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Here, we utilize transcriptome-wide approaches to investigate ac4C localization and function in mRNA. We find that ac4C is widely distributed within the human transcriptome with a majority of sites occurring within coding sequences (CDS).

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In the course of developing efficient CRISPR/Cas9-mediated genetic screens in primary cells, we previously transduced wild-type and Cas9-transgenic activated B cells with retroviruses encoding sgRNAs targeting 12 surface markers, leading to an average knockout frequency of 80% (Chu et al., 2016).