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## Project Hisao Masai Genome Dynamics Project

## **Genome Replication and Maintenance:** In search of unexplored messages in the genome

Precise duplication of genetic materials is central to the stable maintenance of genomes through generations. Defects in the genome copying processes would generate genomic instability which could ultimately result in various diseases including cancer. The goal of our studies is to understand the molecular basis of how the huge genomes are accurately replicated and the precise copies of the genetic materials are inherited to the next generation. Three billion base pairs of the human genome (2 meter long) are replicated with almost no errors during the 6-8 hr time span of the cell cycle. This requires an extreme level of coordination of temporal and spatial arrangements of chromatin organization and signaling events for initiation of DNA replication.



## "We are trying to decipher 'unexplored messages' of the genome that are crucial for shaping the chromosomes, copying and reading out genetic information, and even for causing detrimental diseases."

We recently discovered novel and crucial roles of non-standard DNA structures in regulation of DNA replication and transcription. Notably, we found that G-quadruplex structures, which are widely present on genomes (estimated to be present at more than 370,000 locations on the human genome), regulate organization of chromatin architecture and initiation of DNA replication. Our major goal is to establish a novel principle of the genome by elucidating the fundamental and universal

functions of G-quadruplex and other non-B type DNA structures in regulation of various genome functions. Through these efforts, we will also explore the possibility that mutations found in various diseases including cancer and

neurodegenerative diseases are related to alteration and mal-formation of these non-B DNA structures, which are likely to be essential components of genomes but somehow have been disregarded in the past.







## **Genome Dynamics**