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Beyond the FANTOM4

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RIKEN OSC has a long history of transcriptome analysis using DNA sequencers; we also organize the international consortium Functional Annotation of Mammalian Genome (FANTOM; Figure 1). We have developed a novel method Cap Analysis of Gene Expression (CAGE),

which analyzes capped transcripts in a genome-wide manner by sequencing the 5' end of mRNA. In the recently completed FANTOM4, we analyzed the transcriptional regulation network of human THP-1 cell differentiation at the promoter level with deepCAGE, an

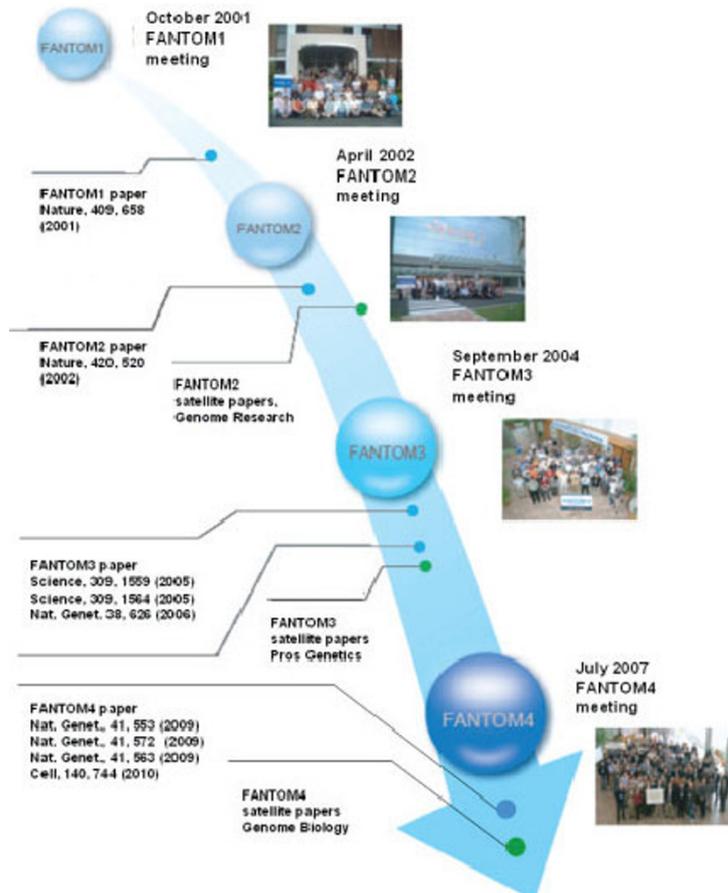


Figure 1 History of FANTOMs.

application of CAGE for the next-generation sequencers. The deepCAGE data were also used to analyze the promoter activity of repeat elements and to discover new small RNA (tiRNA) by integration with the small RNA sequencing.

Although the deepCAGE is a powerful tool for transcriptome analysis, it is limited owing to the need to use a significantly large amount of RNA and it is semi-quantitative. We have addressed these problems and developed NanoCAGE technology and quantitative deepCAGE. OSC aims to expand transcriptome knowledge; we aim to understand promoter and transcriptional regulation. We are about to start the FANTOM5 project.

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