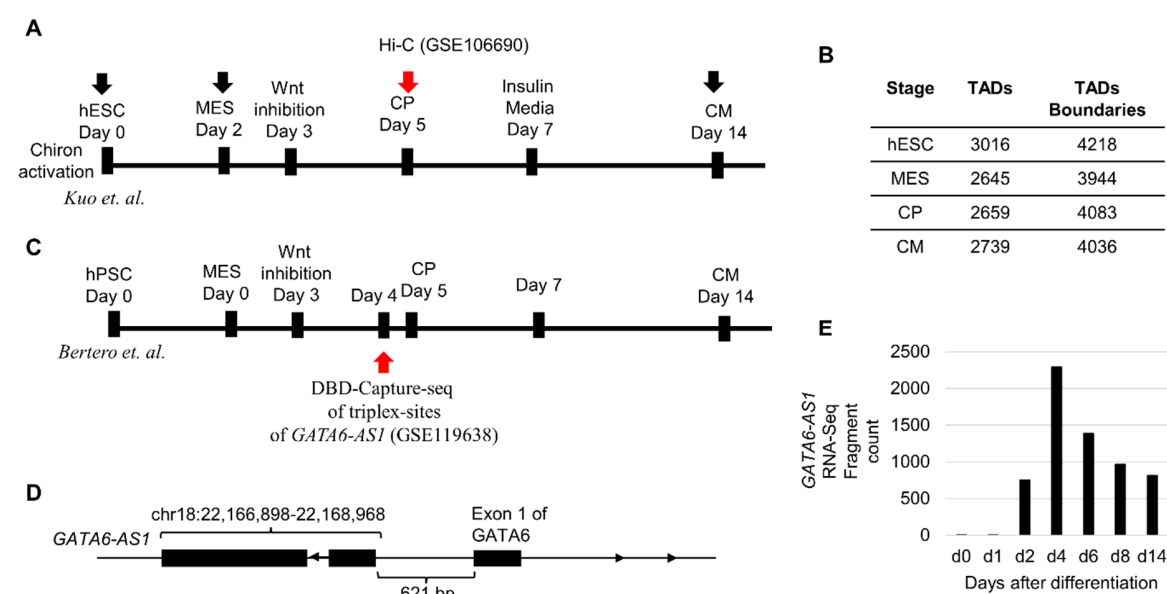


# Association between Triplex-Forming Sites of Cardiac Long Noncoding RNA GATA6-AS1 and Chromatin Organization

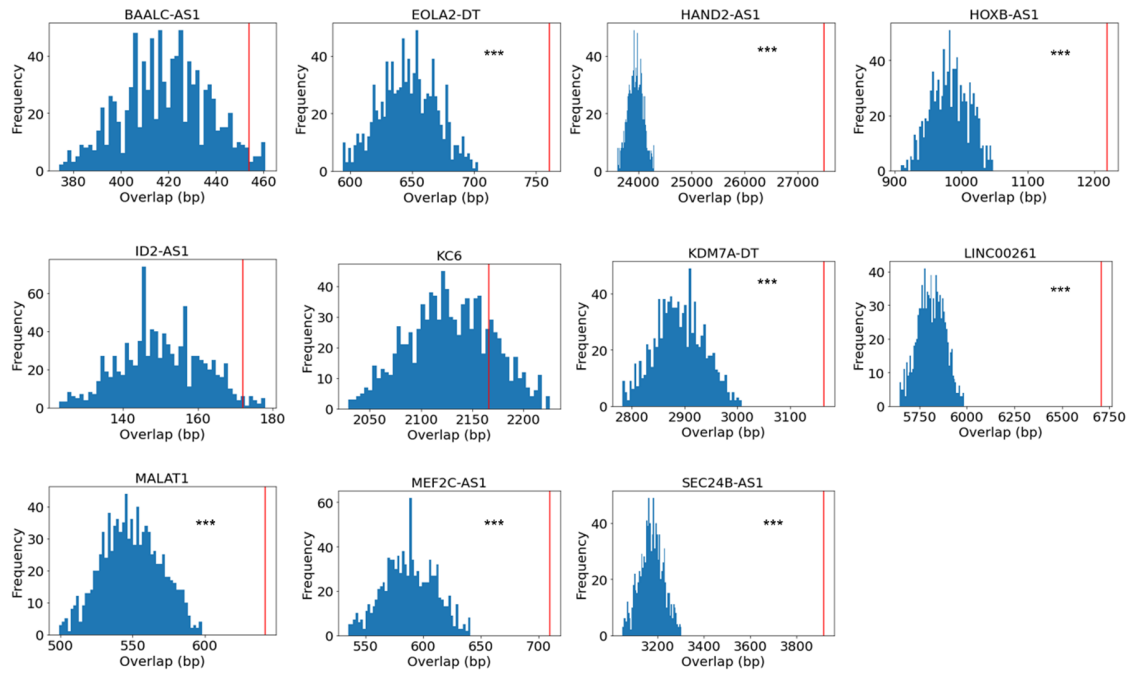
## Supplementary Data



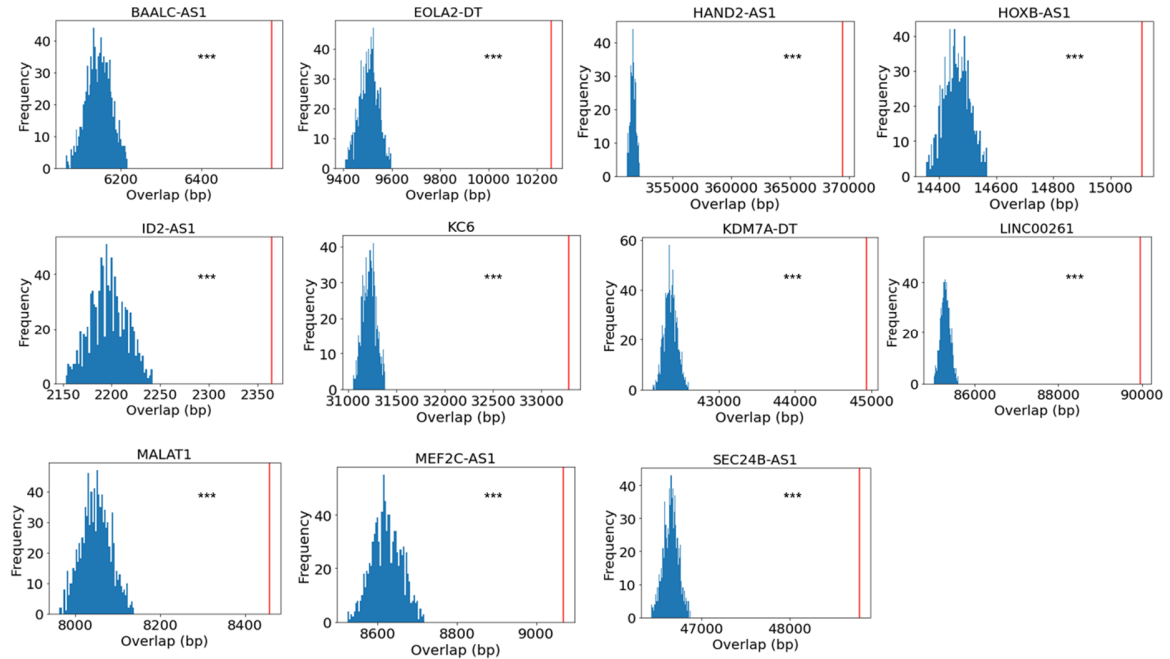
**Figure S1.** LncRNA *GATA6-AS1* in cardiac differentiation from previous studies. **(A)** Different Stages of cardiac differentiation with Hi-C data from the study by Kuo et. al. [19] **(B)** Number of TAD and TAD boundaries at different stages of cardiac differentiation from panel (A). **(C)** DBD-capture-seq data was performed to obtain triplex-forming sites of lncRNA *GATA6-AS1* at day 5 after differentiation in a study by Bertero et. al [18]. **(D)** Genomic location of *GATA6-AS1* relative to protein-coding gene *GATA6*. **(E)** Expression profile of *GATA6-AS1* at different stages of cardiac differentiation.

**Table S1:** LncRNAs with fold change > 2 at CP stage compared to day 0 of cardiac differentiation reported by Kuo et al. [19]. The lncRNAs are provided in order of their rank (highest rank first) assigned by Kuo et al. [19] based on the number of triplex-forming sites, size of triplex-forming domain in the lncRNAs sequences, and amount of elevated expression.

<b>LncRNA</b>	<b>Fold Change</b>	<b>Triplex-forming potential from Kuo et al. [19]</b>
<i>GATA6-AS1</i>	6.22	Yes
<i>JHDM1D-AS1 or KDM7A-DT</i>	3.51	Yes
<i>HOXB-AS1</i>	7.34	Yes
<i>LINC00261</i>	4.87	Yes
<i>KC6</i>	4.41	Yes
<i>SEC24B-AS1</i>	2.72	Yes
<i>ID2-AS1</i>	3.73	Yes
<i>MALAT1</i>	3.06	Yes
<i>HAND2-AS1</i>	7.32	Yes
<i>LINC00890 or SERTM2 (protein-coding gene)</i>	4.43	Yes
<i>ZNF436-AS1</i>	4.35	Yes
<i>MEF2C-AS1</i>	4.05	Yes
<i>LINC00894 or EOLA2-DT</i>	3.64	Yes
<i>BAALC-AS1</i>	2.17	Yes
<i>N4BP2L2-IT2</i>	2.2	Yes
<i>TMCC1-AS1</i>	3.33	No
<i>DICER1-AS1</i>	2.37	No
<i>MANEA-AS1</i>	2.57	No
<i>LINC01473</i>	3.37	No
<i>ACVR2B-AS1</i>	2.35	No
<i>LINC01125</i>	2.28	No
<i>GATA3-AS1</i>	5.56	No
<i>LINC01099</i>	6.91	No
<i>TBX2-AS1</i>	7.46	No
<i>LINC01440</i>	6.02	No
<i>LINC00648</i>	4.05	No
<i>ALOX12-AS1</i>	2.41	No
<i>TAPT1-AS1</i>	2.69	No
<i>CAHM</i>	2.04	No
<i>MIR210HG</i>	2.37	No
<i>VIM-AS1</i>	2.29	No
<i>PTOV1-AS1</i>	2.23	No
<i>MFI2-AS1</i>	2.28	No



**Figure S2.** Enrichment of 9 cardiac lncRNAs' triplex sites in TAD boundaries at CP stage. The distribution of expected coverage (blue) compared to the observed coverage (vertical red line) in TAD boundaries are shown. The x-axis and y-axis represent coverage, and frequency, respectively. A statistical difference between expected coverage and random measurements is indicated by \*\*\* ( $p$ -value < 0.001).



**Figure S3.** Enrichment of 9 cardiac lncRNAs' triplex sites in TADs at CP stage. The distribution of expected coverage (blue) compared to the observed coverage (vertical red line) in TAD domains are shown. The x-axis and y-axis represent coverage, and frequency, respectively. A statistical difference between expected coverage and random measurements is indicated by \*\*\* ( $p$ -value < 0.001).

## References

- 18 Bertero, A.; Fields, P.A.; Ramani, V.; Bonora, G.; Yardimci, G.G.; Reinecke, H.; Pabon, L.; Noble, W.S.; Shendure, J.; Murry, C.E. Dynamics of genome reorganization during human cardiogenesis reveal an RBM20-dependent splicing factory. *Nat. Commun.* **2019**, *10*, 1538. <https://doi.org/10.1038/s41467-019-09483-5>.
- 19 Kuo, C.C.; Hänzelmann, S.; Sentürk Cetin, N.; Frank, S.; Zajzon, B.; Derks, J.P.; Akhade, V.S.; Ahuja, G.; Kanduri, C.; Grummt, I.; et al. Detection of RNA-DNA binding sites in long noncoding RNAs. *Nucleic Acids Res.* **2019**, *47*, e32. <https://doi.org/10.1093/nar/gkz037>.