浙江大学医学院学术报告

Chopping Away at “Junk” DNA: using high-throughput CRISPR/Cas9 to uncover the role of non-coding genome sequence

报 告 人：刁亚锐

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主 持 人：徐素宏 研究员

Yarui received his B.Sc. in Biotechnology (2006) from Nanjing University and his Ph.D. in Biochemistry (2011) from the Hong Kong University of Science and Technology (HKUST). As a graduate student in Dr. Zhenguo Wu's lab, he investigated transcription regulation and signaling transduction in muscle stem cell and rhabdomyosarcoma. His work led to first authored publications in Mol Cell Biol (2009), PNAS (2010), Cell Stem Cell (2012), JBC (2014), and Dev Cell (2017). For postdoc training, Yarui made a bold decision to switch his research filed from stem cell to functional genomics, and joined Dr. Bing Ren's group at UCSD, where he led a project to develop high-throughput CRISPR/Cas9 screen strategies that allow for genome-wide functional characterization of non-coding regulatory sequence in the native chromatin context (Diao et al. 2016, Genome Res; Diao et al. 2017, Nat Methods). He has also made major contributions to map the long-range chromatin interactions in 27 human cell and primary tissue types, to provide a comprehensive, tissue specific, and three-dimensional cis-regulatory landscape to interpret the regulatory target genes of cis-acting elements and genetic variants associated with human diseases and traits (Jung*, Schmitt*, Diao* et al, under revision in Nature). In Sep 2018, Yarui is staring his new lab at Duke University to employ the powerful genomics tools to investigate the transcriptional regulatory network that control tissue regeneration, aging, and tumorigenesis.

Key Publications:

1. Diao Y, Fang R, Li B, Meng Z, Yu J, Qiu Y, Lin KC, Huang H, Liu T, Marina RJ, Jung I, Shen Y, Guan KL, Ren B. **A tiling-deletion-based genetic screen for cis-regulatory element identification in mammalian cells.** *Nat Methods*. 2017

2. Diao Y, Li B, Meng Z, Jung I, Lee AY, Dixon J, Maliskova L, Guan KL, Shen Y, Ren B. **A new class of temporarily phenotypic enhancers identified by CRISPR/Cas9-mediated genetic screening**. *Genome Res*. 2016

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