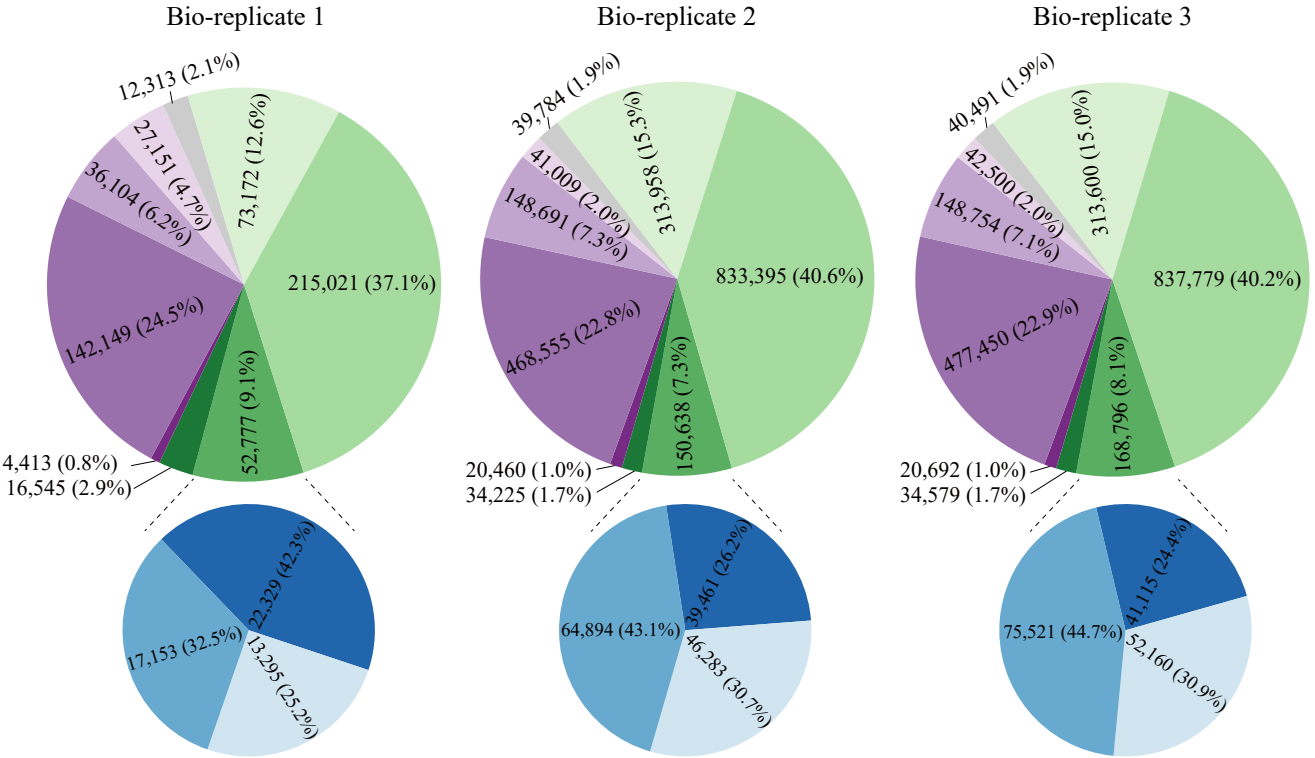


Supplementary Figure S1. Very similar genomic profiles among the 3 biological replicates of K562 small RNA-seq data. Distribution of numbers and fractions of uniquely mapping reads among the different genomic features for each biological replicate. Important, this analysis was done on all uniquely mapping reads, prior to merging shown in the Figure 1.