

advances.sciencemag.org/cgi/content/full/7/1/eabb5414/DC1

## Supplementary Materials for

# Fanconi anemia A protein participates in nucleolar homeostasis maintenance and ribosome biogenesis

Anna Gueiderikh, Frédérique Maczkowiak-Chartois, Guillaume Rouvet, Sylvie Souquère-Besse, Sébastien Apcher, Jean-Jacques Diaz, Filippo Rosselli\*

\*Corresponding author. Email: filippo.rosselli@gustaveroussy.fr

Published 1 January 2021, *Sci. Adv.* 7, eabb5414 (2021) DOI: 10.1126/sciadv.abb5414

#### This PDF file includes:

Figs. S1 to S3 Tables S1 to S5 References







**SiFANCA1** 

siFANCA2

SiFANCA

siFANCA3







¥

<sup>-/-</sup>ɛɔuɛヲ

siFANCG

4

ი

2

0

N° of nucleoli per cell



DAPI





\*\*

\*



FANCA

L

Vinculin FBL

NCL

SiLacZ

# Supplementary Figure S1: Nucleolar abnormalities in FANC pathway-deficient cells.

**A.** Confocal microscopy images showing wide fields of HeLa cells after transfection with untargeted (siLacZ) or FANCA-targeted siRNAs stained with antibodies against the nucleolar proteins UBF (Red) and FBL (Green) and counterstained with DAPI to visualize DNA

**B.** Confocal microscopy images showing wide fields of HeLa cells after transfection with untargeted (siLacZ) or FANCA-targeted siRNAs stained with antibodies against the nucleolar protein NPM1 (yellow) counterstained with DAPI to visualize DNA.

**C.** Confocal microscopy images showing single HeLa cells after transfection with untargeted (siLacZ), FANCA- or FANCD2-targeted siRNAs stained with antibodies against the nucleolar protein FBL (Green) and counterstained with DAPI to visualize DNA.

**D.** Western blot showing the consequence of FANCA or FANCD2 siRNA-mediated depletion in HeLa or U2OS cells 72 h after transfection on FANCA, FANCD2, NPM1, NCL and FBL expression. Vinculin was utilized as a loading control.

**E.** Percentage of cells showing 1, 2 or more nucleoli as a function of FANCA expression in HeLa (top panel) or U2OS (bottom panel) cells. Bars represent the means of 3 independent experiments +/- sem.

**F.** Immunofluorescence microscopy images showing wide fields of HeLa cells 72 h after transfection with untargeted (siLacZ) or one of the three siFANCA1 to siFANCA3 siRNAs that were pooled are shown in Fig. 1a. Cells were stained with antibodies against the nucleolar proteins NCL (Red) and FBL (Green) and counterstained with DAPI to visualize DNA. Top : WB illustrating the shutdown of FANCA expression induced by each single siRNA is shown. Vinculin was utilized as a loading control. Bars represent the means of 3 independent experiments +/- sem. **G and H.** Percentage of HeLa (G) or U2OS (H) cells presenting nucleolar abnormalities (a round or cap-like shape) following transfection with the indicated siRNA. The presented data originate from an independent set of experiments that are presented in Figure 1.

I. Western blots showing the expression of FANCA in human primary fibroblasts.

J. Immunofluorescence microscopy images showing single nuclei of mouse primary fibroblasts from 3- to 5-month-old WT or Fanca<sup>-/-</sup> mice stained as described above.
K. Electronic micrographs showing nucleolar morphology as observed in mouse

primary fibroblasts from WT (i) or Fanca<sup>-/-</sup> mouse fibroblasts (ii and iii). **L.** Percentage of mouse primary fibroblasts presenting canonical nucleolar merphology (irregular shape) or a round or can like shape. Analyzes of fibrobl

morphology (irregular shape) or a round or cap-like shape. Analyses of fibroblasts isolated from two WT and two Fanca<sup>-/-</sup> mice are reported.



# Supplementary Figure S2: rDNA transcription and rRNA processing in FANC pathway-deficient cells.

**A.** Representative experiments showing precursor and mature rRNAs. After 72 h of siRNA transfection, HeLa cells were labelled for 20 min with <sup>32</sup>P-orthophosphate and chased with cold orthophosphate for 1, 2, 3 and 6 h. The EtBr-stained gel is shown at the bottom as a loading control. Bottom, relative level of different rRNA forms in siFANCA- or FANCD2-transfected cells normalized vs the FANC proficient cells settled to 1 each time.

**B.** Example of FACS analysis measuring the level of EU incorporation into cells following 15 min of incubation. The black line represents the profile of HeLa cells transfected with an untargeted siRNA, and the red line shows the profile of HeLa cells 72 h following transfection with siRNAs targeting FANCA.



### Supplementary Figure S3: FANCA partnership in ribosome biogenesis.

**A.** Western blot illustrating that FANCG and NCL proteins coimmunoprecipitate with FANCA in FANCC-deficient and FANCC-proficient human lymphoblasts issued from an FA patient.

**B.** Example FACS analysis measuring the level of OP-puro incorporation into cells following 30 min of incubation. The black line on the left represents the profile of unstained FANC proficient (HSC93) cells.

**C.** Western blot illustrating that FANCA coimmunoprecipitates NCL, NPM1 and RPL18 in HSC93 FANC pathway-proficient lymphoblasts. Two different IPs (IP1 and IP2) realized at one week intervals are reported.

## Supplemetary Table 1: list of the cell lines used.

Cell line	Cell type	FANC pathway stauts	Origin	Research Resource Identifier (RRID)	
HeLa	Human papillomavirus- adenocarcinoma	WT	In house and ATCC	CVCL_0030	
U2OS	Osteosarcoma	WT	In house and ATCC	CVCL_0042	
HEK293	Human embryonic kidney	WT	In house	CVCL_0045	
HSC93	EBV-immortalized lymphoblasts	WT	Gift of M. Buchwald lab, received in the 90s	CVCL_G049	
HSC72	EBV-immortalized lymphoblasts	FANCA Homozygous Ex18-28del	Gift of M. Buchwald lab, received in the 90s & Coriell Repository	CVCL_AK37	
HSC99	EBV-immortalized lymphoblasts	Not determined	Gift of M. Buchwald lab, received in the 90s	CVCL_G050)	
HSC536	EBV-immortalized lymphoblasts	FANCC <sup>-/-</sup> p.Leu554Pro (c.1661T>C); ?	Gift of M. Buchwald lab, received in the 90s & Coriell Repository	CVCL_G045	
HSC72CORR	EBV-immortalized lymphoblasts	FANCA <sup>-/-</sup> +FANCA	Gift of M. Buchwald lab, received in the 90s	#	
HSC536CORR	EBV-immortalized lymphoblasts	FANCC <sup>-/-</sup> +FANCC	Gift of M. Buchwald lab, received in the 90s	#	
EGF004	EBV-immortalized lymphoblasts	FANCG ≁	Gift of J Soulier lab	#	
EGF070	EBV-immortalized lymphoblasts	FANCG ≁	Gift of J Soulier lab	#	
MRC5	Human primary fibroblasts	WT	In house	CVCL_0440	
MRC5-SV	SV40-immortalized fibroblasts	WT	In house	#	
GM03657	EBV-immortalized lymphoblasts	WT	Coriell Repository	CVCL_7398	
GM03348	Human primary fibroblasts	WT	Coriell Repository	CVCL_7382	
GM03652	Human primary fibroblasts	WT	Coriell Repository	CVCL_7397	
GM05757	Human primary fibroblasts	WT	Coriell Repository	CVCL_7437	
GM16754	Human primary fibroblasts	FANCC -/-	Coriell Repository	CVCL_AK43	
GM00449	Human primary fibroblasts	FANCC <sup>-/-</sup> Homozygous c.456+4A>T (IVS4+4A>T)	Coriell Repository	CVCL_F125	
GM02361	Human primary fibroblasts	FANCG <sup>-/-</sup>	Coriell Repository	CVCL_AK22	
GM13136	Human GM00449- SV40-immortalized fibroblasts	FANCC <sup>-≁</sup> Homozygous c.456+4A>T (IVS4+4A>T)	Coriell Repository	CVCL_F126	
GM16635	Human GM00449- SV40-immortalized fibroblasts	FANCG <sup>≁</sup>	Coriell Repository	CVCL_F634	
AS911	Human primary fibroblasts	WT	Gift of A. Sarasin lab	#	
PD352	Human primary fibroblasts	FANCG	In house	#	
EGF47	Human primary fibroblasts	FANCA <sup>-/-</sup> 1263-1264del; ?	Gift of J Soulier lab	#	
EGF47CORR	Human primary fibroblasts	FANCA <sup>-/-</sup> +FANCA	Gift of J Soulier lab	#	
EGF56	Human primary fibroblasts	FANCA <sup>-/-</sup> L1305D; V372fs	Gift of J Soulier lab	#	
EGF56CORR	Human primary fibroblasts	FANCA <sup>-/-</sup> +FANCA	Gift of J Soulier lab	#	
EGF71	Human primary fibroblasts	FANCA <sup>-/-</sup> S725fs; F1306fs	Gift of J Soulier lab	#	
EGF71CORR	Human primary fibroblasts	FANCA <sup>-/-</sup> +FANCA	Gift of J Soulier lab	#	
EGF72	Human primary fibroblasts	FANCA <sup>-/-</sup> S1187fs; ?	Gift of J Soulier lab	#	
EGF72CORR	Human primary fibroblasts	FANCA <sup>-/-</sup> + <i>FANCA</i>	Gift of J Soulier lab	#	
Mouse Primary Fibroblasts			In house	#	

Supplemetary Table 2: list of used siRNA.

GENE	SEQUENCE	SEQUENCE CODE
LACZ	CGUCGACGGAAUACUUCGA	#
	GUACAGCAGCAAUUUCUUA	FANCA1
FANCA	GAUCGUGGCUCUUCAGGAA	FANCA2
	GGACAUCACUGCCCACUUC	FANCA3
	GGAGAUUGAUGGUCUACUA	FANCD2_1
FANCD2	AACAGCCAUGGAUACACUUGATT	FANCD2_2
	CAGAGUUUGCUUCACUCUCUA	FANCD2_3
	GAGAGAAUCAUCUUAAUGG	FANCC_1
FANCC	GGAAUCGUCUUGGCAUUGA	FANCC_2
	GGUAUGCACCUAUAGAUUA	FANCC_3
FANCE	UGCUUCACCAUCAUUAGGAAU	FANCG_1
FANCG	CCUGUGAAAUUUGCCCUAGUU	FANCG_2
ATM	ATM1-492 (Invitrogen)	#
ATR	HSS100876, HSS10877, HSS878 (Invitrogen)	#

## Supplemetary Table 3: list of antibodies used:

Antibody target	Supplier	Code N°	Specie	WB dilution	IF dilution	CHIP	IP
Alexa-Fluor Secondary Antibodies	Life Technologies		D		1:1000		
FANCA	Bethyl	A301-980A	R	1:1000			х
FANCA	FARF	FANCA-1	R	1:1000			
FANCA	Abcam	ab97578	R	1:1000			х
FANCA	R&D	AF6026	G	1 :500			
FANCA	Cell Signalling	#14657	R	1 :1000			х
FANCC	FARF	FANCC-2	R	1:1000			
FANCG	Santa Cruz	sc-393382	М	1 :500			х
FANCD2	Novus	NB100-182	R			4µg	
FANCD2	Abcam	Ab2187	R	1:1000			
FANCD2 (FI17)	Santa Cruz	sc-20022	М	1:1000			
Fibrillarin	Abcam	ab5821	R	1:1000	1:2000		
G4s- (clone1H6)	Merck	MABE	М		1:200		
H2AX	Abcam	ab11175	R	1:1000			
γH2AX (JBW301)	Millipore	05-636	М	1:1000	1:2000		
H3K9me3 (6F12- H4)	Millipore	05-12432	м			4µg	
H3K4me3	Active motif	#61379	М			4µg	
Lamin A/C	Santa Cruz	sc-7292	М	1:1000			
NPM1 (FC61991)	Thermo Fisher	32-5200	М	1:1000	1:500		Х
Nucleolin (4E2)	Abcam	ab13541	М		1:4000		Х
RNAPoll	Abcam	ab101977	R			4µg	
S9.6	P. Pasero's team		М		1:200		
UBF (F9)	Santa Cruz	sc-13125	М	1:1000	1:250		
Vinculin (spm227)	Abcam	ab18058	м	1:4000			
EIF4E2	Abcam	ab238519	R	1:1000			
EIF6	Abcam	ab245532	R	1:1000			
RPL18	Novus	NBP2-13251	R	1 :500			
RPL5	Bethyl	A303-933AM	R	1:1000			
lgG1	Dako	X0931	М			4µg	Х
IGg	Dako	XO903	R				Х
lgG	Cell Signalling	#3900	R				х

FARF: Fanconi Anemia Research Found; R: Rat; M: Mouse; D: Donkey; G: Goat

### Supplemetary Table 4: Northern blot probe used.

Name	Sequence	Position in
		gene
		Genbank
		accession
		#U13369
5'ETS1b	5'-AGACGAGAACGCCTGACACGCACGGCAC-3'	297 to 324

### Supplemetary Table 5: list of the ChIP-qPCR primers used.

Name	Forward	Reverse	Efficiency (10 <sup>(-1/slope)</sup> -1)	Elongation T°	Position
H1	GGCGGTTTGAGTGAGACGAGA	ACGTGCGCTCA2CCGAGAGCAG	0,95	58°	952-1030
H8	AGTCGGGTTGCTTGGGAATGC	CCCTTACGGTACTTGTTGACT	0,90	58°	8204-8300
H27	CCTTCCACGAGAGTGAGAAGCG	CTCGACCTCCCGAAATCGTACA	1,11	58°	27366-27477
H42.9	CCCGGGGGGAGGTATATCTTT	CCAACCTCTCCGACGACA	1,05	58°	42943 to 33

Primers pairs were as in (64).

#### **REFERENCES AND NOTES**

- 1. M. Tsekrekou, K. Stratigi, G. Chatzinikolaou, The nucleolus: In genome maintenance and repair. *Int. J. Mol. Sci.* **18**, 1411 (2017).
- 2. S. Boulon, B. J. Westman, S. Hutten, F.-M. Boisvert, A. I. Lamond, The nucleolus under stress. *Mol. Cell* **40**, 216–227 (2010).
- J. M. Liu, S. R. Ellis, Ribosomes and marrow failure: Coincidental association or molecular paradigm? *Blood* 107, 4583–4588 (2006).
- 4. D. Ruggero, A. Shimamura, Marrow failure: A window into ribosome biology. *Blood* **124**, 2784–2792 (2014).
- 5. M. Bogliolo, J. Surrallés, Fanconi anemia: A model disease for studies on human genetics and advanced therapeutics. *Curr. Opin. Genet. Dev.* **33**, 32–40 (2015).
- 6. R. Ceccaldi, P. Sarangi, A. D. D'Andrea, The Fanconi anaemia pathway: New players and new functions. *Nat. Rev. Mol. Cell Biol.* **17**, 337–349 (2016).
- 7. A. Gueiderikh, F. Rosselli, J. B. C. Neto, A never-ending story: The steadily growing family of the FA and FA-like genes. *Genet. Mol. Biol.* **40**, 398–407 (2017).
- R. Ceccaldi, K. Parmar, E. Mouly, M. Delord, J. M. Kim, M. Regairaz, M. Pla, N. Vasquez, Q. S. Zhang, C. Pondarre, R. Peffault de Latour, E. Gluckman, M. Cavazzana-Calvo, T. Leblanc, J. Larghero, M. Grompe, G. Socie, A. D. D'Andrea, J. Soulier, Bone marrow failure in Fanconi anemia is triggered by an exacerbated p53/p21 DNA damage response that impairs hematopoietic stem and progenitor cells. *Cell Stem Cell* 11, 36–49 (2012).
- D. Walter, A. Lier, A. Geiselhart, F. B. Thalheimer, S. Huntscha, M. C. Sobotta, B. Moehrle, D. Brocks, I. Bayindir, P. Kaschutnig, K. Muedder, C. Klein, A. Jauch, T. Schroeder, H. Geiger, T. P. Dick, T. Holland-Letz, P. Schmezer, S. W. Lane, M. A. Rieger, M. A. G. Essers, D. A. Williams, A. Trumpp, M. D. Milsom, Exit from dormancy provokes DNAdamage-induced attrition in haematopoietic stem cells. *Nature* 520, 549–552 (2015).
- I. V. Rosado, F. Langevin, G. P. Crossan, M. Takata, K. J. Patel, Formaldehyde catabolism is essential in cells deficient for the Fanconi anemia DNA-repair pathway. *Nat. Struct. Mol. Biol.* 18, 1432–1434 (2011).
- 11. F. Langevin, G. P. Crossan, I. V. Rosado, M. J. Arends, K. J. Patel, Fancd2 counteracts the toxic effects of naturally produced aldehydes in mice. *Nature* **475**, 53–58 (2011).
- S. van Twest, V. J. Murphy, C. Hodson, W. Tan, P. Swuec, J. J. O'Rourke, J. Heierhorst, W. Crismani, A. J. Deans, Mechanism of ubiquitination and deubiquitination in the Fanconi anemia pathway. *Mol. Cell* 65, 247–259 (2017).

- D. Adachi, T. Oda, H. Yagasaki, K. Nakasato, T. Taniguchi, A. D. D'Andrea, S. Asano, T. Yamashita, Heterogeneous activation of the Fanconi anemia pathway by patient-derived FANCA mutants. *Hum. Mol. Genet.* 11, 3125–3134 (2002).
- 14. M. Nepal, C. Ma, G. Xie, W. Jia, P. Fei, Fanconi anemia complementation group C protein in metabolic disorders. *Aging* **10**, 1506–1522 (2018).
- 15. A. Benitez, W. Liu, A. Palovcak, G. Wang, J. Moon, K. An, A. Kim, K. Zheng, Y. Zhang, F. Bai, A. V. Mazin, X. H. Pei, F. Yuan, Y. Zhang, FANCA promotes DNA double-strand break repair by catalyzing single-strand annealing and strand exchange. *Mol. Cell* **71**, 621–628.e4 (2018).
- 16. T. Kaddar, M. Carreau, Fanconi anemia proteins and their interacting partners: A molecular puzzle. *Anemia* **2012**, 425814 (2012).
- D. Briot, G. Mace-Aime, F. Subra, F. Rosselli, Aberrant activation of stress-response pathways leads to TNF-alpha oversecretion in Fanconi anemia. *Blood* 111, 1913–1923 (2008).
- F. Rosselli, J. Sanceau, E. Gluckman, J. Wietzerbin, E. Moustacchi, Abnormal lymphokine production: A novel feature of the genetic disease Fanconi anemia. II. In vitro and in vivo spontaneous overproduction of tumor necrosis factor alpha. *Blood* 83, 1216–1225 (1994).
- A. Oppezzo, J. Bourseguin, E. Renaud, P. Pawlikowska, F. Rosselli, Microphthalmia transcription factor expression contributes to bone marrow failure in Fanconi anemia. *J. Clin. Invest.* 130, 1377–1391 (2020).
- 20. H. Zhang, D. E. Kozono, K. W. O'Connor, S. Vidal-Cardenas, A. Rousseau, A. Hamilton, L. Moreau, E. F. Gaudiano, J. Greenberger, G. Bagby, J. Soulier, M. Grompe, K. Parmar, A. D. D'Andrea, TGF-beta inhibition rescues hematopoietic stem cell defects and bone marrow failure in Fanconi anemia. *Cell Stem Cell* 18, 668–681 (2016).
- A. Epanchintsev, P. Shyamsunder, R. S. Verma, A. Lyakhovich, IL-6, IL-8, MMP-2, MMP-9 are overexpressed in Fanconi anemia cells through a NF-kappaB/TNF-alpha dependent mechanism. *Mol. Carcinog.* 54, 1686–1699 (2015).
- 22. N. Matsushita, Y. Endo, K. Sato, H. Kurumizaka, T. Yamashita, M. Takata, S. Yanagi, Direct inhibition of TNF-alpha promoter activity by Fanconi anemia protein FANCD2. *PLOS ONE* 6, e23324 (2011).
- R. Zanier, D. Briot, J. A. Dugas du Villard, A. Sarasin, F. Rosselli, Fanconi anemia C gene product regulates expression of genes involved in differentiation and inflammation. *Oncogene* 23, 5004–5013 (2004).

- 24. M. Moriel-Carretero, S. Ovejero, M. Gerus-Durand, D. Vryzas, A. Constantinou, Fanconi anemia FANCD2 and FANCI proteins regulate the nuclear dynamics of splicing factors. *J. Cell Biol.* **216**, 4007–4026 (2017).
- 25. W. Du, Z. Adam, R. Rani, X. Zhang, Q. Pang, Oxidative stress in Fanconi anemia hematopoiesis and disease progression. *Antioxid. Redox Signal.* **10**, 1909–1921 (2008).
- 26. G. Pagano, A. A. Talamanca, G. Castello, M. d'Ischia, F. V. Pallardo, S. Petrovic, B. Porto, L. Tiano, A. Zatterale, From clinical description, to in vitro and animal studies, and backward to patients: Oxidative stress and mitochondrial dysfunction in Fanconi anemia. *Free Radic. Biol. Med.* 58, 118–125 (2013).
- G. Pagano, P. Degan, M. d'Ischia, F. J. Kelly, B. Nobili, F. V. Pallardo, H. Youssoufian, A. Zatterale, Oxidative stress as a multiple effector in Fanconi anaemia clinical phenotype. *Eur. J. Haematol.* **75**, 93–100 (2005).
- 28. R. A. Schwab, J. Nieminuszczy, F. Shah, J. Langton, D. Lopez Martinez, C. C. Liang, M. A. Cohn, R. J. Gibbons, A. J. Deans, W. Niedzwiedz, The Fanconi anemia pathway maintains genome stability by coordinating replication and transcription. *Mol. Cell* **60**, 351–361 (2015).
- M. Kruhlak, E. E. Crouch, M. Orlov, C. Montano, S. A. Gorski, A. Nussenzweig, T. Misteli, R. D. Phair, R. Casellas, The ATM repair pathway inhibits RNA polymerase I transcription in response to chromosome breaks. *Nature* 447, 730–734 (2007).
- 30. M. van Sluis, B. McStay, A localized nucleolar DNA damage response facilitates recruitment of the homology-directed repair machinery independent of cell cycle stage. *Genes Dev.* **29**, 1151–1163 (2015).
- 31. G. R. Kidiyoor, A. Kumar, M. Foiani, ATR-mediated regulation of nuclear and cellular plasticity. *DNA Repair* 44, 143–150 (2016).
- 32. D. O. Warmerdam, J. van den Berg, R. H. Medema, Breaks in the 45S rDNA lead to recombination-mediated loss of repeats. *Cell Rep.* **14**, 2519–2527 (2016).
- 33. H. Ma, T. Pederson, The nucleolus stress response is coupled to an ATR-Chk1-mediated G2 arrest. *Mol. Biol. Cell* **24**, 1334–1342 (2013).
- 34. R. D. Kennedy, C. C. Chen, P. Stuckert, E. M. Archila, M. A. De la Vega, L. A. Moreau, A. Shimamura, A. D. D'Andrea, Fanconi anemia pathway-deficient tumor cells are hypersensitive to inhibition of ataxia telangiectasia mutated. *J. Clin. Invest.* **117**, 1440–1449 (2007).
- 35. J. H. Guervilly, G. Mace-Aime, F. Rosselli, Loss of CHK1 function impedes DNA damageinduced FANCD2 monoubiquitination but normalizes the abnormal G2 arrest in Fanconi anemia. *Hum. Mol. Genet.* 17, 679–689 (2008).

- 36. M. L. Garcia-Rubio, C. Perez-Calero, S. I. Barroso, E. Tumini, E. Herrera-Moyano, I. V. Rosado, A. Aguilera, The Fanconi anemia pathway protects genome integrity from R-loops. *PLOS Genet.* **11**, e1005674 (2015).
- 37. C. Y. Jao, A. Salic, Exploring RNA transcription and turnover in vivo by using click chemistry. *Proc. Natl. Acad. Sci. U.S.A.* **105**, 15779–15784 (2008).
- 38. A. Cammas, S. Millevoi, RNA G-quadruplexes: Emerging mechanisms in disease. *Nucleic Acids Res.* **45**, 1584–1595 (2017).
- 39. D. Rhodes, H. J. Lipps, G-quadruplexes and their regulatory roles in biology. *Nucleic Acids Res.* **43**, 8627–8637 (2015).
- 40. P. Richard, J. L. Manley, R Loops and links to human disease. *J. Mol. Biol.* **429**, 3168–3180 (2016).
- 41. J. M. Santos-Pereira, A. Aguilera, R loops: New modulators of genome dynamics and function. *Nat. Rev. Genet.* **16**, 583–597 (2015).
- 42. A. C. Hall, L. A. Ostrowski, V. Pietrobon, K. Mekhail, Repetitive DNA loci and their modulation by the non-canonical nucleic acid structures R-loops and G-quadruplexes. *Nucleus* **8**, 162–181 (2017).
- 43. F. Yuan, L. Qian, X. Zhao, J. Y. Liu, L. Song, G. D'Urso, C. Jain, Y. Zhang, Fanconi anemia complementation group A (FANCA) protein has intrinsic affinity for nucleic acids with preference for single-stranded forms. *J. Biol. Chem.* **287**, 4800–4807 (2012).
- 44. H. Chasse, S. Boulben, V. Costache, P. Cormier, J. Morales, Analysis of translation using polysome profiling. *Nucleic Acids Res.* **45**, e15 (2017).
- 45. B. Falini, N. Bolli, A. Liso, M. P. Martelli, R. Mannucci, S. Pileri, I. Nicoletti, Altered nucleophosmin transport in acute myeloid leukaemia with mutated NPM1: Molecular basis and clinical implications. *Leukemia* **23**, 1731–1743 (2009).
- 46. B. Falini, N. Bolli, J. Shan, M. P. Martelli, A. Liso, A. Pucciarini, B. Bigerna, L. Pasqualucci, R. Mannucci, R. Rosati, P. Gorello, D. Diverio, G. Roti, E. Tiacci, G. Cazzaniga, A. Biondi, S. Schnittger, T. Haferlach, W. Hiddemann, M. F. Martelli, W. Gu, C. Mecucci, I. Nicoletti, Both carboxy-terminus NES motif and mutated tryptophan(s) are crucial for aberrant nuclear export of nucleophosmin leukemic mutants in NPMc+ AML. *Blood* 107, 4514–4523 (2006).
- 47. N. Bolli, I. Nicoletti, M. F. De Marco, B. Bigerna, A. Pucciarini, R. Mannucci, M. P. Martelli, A. Liso, C. Mecucci, F. Fabbiano, M. F. Martelli, B. R. Henderson, B. Falini, Born to be exported: COOH-terminal nuclear export signals of different strength ensure

cytoplasmic accumulation of nucleophosmin leukemic mutants. *Cancer Res.* **67**, 6230–6237 (2007).

- 48. W. Du, J. Li, J. Sipple, J. Chen, Q. Pang, Cytoplasmic FANCA-FANCC complex interacts and stabilizes the cytoplasm-dislocalized leukemic nucleophosmin protein (NPMc). *J. Biol. Chem.* **285**, 37436–37444 (2010).
- 49. B. Falini, C. Mecucci, E. Tiacci, M. Alcalay, R. Rosati, L. Pasqualucci, R. La Starza, D. Diverio, E. Colombo, A. Santucci, B. Bigerna, R. Pacini, A. Pucciarini, A. Liso, M. Vignetti, P. Fazi, N. Meani, V. Pettirossi, G. Saglio, F. Mandelli, F. Lo-Coco, P. G. Pelicci, M. F. Martelli; GIMEMA Acute Leukemia Working Party, Cytoplasmic nucleophosmin in acute myelogenous leukemia with a normal karyotype. *N. Engl. J. Med.* 352, 254–266 (2005).
- 50. N. Meani, M. Alcalay, Role of nucleophosmin in acute myeloid leukemia. *Expert Rev. Anticancer Ther.* **9**, 1283–1294 (2009).
- 51. G. D. Bailey, H. M. H. Qutob, A. Akhtar, N. H. Russell, C. H. Seedhouse, DNA damage corrects the aberrant cytoplasmic localisation of nucleophosmin in NPM1 mutated acute myeloid leukaemia. *Br. J. Haematol.* **186**, 343–347 (2019).
- 52. N. B. Collins, J. B. Wilson, T. Bush, A. Thomashevski, K. J. Roberts, N. J. Jones, G. M. Kupfer, ATR-dependent phosphorylation of FANCA on serine 1449 after DNA damage is important for FA pathway function. *Blood* **113**, 2181–2190 (2009).
- 53. T. Taniguchi, I. Garcia-Higuera, B. Xu, P. R. Andreassen, R. C. Gregory, S. T. Kim, W. S. Lane, M. B. Kastan, A. D. D'Andrea, Convergence of the fanconi anemia and ataxia telangiectasia signaling pathways. *Cell* 109, 459–472 (2002).
- 54. D. D. Scott, M. Oeffinger, Nucleolin and nucleophosmin: Nucleolar proteins with multiple functions in DNA repair. *Biochem. Cell Biol.* **94**, 419–432 (2016).
- 55. Y. Zhang, A. C. Duc, S. Rao, X. L. Sun, A. N. Bilbee, M. Rhodes, Q. Li, D. J. Kappes, J. Rhodes, D. L. Wiest, Control of hematopoietic stem cell emergence by antagonistic functions of ribosomal protein paralogs. *Dev. Cell* 24, 411–425 (2013).
- 56. A. J. Finch, C. Hilcenko, N. Basse, L. F. Drynan, B. Goyenechea, T. F. Menne, A. Gonzalez Fernandez, P. Simpson, C. S. D'Santos, M. J. Arends, J. Donadieu, C. Bellanne-Chantelot, M. Costanzo, C. Boone, A. N. McKenzie, S. M. Freund, A. J. Warren, Uncoupling of GTP hydrolysis from eIF6 release on the ribosome causes Shwachman-Diamond syndrome. *Genes Dev.* 25, 917–929 (2011).
- 57. S. Tan, L. Kermasson, A. Hoslin, P. Jaako, A. Faille, A. Acevedo-Arozena, E. Lengline, D. Ranta, M. Poiree, O. Fenneteau, H. Ducou le Pointe, S. Fumagalli, B. Beaupain, P. Nitschke, C. Bole-Feysot, J. P. de Villartay, C. Bellanne-Chantelot, J. Donadieu, C. Kannengiesser, A.

J. Warren, P. Revy, EFL1 mutations impair eIF6 release to cause Shwachman-Diamond syndrome. *Blood* **134**, 277–290 (2019).

- 58. O. Haimov, U. Sehrawat, A. Tamarkin-Ben Harush, A. Bahat, A. Uzonyi, A. Will, H. Hiraishi, K. Asano, R. Dikstein, Dynamic interaction of eukaryotic initiation factor 4G1 (eIF4G1) with eIF4E and eIF1 underlies scanning-dependent and -independent translation. *Mol. Cell. Biol.* 38, e00139-18 (2018).
- 59. M. Badura, S. Braunstein, J. Zavadil, R. J. Schneider, DNA damage and eIF4G1 in breast cancer cells reprogram translation for survival and DNA repair mRNAs. *Proc. Natl. Acad. Sci. U.S.A.* **109**, 18767–18772 (2012).
- 60. Z. Liang, F. Liang, Y. Teng, X. Chen, J. Liu, S. Longerich, T. Rao, A. M. Green, N. B. Collins, Y. Xiong, L. Lan, P. Sung, G. M. Kupfer, Binding of FANCI-FANCD2 complex to RNA and R-loops stimulates Robust FANCD2 monoubiquitination. *Cell Rep.* 26, 564–572.e5 (2019).
- S. B. Sondalle, S. Longerich, L. M. Ogawa, P. Sung, S. J. Baserga, Fanconi anemia protein FANCI functions in ribosome biogenesis. *Proc. Natl. Acad. Sci. U.S.A.* 116, 2561–2570 (2019).
- 62. N. T. Ingolia, G. A. Brar, S. Rouskin, A. M. McGeachy, J. S. Weissman, The ribosome profiling strategy for monitoring translation in vivo by deep sequencing of ribosome-protected mRNA fragments. *Nat. Protoc.* **7**, 1534–1550 (2012).
- V. Gandin, K. Sikstrom, T. Alain, M. Morita, S. McLaughlan, O. Larsson, I. Topisirovic, Polysome fractionation and analysis of mammalian translatomes on a genome-wide scale. *J. Vis. Exp.* 17, 51455 (2014).
- 64. C. Grandori, N. Gomez-Roman, Z.A. Felton-Edkins, C. Ngouenet, D. A. Galloway, R. N. Eisenman, R. J. White, c-Myc binds to human ribosomal DNA and stimulates transcription of rRNA genes by RNA polymerase I. *Nat. Cell Biol.* **7**, 311–318 (2005).