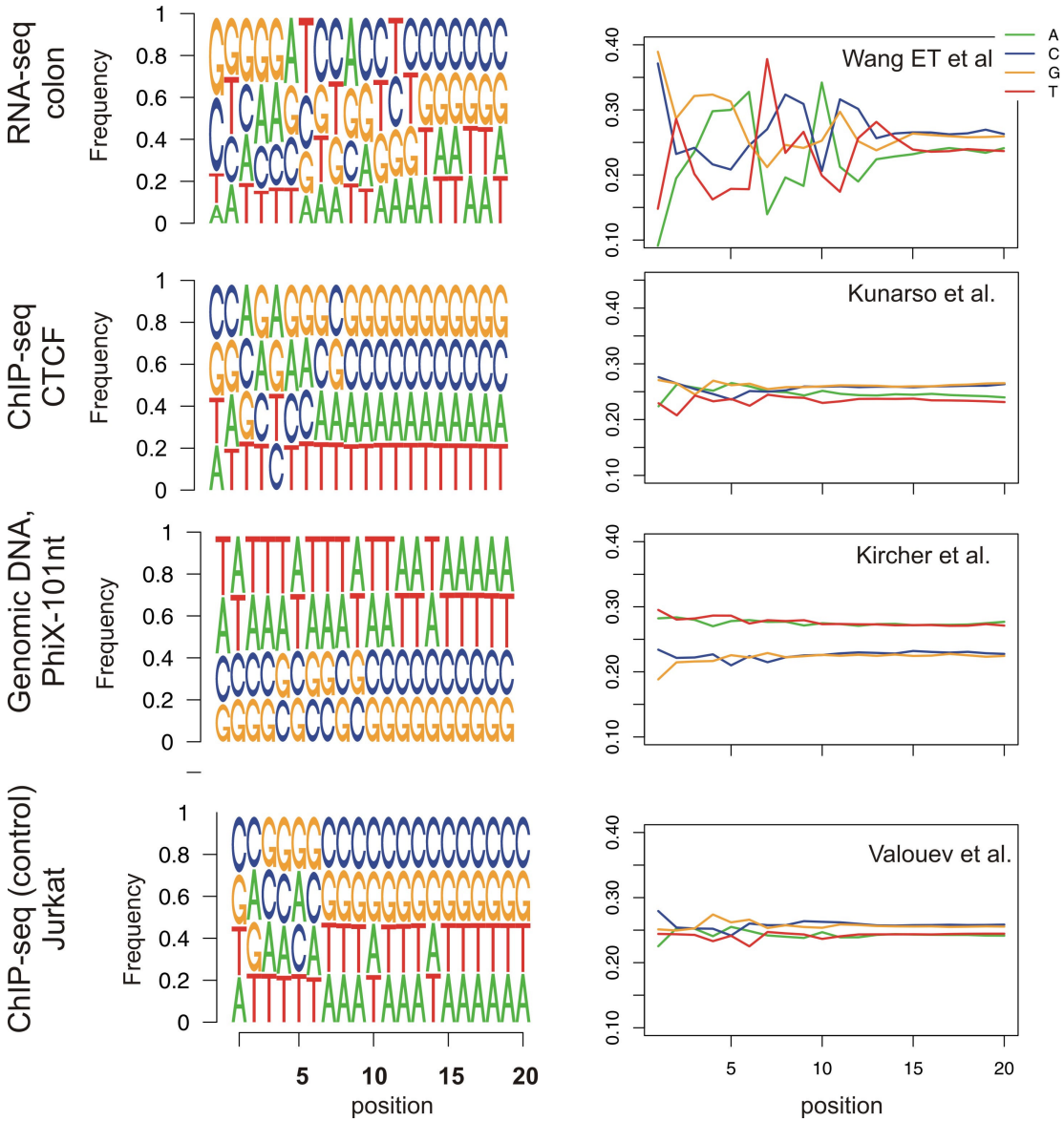
Supplementary Materials: Detection and removal of biases in the analysis of next-generation sequencing reads

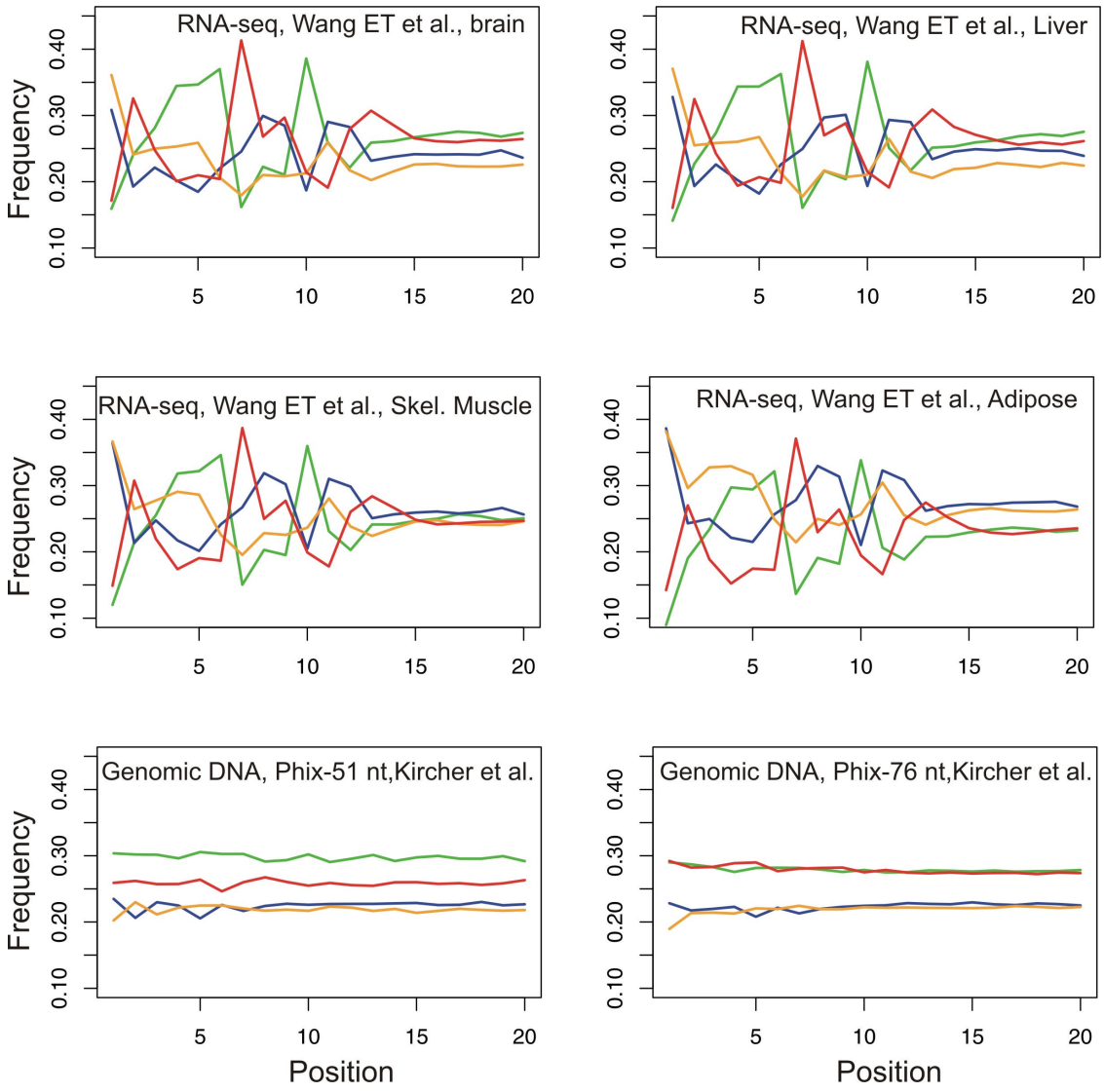
Schraga Schwartz[1,2], Ram Oren[1,2], and Gil Ast[1]

[1]Department of Human Molecular Genetics and Biochemistry, Sackler Faculty of Medicine, Tel-Aviv University, Ramat Aviv 69978, Israel

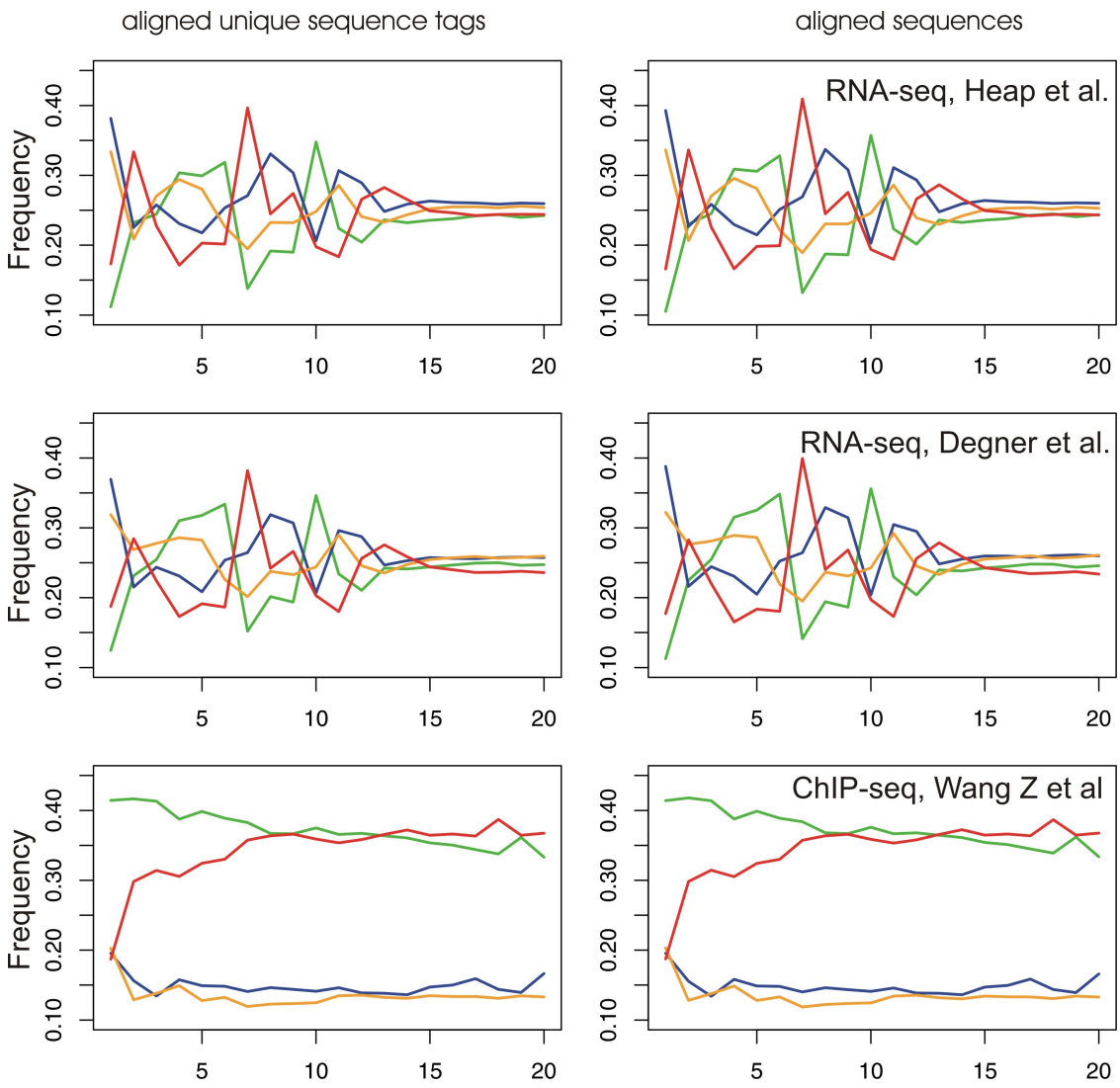
[2]These authors contributed equally.



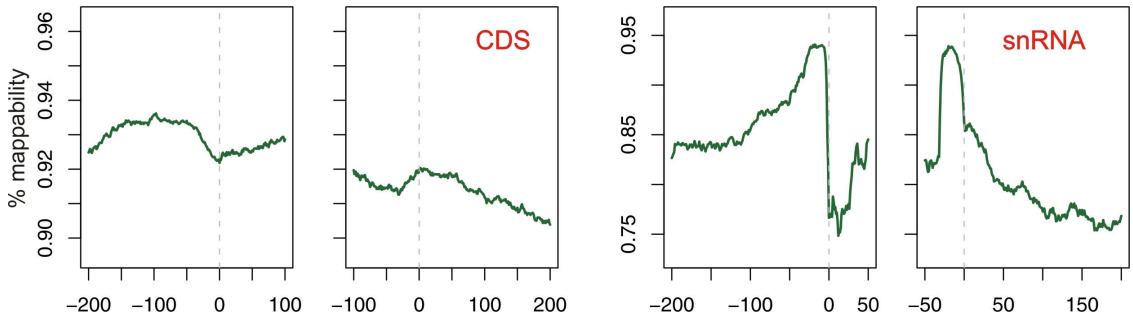
Supplementary Figure 1: Sequence logos and positional nucleotide plots for several additional examined datasets, as in Figure 1.



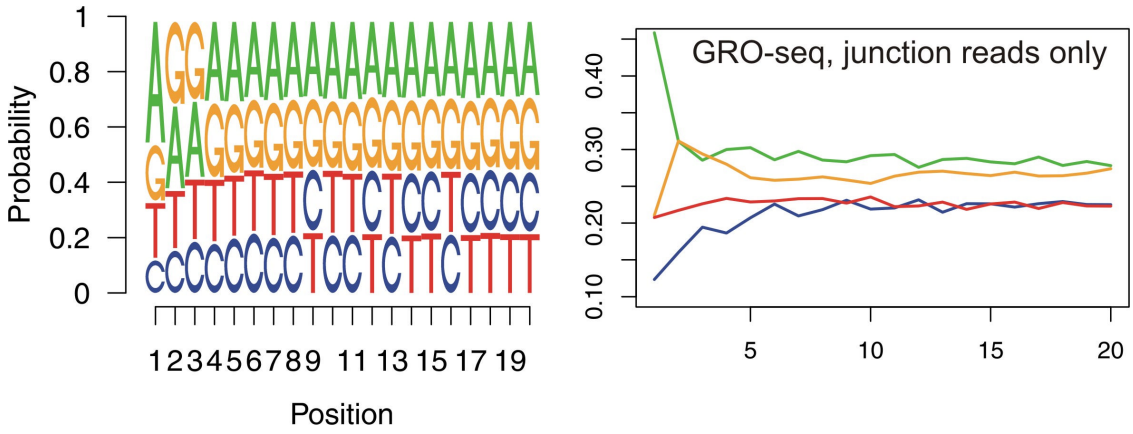
Supplementary Figure 2: Positional nucleotide plots for several additional examined datasets, as in Figure 1 and in Supplementary Figure 1.



Supplementary Figure 3: Comparison of nucleotide composition when examining only unique sequence tags (left column), as opposed to all sequences (as shown in Figure 1 in the manuscript). This analysis demonstrates that the bias in nucleotide composition is not likely to have occurred as a result of biased PCR amplification of few specific amplicons.



Supplementary Figure 4: Mappability density values within the regions surrounding the coding sequence start and end sites, and snRNAs.



Supplementary Figure 5: Sequence logos and positional nucleotide plots for junction reads in GRO-seq data. The similarity of these plots to the ones in Figure 4C-D demonstrates that the bias is presumably not due to biased hydrolysis of BrU containing residues, as it is present also in reads originating from contaminating mRNA.