

# Scientists discover a new gene regulation mechanism

April 19 2021

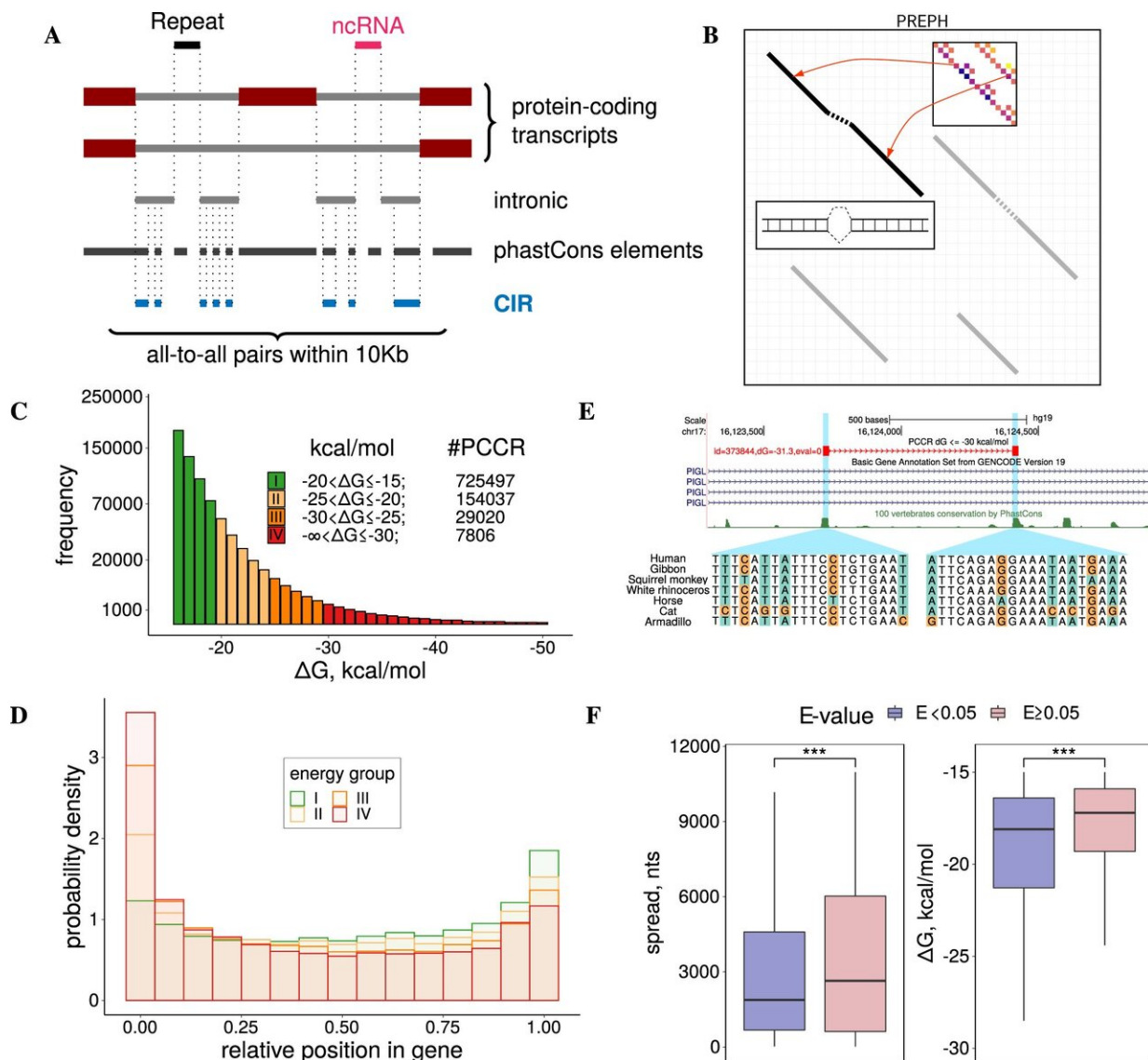


Fig. 1: Pairs of conserved complementary regions (PCCRs). From: Conserved long-range base pairings are associated with pre-mRNA processing of human

genes. Credit: *Nature Communications* (2021). DOI: 10.1038/s41467-021-22549-7

A team of scientists from Russia studied the role of double-stranded fragments of the maturing RNA and showed that the interaction between distant parts of the RNA can regulate gene expression. The research was published in *Nature Communications*.

At school, we learn that DNA is double-stranded and RNA is single-stranded, but that is not entirely true. Scientists have encountered many cases of RNA forming a double-stranded (a.k.a. secondary) structure that plays an important role in the functioning of RNA molecules. These structures are involved in the regulation of gene expression, where the double-stranded regions typically carry specific functions and, if lost, may cause severe disorders. A double-stranded structure is created by sticky complementary regions. For the strands to stick to each other, U and G should appear opposite A and C, respectively. The majority of the sticking regions are located close to one another, but the role of those located far apart has not been well understood.

Scientists from the Skoltech Center for Life Sciences (CLS) led by professor Dmitri Pervouchine and their colleagues from Russian and international laboratories used molecular and bioinformatics techniques to analyze the structure and roles of complementary RNA regions spaced far apart but capable of forming secondary structures. It transpired that the secondary structure plays an important role in the maturation of information-carrying RNA molecules and particularly in splicing, a process in which non-coding regions are cut out, and the coding regions are stitched together. The team showed that the RNA secondary structures can regulate splicing and thus contribute strongly to gene regulation.

"This paper culminates years of research on the RNA secondary [structure](#) and its role in the regulation of [gene expression](#). We have published an extensive computation-based catalog of potentially important RNA structures, but the [experimental research](#) in this direction is just starting," professor Pervouchine says.

**More information:** Svetlana Kalmykova et al. Conserved long-range base pairings are associated with pre-mRNA processing of human genes, *Nature Communications* (2021). [DOI: 10.1038/s41467-021-22549-7](https://doi.org/10.1038/s41467-021-22549-7)

Provided by Skolkovo Institute of Science and Technology

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