Researchers map out the atlas of gene regulators in human cardiac cells for the first time

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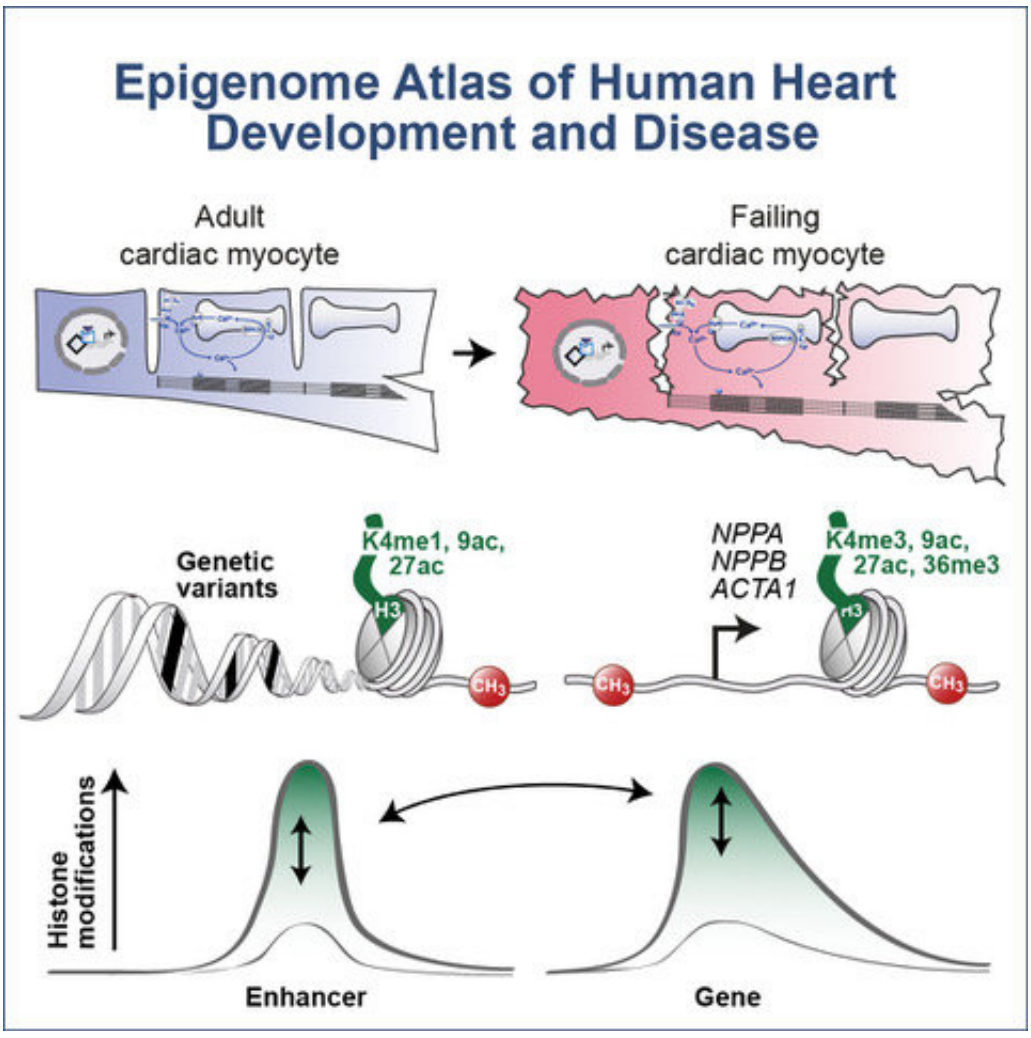

Credit: Graphic: Lutz Grein

Information for building cells is stored in DNA, the blueprints for the more than 20,000 proteins in the human body. Every cell requires several thousand proteins in order to function. If you were to roll every single protein blueprint into one, the information they contain would occupy less than 2 percent of all DNA. What is the remaining 98 percent of the genome needed for? It contains the switches that control gene activity. For the first time, a research team led by Dr. Ralf Gilsbach and Prof. Dr. Lutz Hein from the University of Freiburg have mapped out the gene regulators in the DNA of human cardiac muscle cells.

The findings have been published in the journal *Nature Communications*.

In order to locate all gene switches, the Freiburg research team used modern sequencing methods to examine the entire genome—DNA, epigenetic markers and RNA—during the development, maturation and disease of human cardiac muscle cells. By analyzing more than a trillion sequencing letters, the team found over 100,000 gene switches. The multitude of data now yields a complete atlas of gene regulators in the life of a cardiac muscle cell. During development and growth, DNA methylation and histone markers control which genes are turned on or off. The atlas also provides insight into mechanisms that are misdirected in heart disease. Some regulatory elements are altered in cardiac arrhythmias at the DNA level, for example. In contrast, histones take control in chronic heart failure. In the future, the Freiburg researchers want to identify the most important switches in this atlas in order to treat heart disease.

More information: Ralf Gilsbach et al, Distinct epigenetic programs regulate cardiac myocyte development and disease in the human heart in vivo, *Nature Communications* (2018). DOI: 10.1038/s41467-017-02762-z