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Zhang, Cheng, Wang, Juan, Song, Xiaoye, Yu, Deen, Guo, Baoqiang , Pang, Yaoyu, Yin, Xiaomei, Zhao, Shasha, Deng, Huan, Zhang, Shihua and Deng, Wensheng (2023) STAT3 potentiates RNA polymerase I-directed transcription and tumor growth by activating RPA34 expression. British Journal of Cancer, 128 (5). pp. 766-782. ISSN 0007-0920

### DOI: https://doi.org/10.1038/s41416-022-02098-6

**Publisher:** Springer Nature [academic journals on nature.com]

Version: Supplemental Material

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# STAT3 potentiates RNA polymerase I-directed transcription and tumor growth by activating RPA34 expression

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**Fig. S1 Filamin A silencing reduced STAT3 expression**. **A**, Analysis of FLNA mRNA reads using the RNA-seq data of SaOS2 cells stably expressing FLNA shRNA or control shRNA. **B**, Analysis of STAT3 mRNA reads using the RNA-seq data of SaOS2 cells stably expressing FLNA shRNA or control shRNA. **C**, STAT3 protein was detected by Western blot using SaOS2 cells stably expressing FLNA shRNA or control shRNA. **C** of three biological replicates , \*\*, *P*<0.01. *P* values were obtained by Student's *t* test performed with control and treatment groups

Fig. S2



293T

37KD

J

GAPDH

К

Ctrl shRNA 1.5 STAT3 shRNA Relative expression (fold) 1.0 0.5 0.0 185 RNA 285 FRWA PresiRNA GAPOH STATS







HeLa



HeLa



Fig. S2 STAT3 knockdown reduced the synthesis of Pol I products. A and B, STAT3 siRNA transfection reduced the expression of Pol I products. SaOS2 cells were transfected with STAT3 siRNA; after 48h, cells were harvested and STAT3 expression was analyzed by Western blot (A), where Pol I products was detected by RT-qPCR (B). C and D, STAT3 siRNA transfection decreased the expression of Pol I products in HepG2 cells. STAT3 siRNA transfection was performed with HepG2; STAT3 (C) and Poll products (D) were analyzed by Western blot and RT-qPCR, respectively. E and F, STAT3 siRNA transfection decreased the expression of Pol I products in HeLa cells. STAT3 siRNA transfection was performed with HepG2; STAT3 (E) and Pol I products (F) were analyzed by Western blot and RT-qPCR, respectively. G and H, STAT3 shRNA stable expression reduced the synthesis of Pol I products in 293T cells. 293T cell lines stably expressing STAT3 shRNA or control shRNA were generated using lentiviral particles. STAT3 expression was detected by Western blot (G), where Pol I products were analyzed by RT-qPCR (H). I and J, STAT3 shRNA stable expression decreased the synthesis of Pol I products in HeLa cells. HeLa cell lines expressing STAT3 shRNA or control shRNA were generated using lentiviral particles. STAT3 expression were analyzed by Western blot (I), where Pol I products were monitored by RT-qPCR (J). K and L, Effect of STAT3 silencing on rRNA synthesis was determined by EU assays. HeLa cell lines expressing STAT3 shRNA or control shRNA were labeled by EU, and the EU-labeled cells were monitored by an EU detection kit. Images were captured under a fluorescence microscope (K). The relative fluorescence intensity for nucleoli was obtained by ImageJ software (L). The scale bars in images represent 5 µm. Each column in histograms represents the mean  $\pm$  SD of three independent experiments. \*, P<0.05; \*\*, P<0.01. P values were obtained by Student's t test performed with control and treatment groups

Fig. S3



Fig. S3 STAT3 overexpression enhanced the synthesis of Pol I products. A and B, STAT3 overexpression increased the synthesis of Pol I product in HeLa cells. A HeLa cell line stably expressing mCherry -STAT3 and its control cell line were generated by a lentiviral infection system. STAT3 protein expression and Pol I products were detected by Western blot (A) and RT-qPCR (B), respectively. C and D, STAT3 overexpression enhanced the synthesis of Pol I products in 293T cells. A 293T cell line expressing mCherry-STAT3 and its control cell line were generated as for HeLa cells. STAT3 protein expression and Pol I products were analyzed by RT-qPCR (C) and Western blot (D), respectively. E and F, EU assays showing the effect of STAT3 overexpression on rRNA synthesis was examined. A HeLa cell line expressing mCherry-STAT3 and its control cell line were labeled by EU, and the EU-labeled cells were monitored by the EU detection kit. Images were captured under a fluorescence microscope (E), and the relative fluorescence intensity for nucleoli was obtained by the ImageJ software (F). The scale bars in the images represent 5  $\mu$ m. Each column in the bar graphs represents the mean  $\pm$  SD of three independent experiments. \*, *P*<0.05; \*\*, *P*<0.01. *P* values were obtained by Student's *t* test performed with control and treatment groups

Fig. S4



Fig. S4 Cancer cell lines exhibited the increased STAT3 phosphorylation and Pol I –directed transcription compared to their normal cells. A, Qantification of Western blot data obtained from Fig 2K and other repeated assays. B and C, STAT3 expression and phosphorylation were analyzed by Western blot using HUCEC and HeLa cells. Western blot data was quantified and presented graphically in C. D, HeLa cells showed the increased Pol I-directed transcription compared to HUCEC. Each column in the bar graphs represents the mean  $\pm$  SD of three independent experiments. \*, *P*<0.05; \*\*, *P*<0.01. *P* values were obtained by Student's *t* test performed with control and treatment groups.

Fig. S5

G

Ctrl vector

dCas9-KRAB

Hoechst 33342













F

Rate of EdU positive cells (%)





В



Η



STA<sup>73</sup>entrua

CHISHRWA

**Fig. S5 STAT3 downregulation reduced cell proliferative activity . A** and **B**, STAT3 knockdown reduced HeLa cell proliferation. HeLa cell lines expressing STAT3 shRNA or control shRNA were cultured for proliferation analysis using cell counting (A) and CCK8 (B) methods. **C** and **D**, STAT3 knockdown decreased 293T cell proliferation. The 293T cell lines stably expressing STAT3 shRNA or control shRNA were cultured for proliferation analysis with cell counting (C) an CCK8 (B)methods. **E** and **F**, The effect of STAT3 knockdown on HeLa cell proliferation was analyzed by EdU assays. EdU assays were performed using HeLa cell lines expressing STAT3 shRNA or control shRNA. Images were captured under a fluorescence microscope (E), and EdU-labelled cells from the images were subjected to statistical analysis (F). The scale bars in the images represent 100  $\mu$ m. **G** and **H**, Endogenous STAT3 downregulation caused by dcas9-KRAB expression inhibited HepG2 cell proliferation. EdU assays were performed using HepG2 cells transfected with the vector expressing STAT3 promoter gRNA and dcas9-KRAB. The quantification result from EdU images (G) is presented in H. The scale bars in the images represent 100  $\mu$ m. Each point/column in histograms represents the mean  $\pm$  SD of three independent experiments. \*, *P*<0.05; \*\*, *P*<0.01. *P* values were obtained by two-way ANOVA (A-D) or Student's *t* test (F and H).

Fig. S6















F

Η











Merge

HepG2

Fig. S6 STAT3 upregulation promoted cell proliferation . A-D, STAT3 overexpression enhanced HeLa cell proliferation. A HeLa cell line expressing mCherry-STAT3 and its control cell line were cultured for proliferation analysis using cell counting (A) and CCK8 (B). C and D, STAT3 overexpression enhanced 293T cell proliferation . A 293T cell line expressing mCherry-STAT3 and its control cell line were cultured for proliferation analysis using cell counting (C) and CCK8 (D) methods. E and F, The effect of STAT3 overexpression on HeLa cell proliferation was analyzed by EdU assays. EdU assays were performed using a HeLa cell line expressing mCherry-STAT3 and its control cell line. Images were captured under a fluorescence microscope (E), and EdU-labelled cells from the images were subjected to statistical analysis (F). Scale bars in the images represent 100 μm. G and H, The effect of endogenous STAT3 upregulation on cell proliferative activity. EdU assays were performed using HepG2 cells transfected with the vectors expressing the STAT3 promoter gRNA and dcas9-VP48. Images were captured under a fluorescence microscope (G), and EdU-labelled cells from the images were subjected to statistical analysis (H). Scale bars in the images represent  $100 \,\mu m$ . Each point/column in graphs represents the mean  $\pm$  SD of three independent experiments. \*, P<0.05; \*\*, P<0.01. P values were obtained by two-way ANOVA (A-D) or Student's *t* test (F and H).

## Fig. S7











**Fig. S7 STAT3 positively regulates cell survival and growth**. **A-C**, STAT3 knockdown in HepG2 cells reduced the number of colony formation and the sizes of colonies. HepG2 cell lines expressing STAT3 shRNA or control shRNA were seeded in 6-well plates. After growing 10 days, cells were stained with 0.2% crystal violet and photographed with a camera (A). The number of colonies in each well was counted (B), and the sizes of individual colonies were obtained by calculating the area of each colony (C). The data obtained were subjected to statistical analysis. **D-F**, STAT3 overexpression in HepG2 cells increased the number of colony formation and the colony size. A HepG2 cell lines stably expressing mCherry-STAT3 and its control cell line were grown in 6-well plates. After growing 10 days, cells were stained and photographed (D). The number of colonies in each well was counted (E), and the sizes (area) of individual colonies randomly selected was calculated (F). The data obtained were subjected to statistical analysis. Each column in histograms represents the mean  $\pm$  SD of three biological replicates. \*, *P*<0.05; \*\*, *P*<0.01. *P* values were obtained Student's *t* test



**Fig. S8** Pol I-specific inhibitor represses cell proliferation and pre-rRNA synthesis. **A**, Effect of CX-5461 on the expression of pre-rRNA in HeLa cells. HeLa cells were seeded in 6-well plates and cultured in the medium containing 5  $\mu$ M CX-5461. Cells were harvested at different time points, and pre-rRNA expression was analyzed by RT-qPCR. **B**, Effect of CX-5461 on the expression of pre-rRNA in HepG2 cells. Cell culture and RT-qPCR were performed as described for A. **C**, CX-5461 inhibited the enhancement of proliferation induced by STAT3 overexpression. **D**, CX-5461 inhibited the activation of Pol I-directed transcription induced by STAT3 overexpression. Each point/column in graphs represents the mean  $\pm$  SD of three independent experiments. \*, *P*<0.05; \*\*, *P*<0.01. *P* values in C and D were obtained by two-way ANOVA



**Fig. S9 STAT3-IN-3 inhibited HeLa cell proliferation**. HeLa cells were seeded in 12-well and 96-well plates, and cell proliferative activity was assessed by cell counting **(A)** and CCK-8 **(B)** methods. Each point or column in histograms represents the mean  $\pm$  SD of three independent experiments. \*, *P*<0.05; \*\*, *P*<0.01. *P* values were obtained by two-way ANOVA.

Fig. S10



D



Fig. S10 Combination of STAT3-IN-3 and Pol I transcription inhibitors showed additive effect on HepG2 cell growth compared to the application of single drug. A and B, Effect of STAT3-IN-3 (500 nM) and BMH-21 (100 nM) on HepG2 cell growth. Cell growth was monitored by cell counting (A) and CCK8 (B) methods. C and D, Effect of STAT3-IN-3 (500 nM)and Actinomycin D (2.5 nM) on HepG2 cell growth. Cell growth was monitored by cell counting (C) and CCK8 (D) methods. E and F, Effect of STAT-IN-3 and CX-5461 on the expression of CDKN1B, caspas-3 and cleaved caspas-3. F represents the quantified result of the Western blot in E. Each point or column in histograms represents the mean  $\pm$ SD of three independent experiments. \*, *P*<0.05; \*\*, *P*<0.01. *P* values were obtained by two-way ANOVA.

Fig. S11



Fig. S11 The co-localization analysis of STAT3 and Fibrillarin in HeLa and HepG2 cells. A, The co-localization analysis between STAT3 and Fibrillarin in HeLa cells using the antibodies against STAT3 or Fibrillarin. Images were captured by a confocal fluorescence microscope. The scale bars in images represent 2.5  $\mu$ m. B, The co-localization analysis between STAT3 and Fibrillarin in HepG2 cells using the antibodies against STAT3 or Fibrillarin. Images were captured by a confocal fluorescence microscope. The scale confocal fluorescence microscope. The scale bars in HepG2 cells using the antibodies against STAT3 or Fibrillarin. Images were captured by a confocal fluorescence microscope. The scale bars in the images represent 2.5  $\mu$ m.



Α





**Fig. S12 STAT3 silencing affected expression of the genes that are related to ribosome activity in HepG2 cells. A**, Analysis of gene ontology based on the significant differential expression genes obtained from the RNA-seq data of HepG2 cell lines expressing STAT3 shRNA or control shRNA; **B**, Analysis of KEGG (Kyoto enclopedia of genes and genomes) pathways based on the significant differential expression genes obtained from the RNA-seq data of HepG2 cell lines expressing STAT3 shRNA or control shRNA; B, Analysis of KEGG (Kyoto enclopedia of genes and genomes) pathways based on the significant differential expression genes obtained from the RNA-seq data of HepG2 cell lines expressing STAT3 shRNA or control shRNA.



HepG2

Fig. S13 STAT3 silencing reduced the localization of RPA34 in the nucleoli of HepG2 cells. Immunofluorescence staining assays were performed using HepG2 cells expressing STAT3 shRNA or control shRNA cultured on the round coverslips with 14-mm in diameter and antibodies against RPA34 and fibrillarin. Images were captured under a confocal fluorescence microscope; scale bars in the images represent 2.5  $\mu$ m.

Fig. S14



**Fig. S14 Pearson correlation analysis between RPA34 and STAT3 in cancer tissues**. Pearson based on the TCGA dataset of clinical cancer samples, including thymoma (**A**), diffuse large B-cell lymphoma (**B**) and thyroid carcinoma (**C**), using the GEPIA online tool (<u>http://gepia2.cancer-pku.cn/#index</u>)



**Fig. S15 RPA34 expression was analyzed by Western blot**. **A**, RPA34 expression in HeLa cells is higher than that in HUCEC cells. **B**, RPA34 expression in HepG2 cells is higher than that in HL-7702 cells. **C**, STAT3-IN-3 inhibited RPA34 expression in HeLa cells. **D**, STAT3-IN-3 inhibited RPA34 expression in HepG2 cells.









Fig. S17 RPA34 is required for the regulation of Pol I-directed mediated by STAT3. A, Western blot showing the generation of a HeLa cell line expressing both STAT3 shRNA and mCherry-RPA34. A HeLa cell line expressing STAT3 shRNA was incubated with lentiviral particles expressing mCherry-RPA34. Cells were selected by puromycin, and expression of STAT3 and mCherry-RPA34 was examined by Western blot with antibodies as indicated. **B**, mCherry-RPA34 expression reversed the inhibition of Pol I-directed transcription caused by STAT3 silencing. Pol I products were detected by RT-qPCR. C and D, mCherry-RPA34 expression alleviated the inhibition of cell proliferation caused by STAT3 silencing. Cell proliferation assays was performed using cell counting and CCK-8 methods. E and F, RPA34 knockdown reduced the synthesis of Pol I products. RPA34 and Pol I products were analyzed by Western blot (E) and RT-gPCR (F), respectively. G and H, RPA34 overexpression increased the synthesis of Pol I products. RPA34, mcherry-RPA34 and Pol I products were analyzed by Western blot (G) and RT-qPCR (H), respectively. I and J, STAT3 overexpression enhanced the RPA34 promoter activity. Luciferase assays were performed using HeLa (I) or HepG2 (J) cell lines expressing mCherry-STAT3 and their corresponding control cells, where cells were transfected with the RPA34 promoter-driven reporter vector. Luciferase activity was monitored using a luciferase detection kit (Promega). Relative luciferase activity (RLA) was obtained by comparing luciferase activity in treatments to that of controls, where the luciferase activity in control was arbitrarily set as 1. Each column or point in histograms represents the mean  $\pm$  SD of three independent experiments. \*, P<0.05; \*\*, P<0.01. P values were obtained by two-way ANOVA (C-D) or Student's t test (B, E, F, H and J).