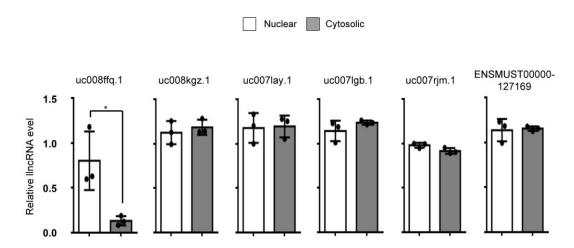
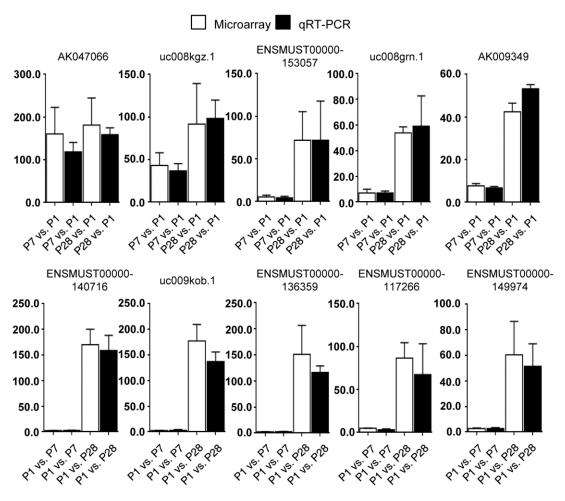
## Profiling analysis of long non-coding RNAs in early postnatal mouse hearts

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**Supplementary Figures and Figure Legends** 

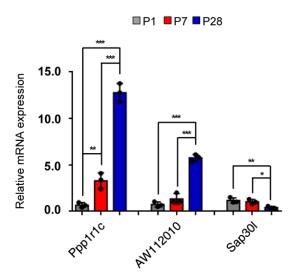


Supplementary Figure S1. The cytosolic and nuclear distribution of lncRNAs determined by qRT-PCR analysis. The RNA levels of lncRNAs in both cytoplasm and nucleus were determined via real time qRT-PCR. Data are presented as mean  $\pm$  S.D. \* indicates p < 0.05, which denote statistical comparison between the two marked groups. Paired two-tailed Student's t-test was used (n = 3 cultures per group).

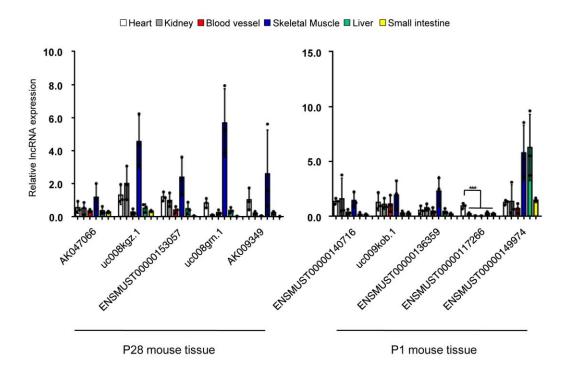


Supplementary Figure S2. Microarray validation of the top 10 lncRNAs by real time qRT-PCR. Fold changes between P1 and P7 or P1 and P28 of the top 10 lncRNAs are shown

for both microarray and qRT-PCR data, respectively. Data are presented as mean  $\pm$ S.D.



Supplementary Figure S3. Microarray validation of the 3 differentially expressed neighboring genes by real time qRT-PCR. The mRNA levels of Ppp1r1c, AW112010 and Sap30l, related to lncRNA uc008kgz.1, uc008grn.1, and ENSMUST00000117266, respectively, in P1, P7 and P28 mouse heart were validated by real time qRT-PCR. Data are normalized to 18S. Data are shown as mean  $\pm$  S.D. \*, \*\* and \*\*\* indicate p < 0.05, p < 0.01 and p < 0.001, respectively, which denote statistical comparison between the two marked groups. One-way ANOVA (post hoc: LSD multiple comparison test) was used.



Supplementary Figure S4. Tissue specificity validation of the top 10 lncRNAs by using 18S as an internal control. The expression levels of the top 10 lncRNAs in different mouse

tissues that contain smooth muscle cells were determined by real time qRT-PCR. Data were normalized to *18S*. Data are shown as mean  $\pm$  S.D. \*, \*\* and \*\*\* indicate p < 0.05, p < 0.01 and p < 0.001, respectively, which denote statistical comparison between the two marked groups. One-way ANOVA (*post hoc*: LSD multiple comparison test) was conducted. (n = 3 samples per time point).