m6A-seq and MAZTER-seq peaks lift-over to SK1 reference genome

1. Download genome annotation in supplementary table 5 from Schwartz et al Cell 2013 (https://doi.org/10.1016/j.cell.2013.10.047) (https://ars.els-cdn.com/content/image/1-s2.0-S0092867413013652-mmc5.xlsx) and convert to tsv format. This table is basically a bed file of gene genomic coordinates, and has the gene name, the start sites, end sites, and the strand for the reference genome used by Schwartz et al.

2. Download m6A-seq sites in supplementary table 1 from Schwartz et al Cell 2013 (https://doi.org/10.1016/j.cell.2013.10.047). (https://ars.els-cdn.com/content/image/1-s2.0-S0092867413013652-mmc1.xlsx) and convert to tsv format. This is a file that has the gene id, gene name, and m6A site in genomic coordinates. This file is reported to be in the same reference genome as supplementary table 5.

3. Download MAZTER-seq sites in supplementary table 4 from Garcia-Campos et al Cell 2019 (https://doi.org/10.1016/j.cell.2019.06.013) (https://ars.els-cdn.com/content/image/1-s2.0-S0092867419306762-mmc4.xlsx) and convert to tsv format. This is a file that has the gene id, and genomic coordinates for each MAZTER-seq site, in addition to a confidence score at each time point. This file is reported to be in the same reference genome as supplementary table 5.

4. Calculate the distance between the start codon as reported in the genome annotation (supp. table 5 of Schwartz et al.) and the m6A peaks. Then, for each gene, map the start sites from supp. table 5 to the start sites in the bed12 file for sk1 reference genome, which was generated as an intermediate to creating a reference gtf file (see Methods). Then use the start codon in bed12 file for sk1 reference genome and the difference calculated before to remap the m6A-seq sites into the sk1 coordinates we are using. The MAZTER-seq sites with a confGroup greater than 1 were converted to the new coordinates in the same way as the m6A-seq peaks.
   To do this, convert_m6a_to_sk1.py was used with command:

   convert_m6A_to_sk1.py --bed alignments.bed --annotation annotation.tsv --m6a m6A-seq.tsv --mazter MAZTER-seq.tsv --outfile m6A_peaks_lifted-over.bed, with:

   alignments.bed: file generated for the sk1 reference genome
   annotation.tsv: supplementary table 5 from Schwartz et al Cell 2013
   m6a: m6A-seq site peaks supplementary table 1 from Schwartz et al Cell 2013
   mazter: MAZTER-seq peaks supplementary 4 table from Garcia-Campos et al Cell 2019
   outfile: file to save the converted m6A sites.