



# Long Non-Coding RNAs Functions in Genomics Regulation

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## Abstract

We have broadly mapped genome elements over the years in FANTOM projects. FANTOM6 directly tested lncRNA functions by systematically knocking down several hundreds of lncRNAs in human primary fibroblasts and ES cells, suggesting function for >30% of lncRNA tested in each cell type. To dig deeper, we broadly map RNA bound to chromatin, using RADICL-seq, revealing unexpected pattern of interactions driven by enhancer RNAs, intronic RNAs, lncRNAs and RNAs from retrotransposon elements.

Moving transcriptome technologies at single-cell level, we comprehensively map transcription and its regulation in all human cells focusing Asian genetic backgrounds in Human Cell Atlas project.

## Publication Highlights

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