucleoli	

27	Rpl27	Nucleoli	
28	Rpl22	Nucleoli	
29	Rpl5	Nucleoli rim, Nucleoli	
30	Rps6	Nucleoli	Ribosome biogenesis
31	Rps25	Nucleoli	
32	Rps27a	Nucleoli	
33	Ddx18	Nucleoli rim, Nucleoli	rRNA processing,
34	Ddx56	Nucleoli	nucleolar structure
35	Nono	FC, Nucleoli	DNA damage response at
			rDNA

Table S2: List of nucleolar proteins interacting with PC4.

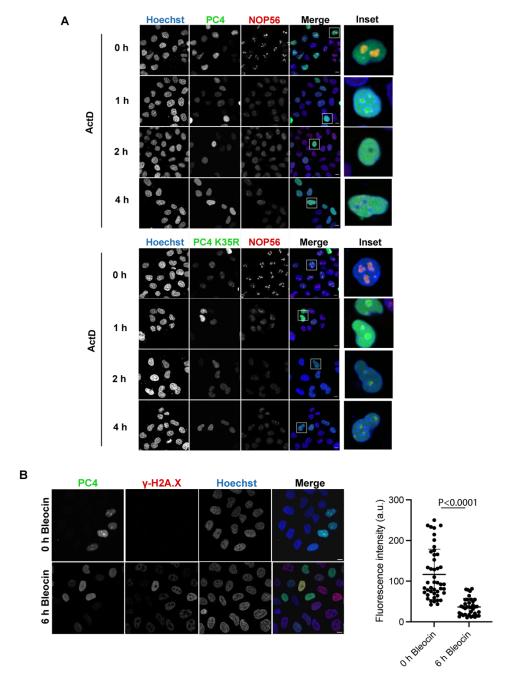


Figure S1. Time-dependent dynamics of PC4 and NOP56 under ActD treatment. A. Sub-cellular localization of WT PC4 (green) and NOP65 (red) under ActD treatment of 0, 1, 2, and 4 hours (h) duration. N=1. B. PC4-GFP (green) and γ -H2A (red) localization upon 5 μ M Bleocin treatment for 6 h. Nucleolar fluorescence intensities were plotted in the graph alongside. DMSO control, n=45, Bleocin, n=37. Unpaired t-test was performed. N=3. Scale bar = 10 μ m.

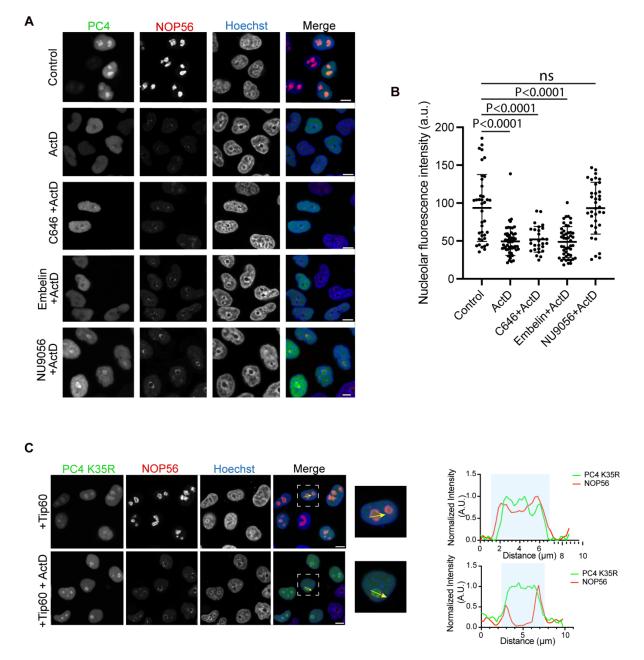


Figure S2. Tip60-mediated acetylation of PC4 on K35R determines its subnuclear localization. A. Subcellular localization of PC4 (green) and Nop56 (red) in HeLa cells treated with10 μM C646 for 2h, 20 μM Embelin for 24 h, or 10 μM NU9056 for 6 h in addition to ActD treatment. Nuclei was counterstained with Hoechst (blue). B. Graphical representation of the nucleolar intensities of control cells (n=39 nucleoli in 22 cells) or cells treated with ActD (n=55 nucleoli in 31 cells), C646+ ActD (n=28 in 20 cells), Embelin+ActD (n=48 nucleoli in 33 cells), or ActD+NU9056 (n=36 nucleoli in 26 cells).

N=2. PC4 K35R (green) and Nop56 (red) subnuclear localization in cells overexpressing Tip60 with or without ActD. Nuclei was counterstained with Hoechst (blue). Line plots across the yellow arrows were plotted to show the colocalization between PC4 and Nop56 nucleolar protein. The nucleolar regions are shaded in blue. N=1. Scale bar = $10 \mu m$.

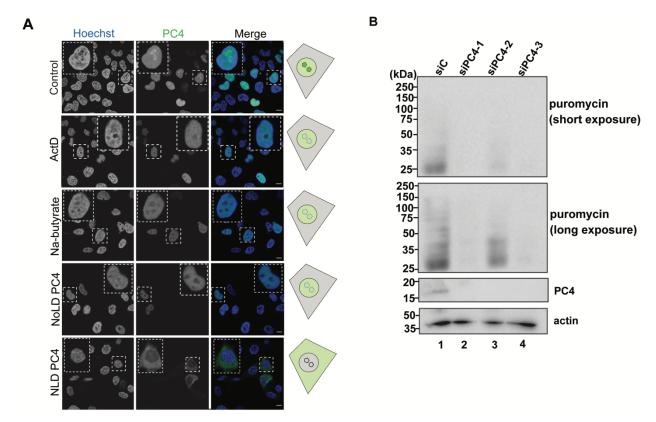


Figure S3: Loss of nucleolar PC4 leads to abrogation of protein synthesis. A. Subcellular localization of WT PC4 and the PC4 localization mutants (nucleolar localization defective mutant (NoLD), and nuclear localization defective mutant (NLD)). PC4 tagged with GFP and DNA were stained green and blue respectively in the merged images. Scale bar = $10 \mu m$. N=3. Scale bar = $10 \mu m$. B. Western blotting analysis of puromycin labelling assay performed on Hela cells following siRNA knockdown of PC4. siRNA against a scrambled sequence was used a control. N=2.

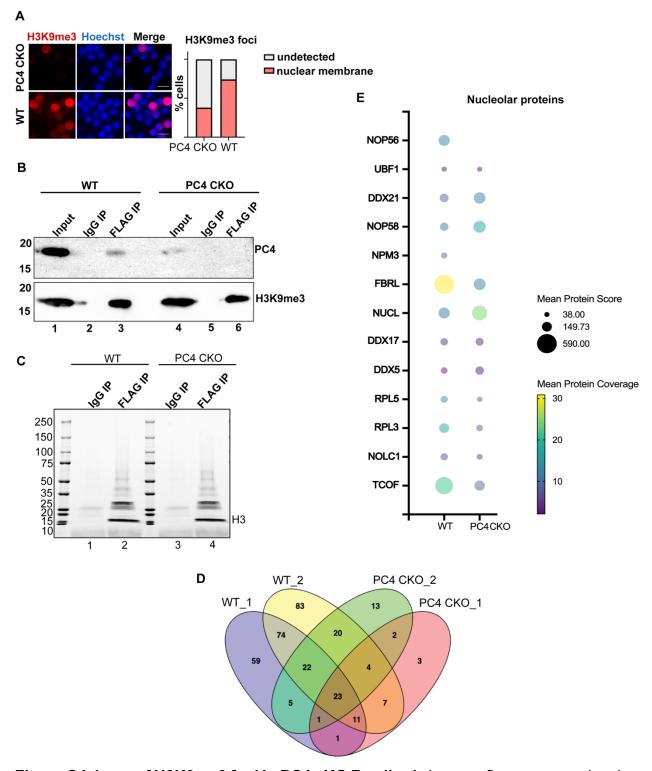
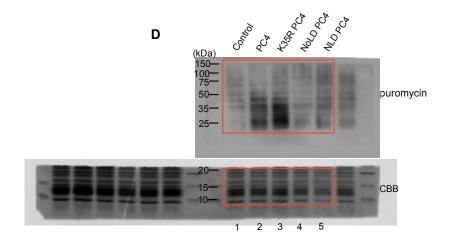
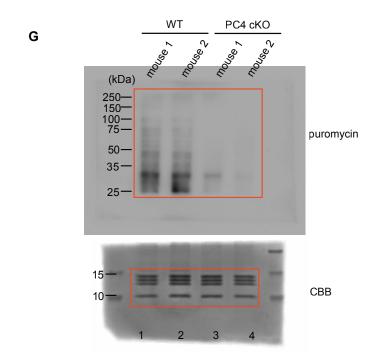


Figure S4. Loss of H3K9me3 foci in PC4 cKO B cells. A. Immunofluorescence showing H3K9me3 foci (red) in WT and PC4 cKO B cells. The nuclei were counterstained with Hoechst (blue). B. Western blotting analysis of H3K9me3 IP in WT and PC4 cKO B cells. C. Protein profile of the H3K9me3 IP in WT and cKO B cells. D. Venn diagram

representing the proteins identified in the H3K9me3 IP. E. Graphical representation of the mean protein score and protein coverage of nucleolar proteins present in the H3K9me3 IP from WT and PC4 cKO B cells. Data from N=3 independent biological repeats.

Uncropped blots and gel Figure 3





Uncropped blots Figure S3

