



THE CHINESE UNIVERSITY OF HONG KONG
BIOCHEMISTRY PROGRAMME, SCHOOL OF LIFE SCIENCES

Chromatin run-on reveals nascent RNAs that
differentiate normal and malignant brain tissue

by

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Our genomes encode a variety of poorly understood RNA species which remain challenging to identify using existing genomic tools. We developed chromatin run-on and sequencing (ChROseq) to map the location of RNA polymerase using virtually any input sample, including samples with degraded RNA that are intractable to conventional RNA-seq. We used ChRO-seq to develop the first maps of nascent transcription in primary human glioblastoma (GBM) brain tumours. ChRO-seq can now be used to map regulatory programmes contributing to a variety of solid tumors and other complex tissues.

Mr. Chu is a 2013 graduate of the Biochemistry Programme of The Chinese University of Hong Kong. He is now a Croucher Foundation Graduate Fellow.

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