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10x Multiome Sample Processing

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dx.doi.org/10.17504/protocols.io.bp2l61mqrvqe/v1**Allen Institute for Brain Science**

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Protocol is used to profile all the open chromatin regions at a single nuclei level through the rapid generation of NGS-ready libraries, and for rapid generation of 3' transcriptomic-NGS-ready-single-cell-libraries from the same pool of transposed nuclei.

[MB0204_10x_Multiome_Sample_Processing.docx](#) [CG000338_ChromiumNext_GEM_Multiome_ATAC_GEX_User_Guide_RevE.pdf](#)

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