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Dynamic organization of lncRNA and circular RNA regulators collectively controlled cardiac differentiation in humans

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Highlights

- Dynamic lncRNA and circRNA transcriptomes from the early embryonic to cardiomyocyte stages were constructed based on high-throughput sequencing data.
- Numerous key lncRNA and circRNA regulators whose expression was significantly stage-specific and shifted gradually and continuously during heart differentiation were identified.
- Functional enrichment analysis revealed that lncRNAs and circRNAs play critical roles in pathways that are activated specifically during heart differentiation.
- Regulatory network analysis revealed the dynamic organization of lncRNAs and circRNAs collectively controlled cardiac differentiation.

Research in context

Understanding noncoding RNA (ncRNA) transcription and regulation during cardiac differentiation remains elusive. This study performed transcriptome analysis for both long noncoding RNAs (lncRNAs) and circular RNAs (circRNAs) during four important development stages ranging from early embryonic to cardiomyocyte. A method was developed to identify numerous lncRNA and circRNA regulators whose expression was significantly stage-specific and shifted gradually and continuously during heart differentiation. These ncRNAs were regulated by stage-specific transcription factors and candidate TF-ncRNA-gene network modules were identified. These data suggest the dynamic organization of lncRNAs and

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