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Corrigendum: The tRNA methyltransferase NSun2 stabilizes p16^{INK4} mRNA by methylating the 3′-untranslated region of p16

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Concern was raised over the level of processing of the images in Fig. 2b in this Article. Because the original blots were no longer available, the experiment was repeated and the results presented in the new Fig. 9 below. As shown in this figure, fragments FL, B and Bc interacted with NSun2, but fragments CR (coding region), A, C, Ba and Bb did not. HuR interacted with fragments FL, A, B and Bb, whereas GAPDH did not interact with any of the fragments used. These additional data are consistent with Fig. 2b and thus support our original conclusions.

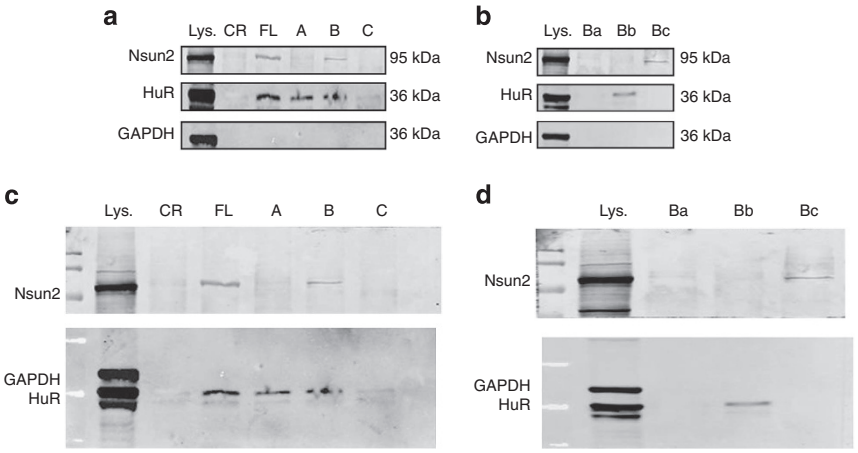

Figure 9 | NSun2 associates with the 3′UTR of p16 mRNA. (**a**) Biotin pull-down assays using p16 mRNA fragments CR, FL, as well as 3′UTR fragments A, B and C (Fig. 2a, schematic), to detect bound cellular NSun2 and HuR by western blotting. Controls included a 10 μg aliquot of whole-cell lysate (Lys.) and immunoblotting for GAPDH. (**b**) Biotin pull-down assays were used to assess the association of NSun2 and HuR with p16 3′UTR fragments Ba, Bb and Bc (Fig. 2a, schematic), as described in **a**. (**c**,**d**) Full blots for panel a (**c**) and panel b (**d**). Western blot analysis was performed using 0.5 μg ml^{-1} polyclonal anti-NSun2 antibody (Abcam), 0.2 μg ml^{-1} monoclonal anti-HuR antibody (Santa Cruz Biotechnology) and 0.2 μg ml^{-1} monoclonal anti-GAPDH antibody (CWBIO, Beijing).