



Corrigendum: Long Non-coding RNA Structure and Function: Is There a Link?

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A Corrigendum on

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In the original article, there was a mistake in **Table 1** as published. A previous version of the Table was published that was not revised and did not include updated references. The corrected **Table 1** appears below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

TABLE 1 | Structural Determination of lncRNAs.

LncRNA (size)	Mode of action	Function	Structure	Probing techniques	References
Xist (17,000 nucleotides)	cis	X-chromosome inactivation.	Regions A-F with distinct repeat sequences.	In vivo and in vitro SHAPE-MaP. Targeted structure Seq. PARIS	Simon et al., 2013; Fang et al., 2015; Lu et al., 2016; Smola et al., 2016
RepA (1,600 nucleotides)	cis	Encoded by an internal promoter on the Xist gene sense strand.	Three folding modules.	In vitro using chemical probing with SHAPE and DMS reagents.	Liu et al., 2017a
Rox1 (3,700 nucleotides)	cis and trans	Male specific nuclear RNAs. Dosage compensation.	Rox1: three stable helices connected by flexible linker regions. Rox2: two clusters of tandem stem-loops.	In vitro using chemical probing with SHAPE and PARS analysis. Both methods independently support the rox2 structure model.	Ilik et al., 2013
Rox2 (1,200 nucleotides)					
SRA (870 nucleotides)	trans	Interacts with SRA protein to regulate cardiac muscle differentiation.	Four distinct domains.	In vitro SHAPE and DMS chemical probing. Good agreement with RNase V1 enzymatic probing.	Novikova et al., 2012
HOTAIR (2,148 nucleotides)	trans	Associated with sporadic thoracic aortic aneurysm and non-end stage heart failure. Circulating biomarker for acute myocardial infarction and congenital heart diseases.	Four structural modules.	In vitro using chemical probing with SHAPE and DMS reagents.	Somarowthu et al., 2015; Greco et al., 2016; Gao et al., 2017; Guo et al., 2017; Jiang et al., 2018
Braveheart (590 nucleotides)	trans	Cardiovascular lineage commitment.	Three domains. Critical structure: a 5' asymmetric G-rich internal loop (AGIL).	In vitro using chemical probing with SHAPE and DMS reagents.	Xue et al., 2016

REFERENCES

- Fang, R., Moss, W. N., Rutenberg-Schoenberg, M., and Simon, M. D. (2015). Probing Xist RNA structure in cells using targeted structure-Seq. *PLoS Genet.* 11:e1005668. doi: 10.1371/journal.pgen.1005668
- Gao, L., Liu, Y., Guo, S., Yao, R., Wu, L., Xiao, L., et al. (2017). Circulating long noncoding RNA HOTAIR is an essential mediator of acute myocardial infarction. *Cell Physiol. Biochem.* 44, 1497–1508. doi: 10.1159/000485588
- Greco, S., Zaccagnini, G., Perfetti, A., Fuschi, P., Valaperta, R., Voellenkle, C., et al. (2016). Long noncoding RNA dysregulation in ischemic heart failure. *J. Transl. Med.* 14:183. doi: 10.1186/s12967-016-0926-5
- Guo, X., Chang, Q., Pei, H., Sun, X., Qian, X., Tian, C., et al. (2017). Long non-coding RNA-mRNA correlation analysis reveals the potential role of HOTAIR in pathogenesis of sporadic thoracic aortic aneurysm. *Eur. J. Vasc. Endovasc. Surg.* 54, 303–314. doi: 10.1016/j.ejvs.2017.06.010
- Ilik, I. A., Quinn, J. J., Georgiev, P., Tavares-Cadete, F., Maticzka, D., Toscano, S., et al. (2013). Tandem stem-loops in roX RNAs act together to mediate X chromosome dosage compensation in *Drosophila*. *Mol. Cell* 51, 156–173. doi: 10.1016/j.molcel.2013.07.001
- Jiang, Y., Mo, H., Luo, J., Zhao, S., Liang, S., Zhang, M., et al. (2018). HOTAIR is a potential novel biomarker in patients with congenital heart diseases. *Biomed. Res. Int.* 2018:2850657. doi: 10.1155/2018/2850657
- Liu, F., Somarowthu, S., and Pyle, A. M. (2017a). Visualizing the secondary and tertiary architectural domains of lncRNA RepA. *Nat. Chem. Biol.* 13, 282–289. doi: 10.1038/nchembio.2272
- Lu, Z., Zhang, Q. C., Lee, B., Flynn, R. A., Smith, M. A., Robinson, J. T., et al. (2016). RNA duplex map in living cells reveals higher-order transcriptome structure. *Cell* 165, 1267–1279. doi: 10.1016/j.cell.2016.04.028
- Novikova, I. V., Hennelly, S. P., and Sanbonmatsu, K. Y. (2012). Structural architecture of the human long non-coding RNA, steroid receptor RNA activator. *Nucleic Acids Res.* 40, 5034–5051. doi: 10.1093/nar/gks071
- Simon, M. D., Pinter, S. F., Fang, R., Sarma, K., Rutenberg-Schoenberg, M., Bowman, S. K., et al. (2013). High-resolution Xist binding maps reveal two-step spreading during X-chromosome inactivation. *Nature* 504, 465–469. doi: 10.1038/nature12719
- Smola, M. J., Christy, T. W., Inoue, K., Nicholson, C. O., Friedersdorf, M., Keene, J. D., et al. (2016). SHAPE reveals transcript-wide interactions, complex structural domains, and protein interactions across the Xist lncRNA in living cells. *Proc. Natl. Acad. Sci. U.S.A.* 113, 10322–10327. doi: 10.1073/pnas.1600008113
- Somarowthu, S., Legiewicz, M., Chillón, I., Marcia, M., Liu, F., and Pyle, A. M. (2015). HOTAIR forms an intricate and modular secondary structure. *Mol. Cell* 58, 353–361. doi: 10.1016/j.molcel.2015.03.006
- Xue, Z., Hennelly, S., Doyle, B., Gulati, A. A., Novikova, I. V., Sanbonmatsu, K. Y., et al. (2016). A G-rich motif in the lncRNA braveheart interacts with a zinc-finger transcription factor to specify the cardiovascular lineage. *Mol. Cell* 64, 37–50. doi: 10.1016/j.molcel.2016.08.010
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