PLOS | GENETICS

CORRECTION

Correction: RNA-Binding Protein FXR1 Regulates p21 and TERC RNA to Bypass p53-Mediated Cellular Senescence in OSCC

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In panel G of Fig 4, the specified hours (in the inset) for shControl-$t_{1/2}$ and shFXR1-$t_{1/2}$ are incorrectly switched. Please see the correct figure here.

Citation: Majumder M, House R, Palanisamy N, Qie S, Day TA, Neskey D, et al. (2016) Correction: RNA-Binding Protein FXR1 Regulates p21 and TERC RNA to Bypass p53-Mediated Cellular Senescence in OSCC. PLoS Genet 12(10): e1006411. doi:10.1371/journal.pgen.1006411

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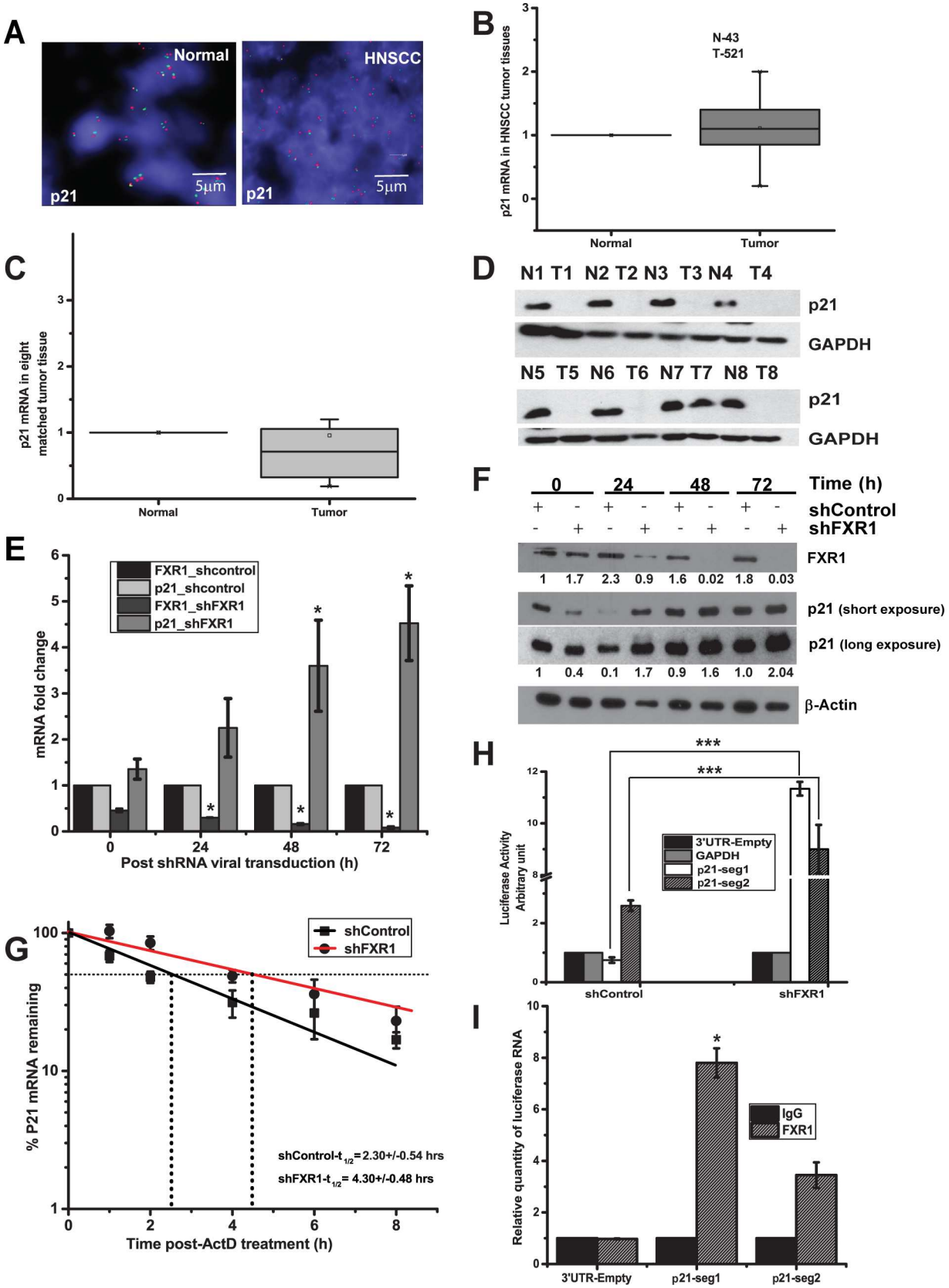
A
Normal
HNSCC
p21
5μm
p21
5μm
B
N-43
T-521
p21 mRNA in HNSCC tumor tissues
Normal
Tumor
C
p21 mRNA in eight matched tumor tissue
Normal
Tumor
D
N1 T1 N2 T2 N3 T3 N4 T4
p21
GAPDH
N5 T5 N6 T6 N7 T7 N8 T8
p21
GAPDH
E
FXR1_shcontrol
p21_shcontrol
FXR1_shFXR1
p21_shFXR1
mRNA fold change
Post shRNA viral transduction (h)
F
Time (h)
shControl
shFXR1
FXR1
1 1.7 2.3 0.9 1.6 0.02 1.8 0.03
p21 (short exposure)
p21 (long exposure)
1 0.4 0.1 1.7 0.9 1.6 1.0 2.04
β-Actin
G
shControl
shFXR1
% P21 mRNA remaining
shControl-t1/2= 2.30+/-0.54 hrs
shFXR1-t1/2= 4.30+/-0.48 hrs
Time post-ActD treatment (h)
H
Luciferase Activity Arbitrary unit
3'UTR-Empty
GAPDH
p21-seg1
p21-seg2
shControl
shFXR1
I
Relative quantity of luciferase RNA
IgG
FXR1
3'UTR-Empty
p21-seg1
p21-seg2

Fig 4. FXR1 destabilizes *p21* mRNA. (A) FISH analysis of p21 in a HNSCC TMA. Green indicates p21 and red denotes the control loci (scale bar 5μm). (B) Relative *p21* expression data obtained from cancer genome browser (N-43, T-521) (S4 Table). (C) Relative mRNA quantity of *p21* in eight matched HNSCC tumor compared to normal adjacent tissue samples estimated using qRT-PCR. GAPDH serves as a control. (D) Immunoblot analysis of p21 protein from eight representative matched HNSCC tumor and normal adjacent samples. GAPDH is used as a loading control. (E) Relative quantity of *FXR1* and *p21* levels estimated by qRT-PCR in UMSCC74B cells after treatment with FXR1 shRNA. Cells were collected at indicated time points. *FXR1* and *p21* levels in shControl treated UMSCC74B cells were taken as 1 for each time points. (F) Immunoblot analysis of p21 protein at different time points, as, mentioned in Fig 4E. (G) The mRNA decay rate of *p21* as indicated in UMSCC74B cells by qRT-PCR after silencing FXR1 followed by transcription inhibition with actinomycin-D for mentioned time points in the graph. Actin serves as a control. Data here represents the mean of n = 3 experiments. (H) Forty-eight hours after transfection of UM74B FXR1 KD and control cells with empty 3'UTR luciferase plasmid, luciferase-fused *GAPDH* 3′UTR plasmid or different segments of *P21* 3′UTR, the lysates were analyzed for luciferase activity using luminometer. The empty 3'UTR luciferase plasmid and luciferase-fused *GAPDH* 3′UTR served as a transfection and loading control. Values are the means ± SD from three independent experiments by using unpaired two sample t-test. (I) Binding of FXR1 with the 3′UTR of *p21seg1* and *p21seg2*RNAs at the G4 region. RNP IP was performed 48 h post-transfection of UMSCC74B cells with *seg1* and *seg2* 3′UTR fused to a luciferase reporter construct. Luciferase mRNA was detected using qRT-PCR. The luciferase gene in the empty-3′UTR was used as a transfection and qRT-PCR control. (*p<0.05, **p<0.005, ***p<0.0005).

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Reference

1. Majumder M, House R, Palanisamy N, Qie S, Day TA, Neskey D, et al. (2016) RNA-Binding Protein FXR1 Regulates p21 and TERC RNA to Bypass p53-Mediated Cellular Senescence in OSCC. PLoS Genet 12(9): e1006306. doi:10.1371/journal.pgen.1006306 PMID: 27606879