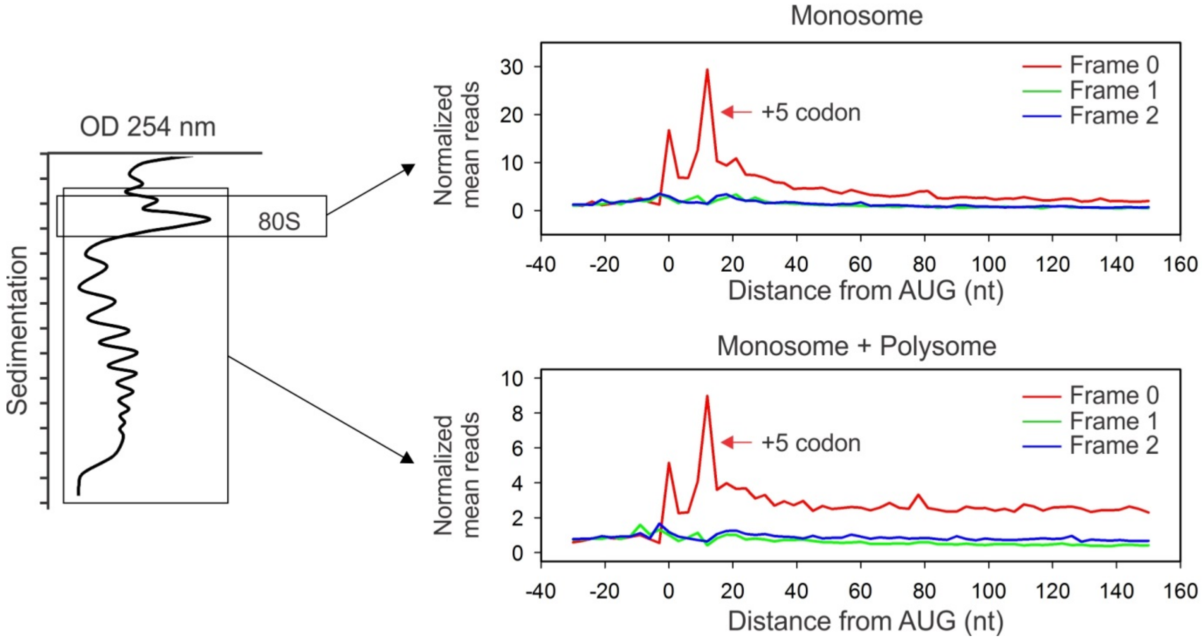

Figure S7. Monosome fraction maintains post-initiation pausing. Ribo-seq was conducted for separated monosome fractions (top) and the total ribosome fractions (bottom). All mapped reads are aligned at the annotated start codon AUG and stratified by frames. The reads density at each nucleotide position is averaged using the P-site of RPFs. The red arrow indicates the 5th codon position.