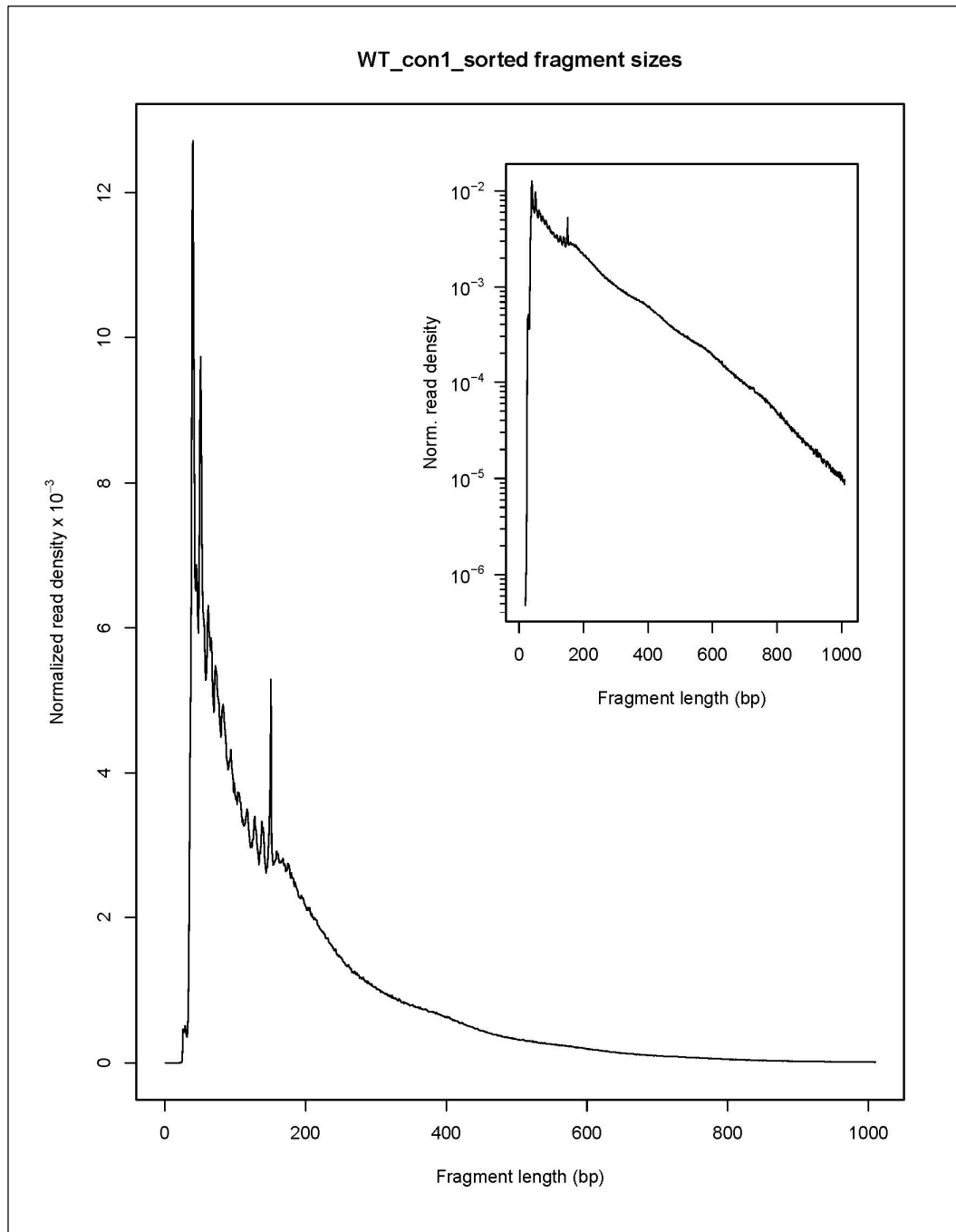


Supplemental Table S1. Mapped reads for ATAC-Seq dataset

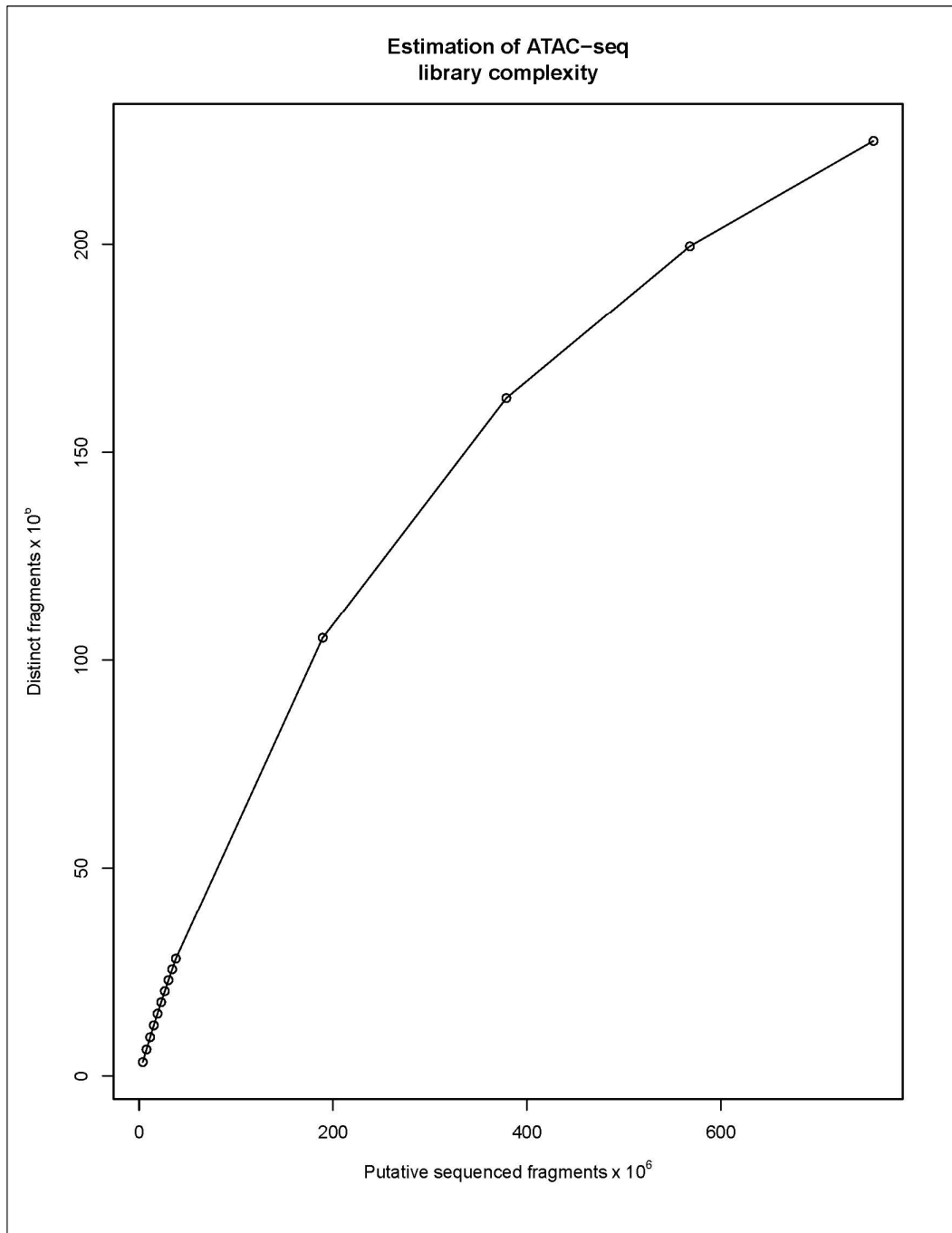
Dataset	No. Reads	No. Mapped	Percentage (%)
WT_1	46,036,987	40,360,835	88
WT_2	59,175,288	51,987,516	88
RSV_1	58,691,358	51,326,986	87
RSV_2	56,720,822	49,220,216	87

Supplemental Figure S1. Quality assessment of ATAC-Seq data. For each replicate, Fragment size and library complexity is plotted.

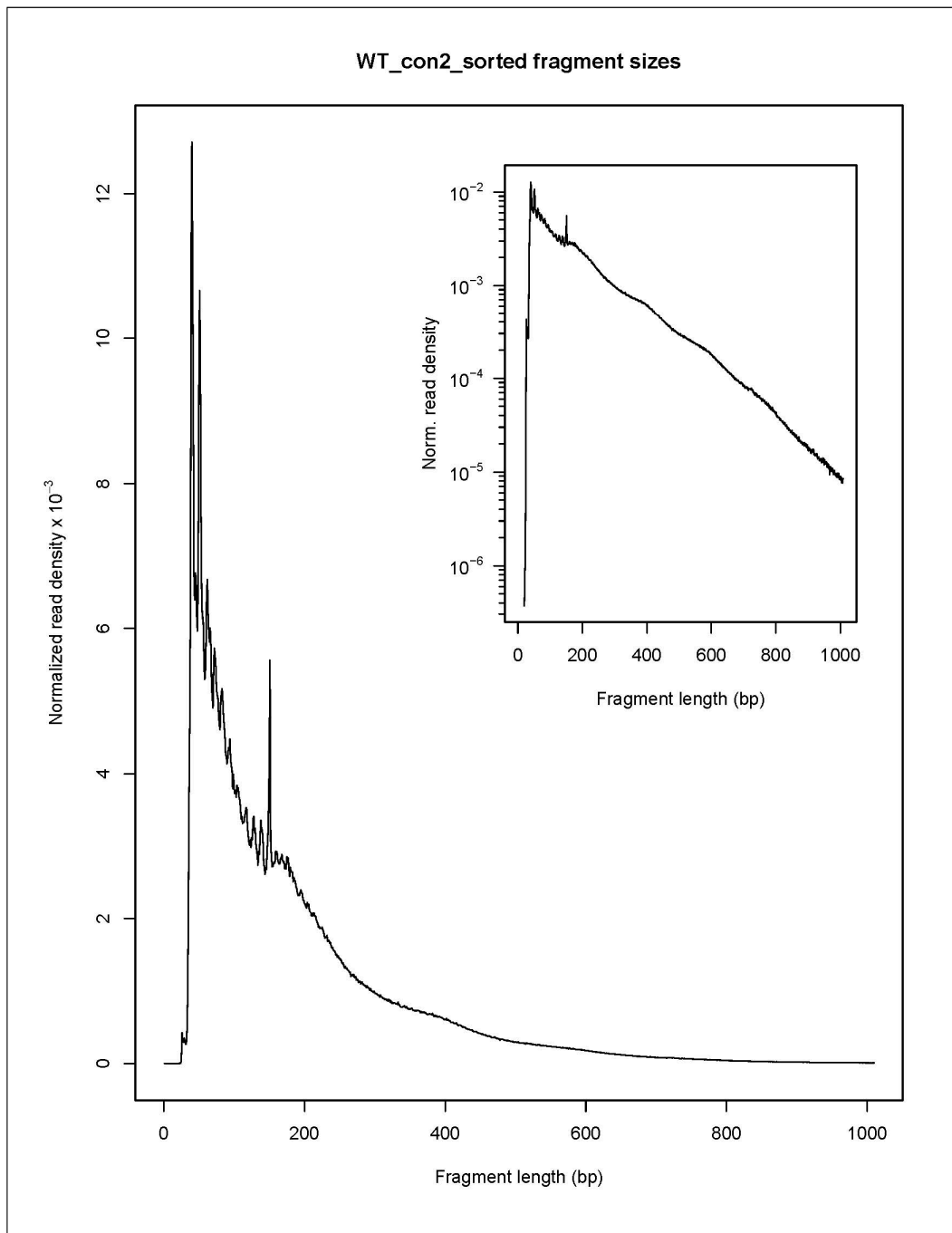
S1A. Fragment size, control sample, replicate 1



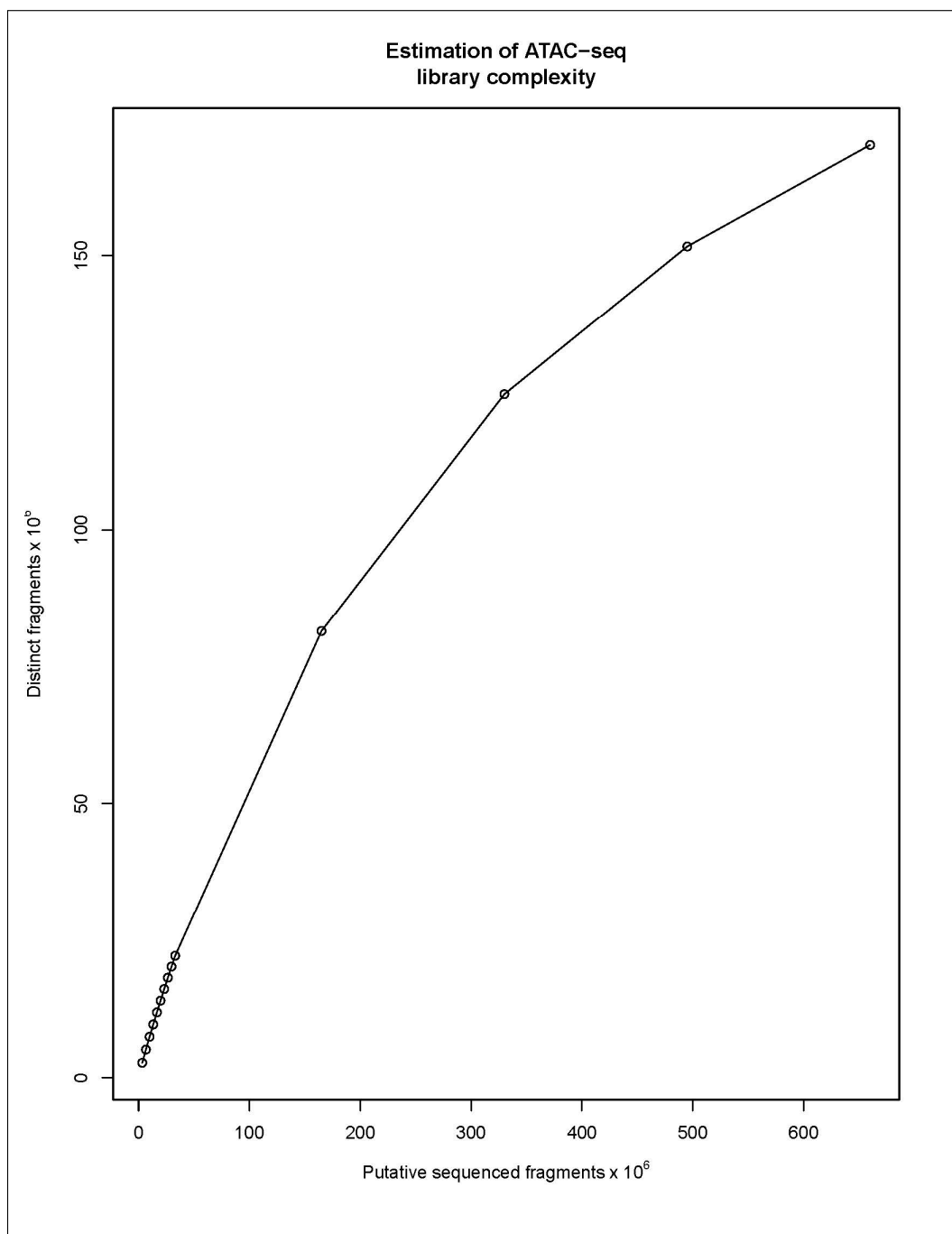
S1B. Library complexity, control sample, replicate 1



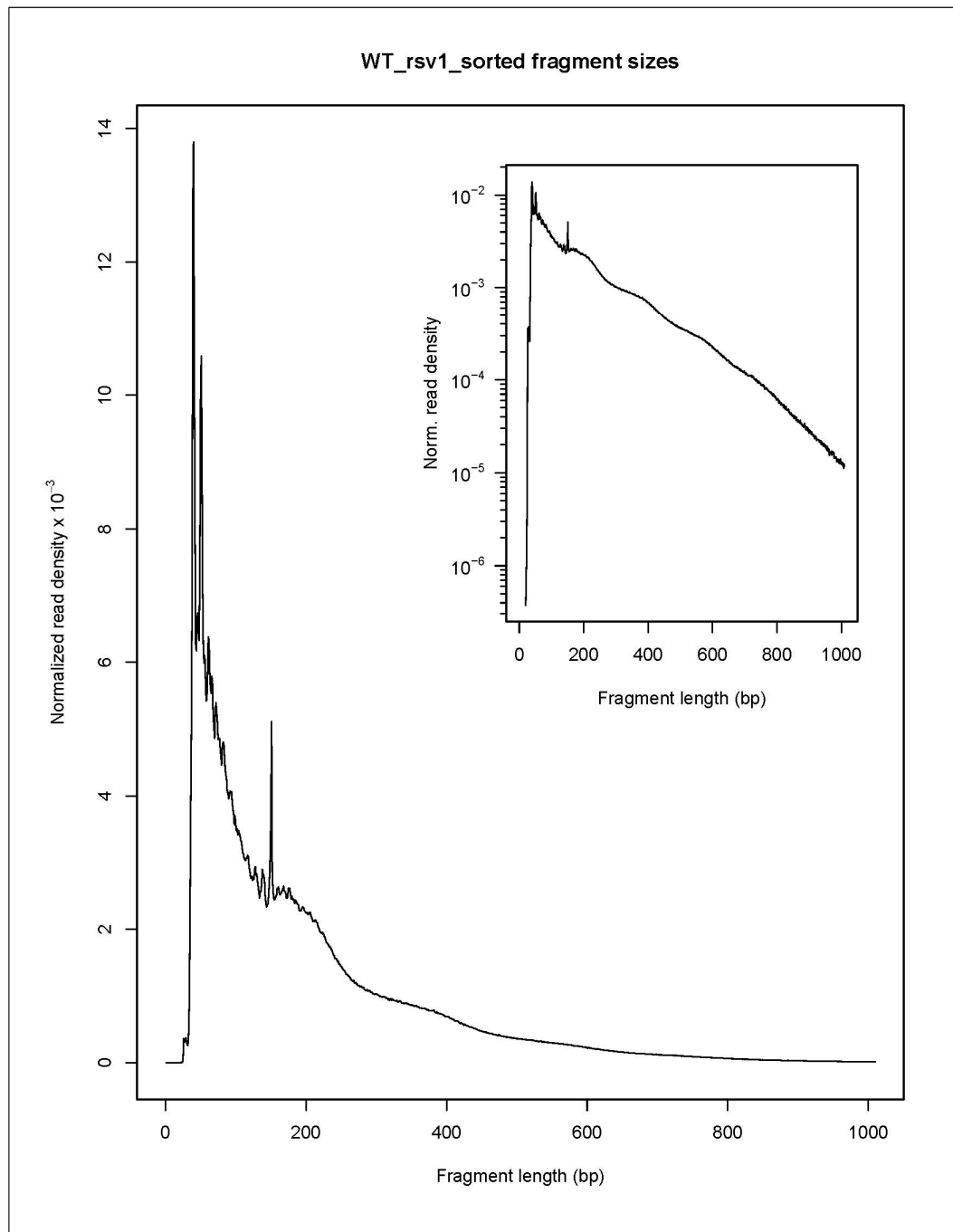
S1C. Fragment size, control sample, replicate 2



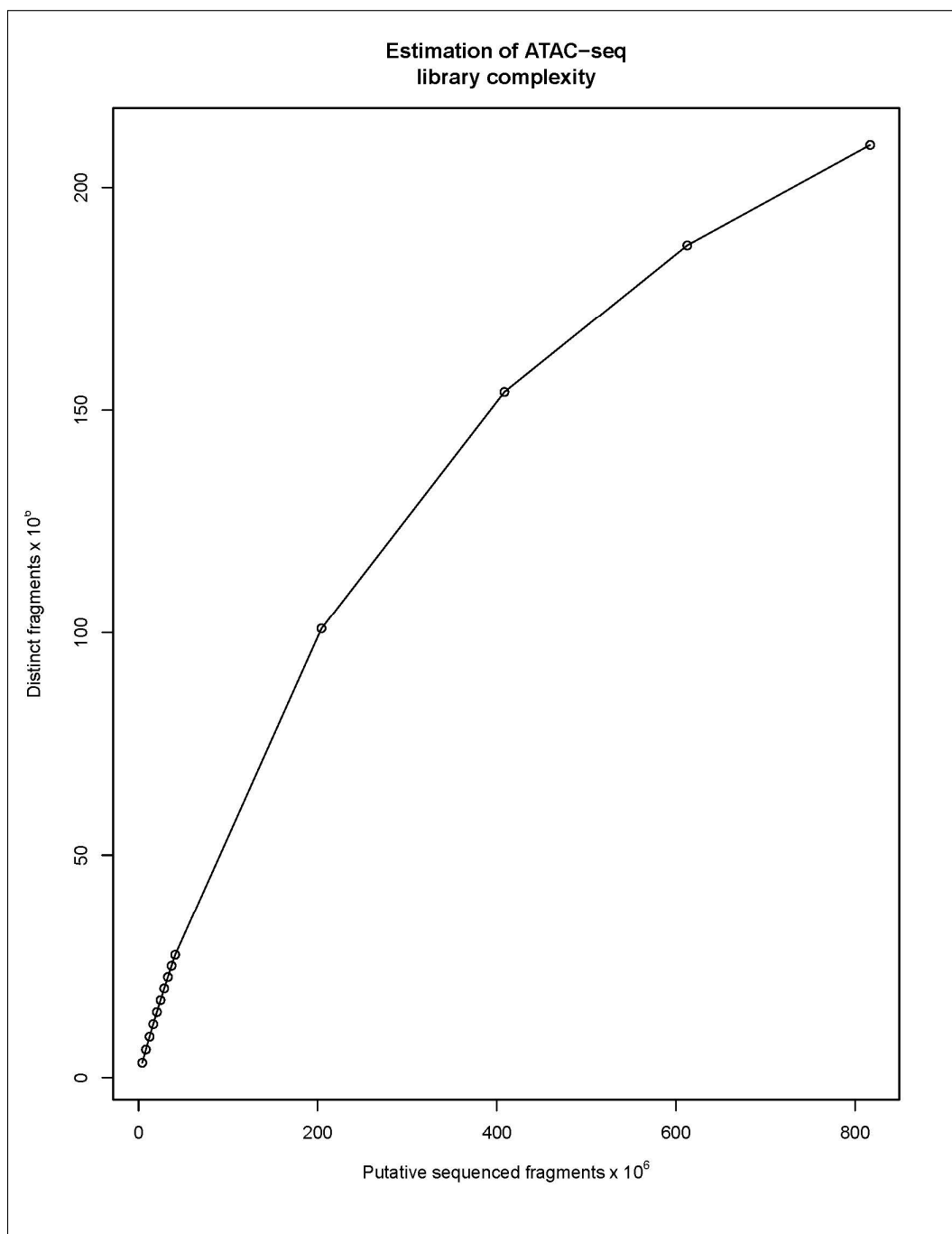
S1D. Library complexity, control sample, replicate 2



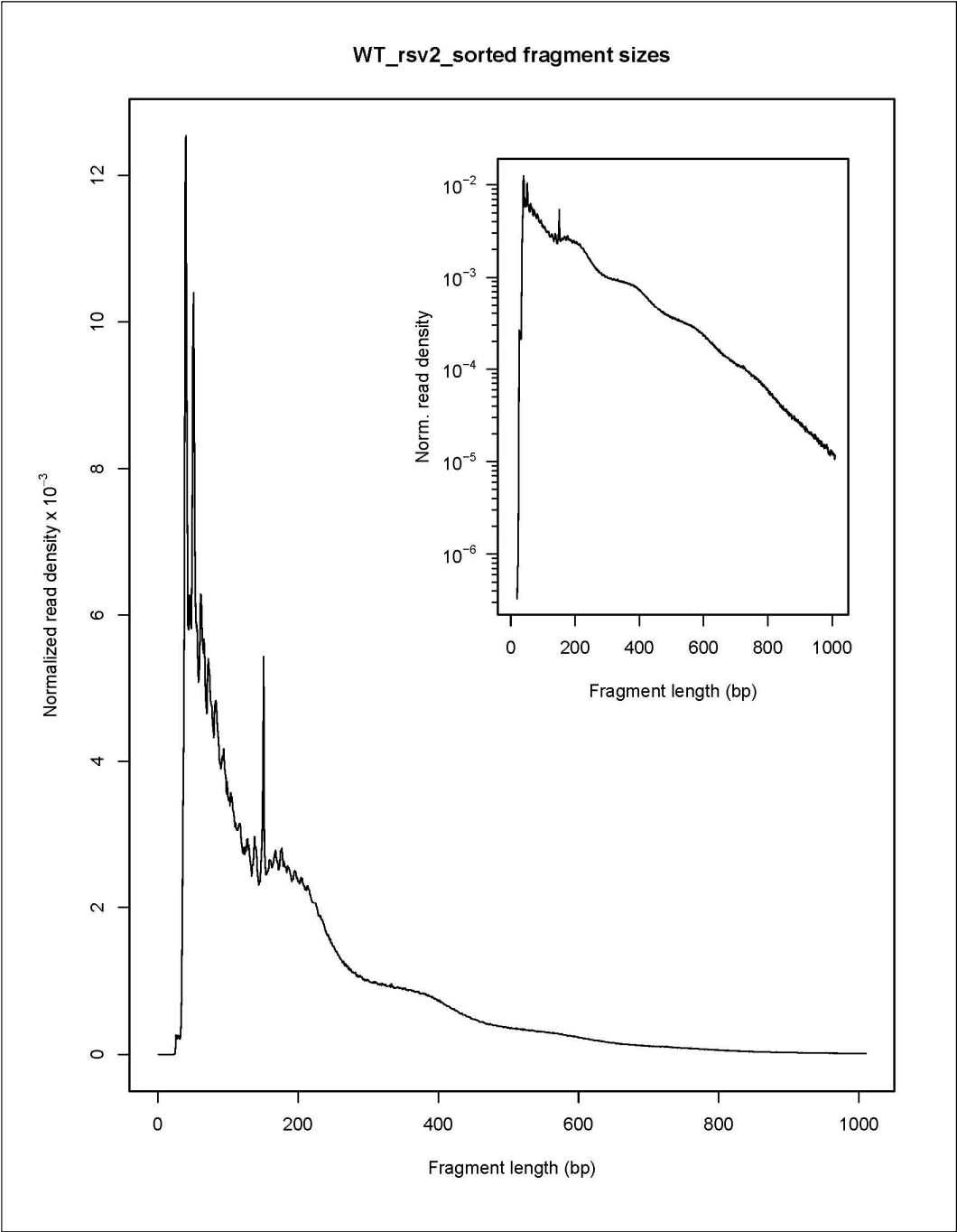
S1E. Fragment size, RSV infected, replicate 1



S1F. Library complexity, RSV sample, replicate 1

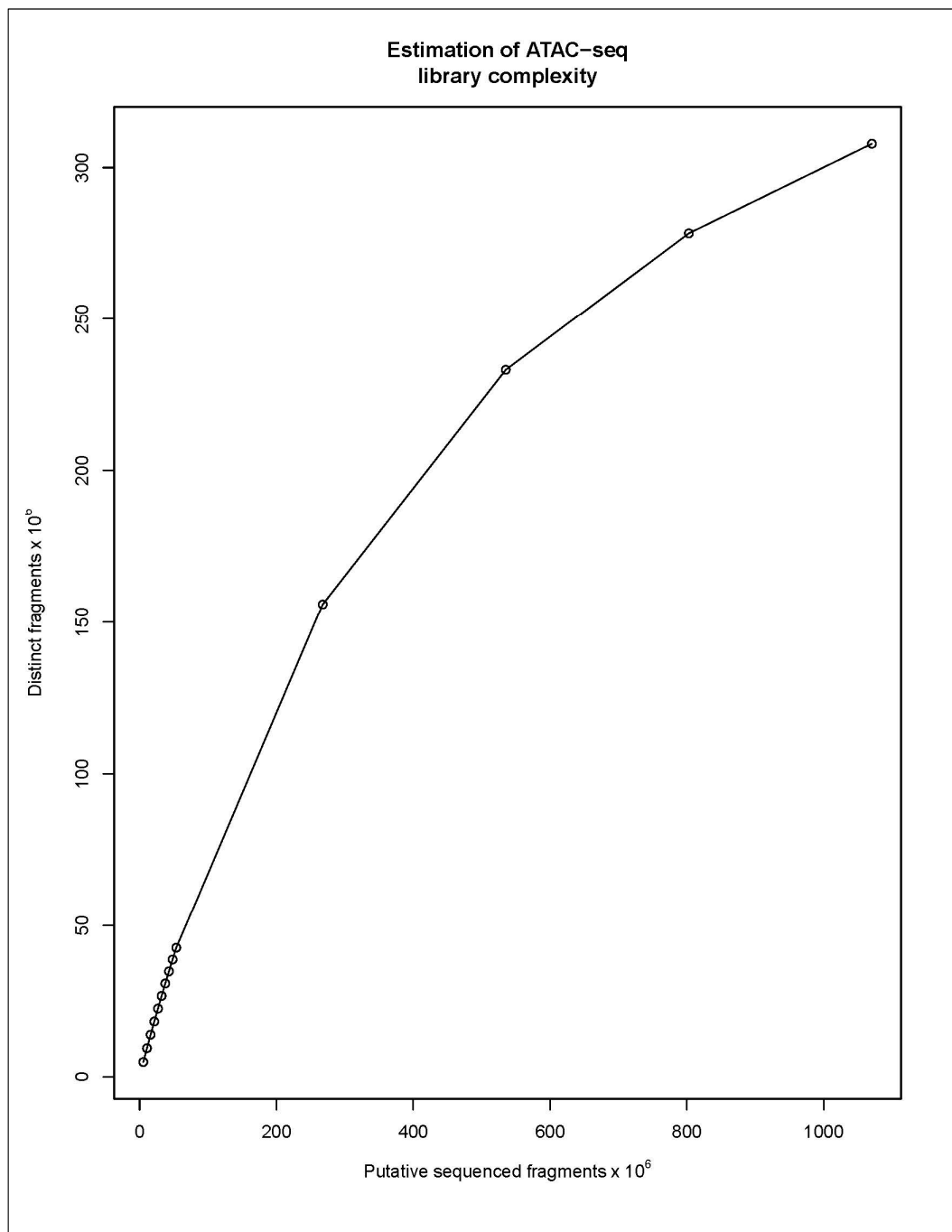


S1G. Fragment size, RSV sample, replicate 2

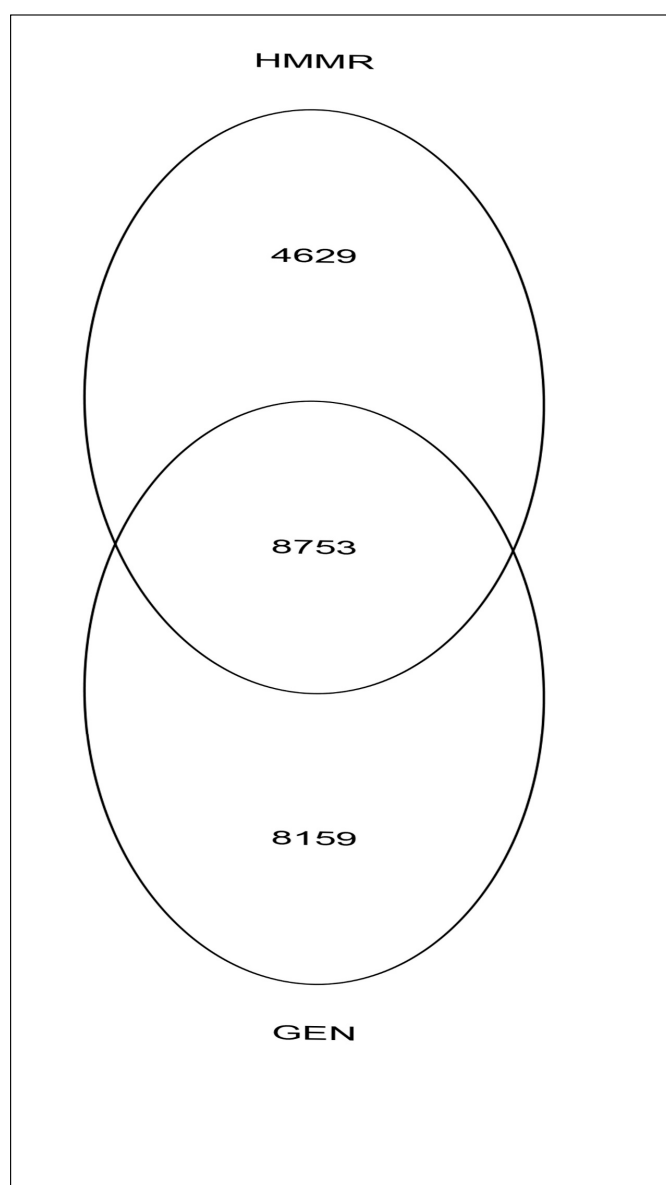




S1H. Library complexity, RSV sample, replicate 2



Supplemental Figure 2. Overlap of read calling algorithms for occupancy analysis. Shown are number of unique genes with ATAC-Seq peaks  $\pm 3$  kb of TSS identified in uninfected hSAECs.



Supplemental Figure 3. Overlap of read calling algorithms for differential analysis. Shown are number of unique genes with ATAC-Seq peaks  $\pm 3$  kb of TSS identified in RSV-infected vs uninfected hSAECs.

