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Epigenomic profiling of neuroblastoma cell lines

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Abstract

This protocol explains the process of how we collected MYCN, MYC, and Histone ChIP-Seq data, as well as ATAC-Seq data for neuroblastoma cell lines. This protocol is comprised of three sections: Cell Growth and Expansion for care of neuroblastoma cell lines, ChIP-Seq protocol, and ATAC-Seq Protocol. Table 1, within the document, outlines which data was collected for each cell line.

Attachments

PDF

ChIP-Seq-ATAC-Seq-Pr...

621KB

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