m6A is the most abundant internal mRNA modification and plays important roles in regulating RNA function. However, methods for detecting m6A in cells have suffered from the need for large amounts of input RNA. Recently, our lab developed DART-seq (deamination adjacent to RNA modification targets) to overcome this challenge. DART-seq uses a fusion protein consisting of the m6A-binding YTH domain tethered to the cytidine deaminase APOBEC1. When this APOBEC1-YTH fusion protein encounters methylated RNA, it binds to m6A and directs C-to-U editing at nearby cytidine residues. We recently demonstrated that expression of APOBEC1-YTH in cells can achieve single-cell m6A identification, revealing new features of m6A distribution that have been missed by other m6A profiling methods. Additionally, we have further leveraged the power of APOBEC1-mediated editing to develop new strategies for investigating RNA:protein interactions in cells at the single-molecule level. We have applied these tools to the cytoplasmic m6A reader proteins YTHDF1, 2, and 3 and discovered that individual mRNA molecules can be bound by more than one YTHDF protein throughout their lifetime, providing new insights into the function of YTHDF proteins in cells.