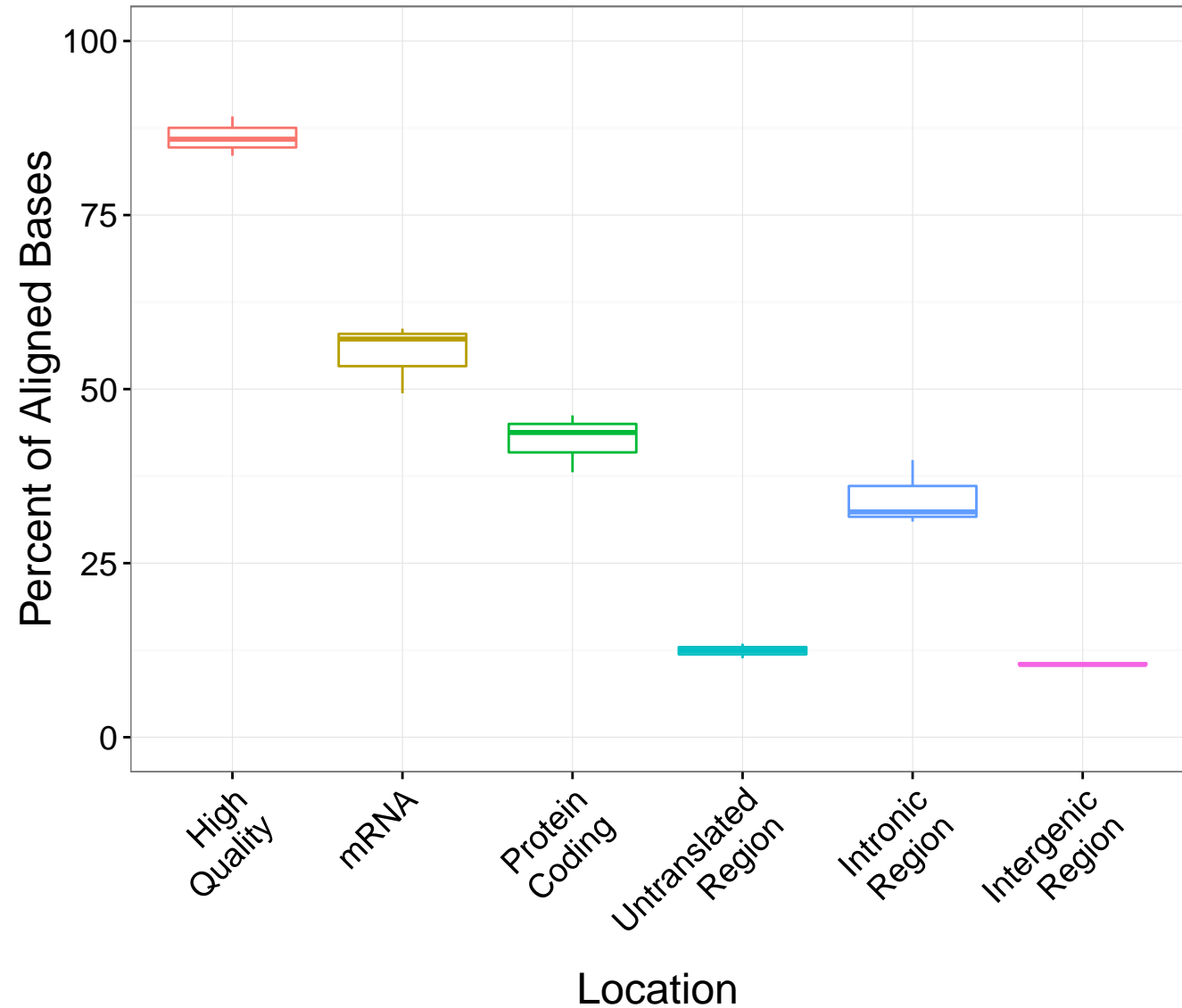
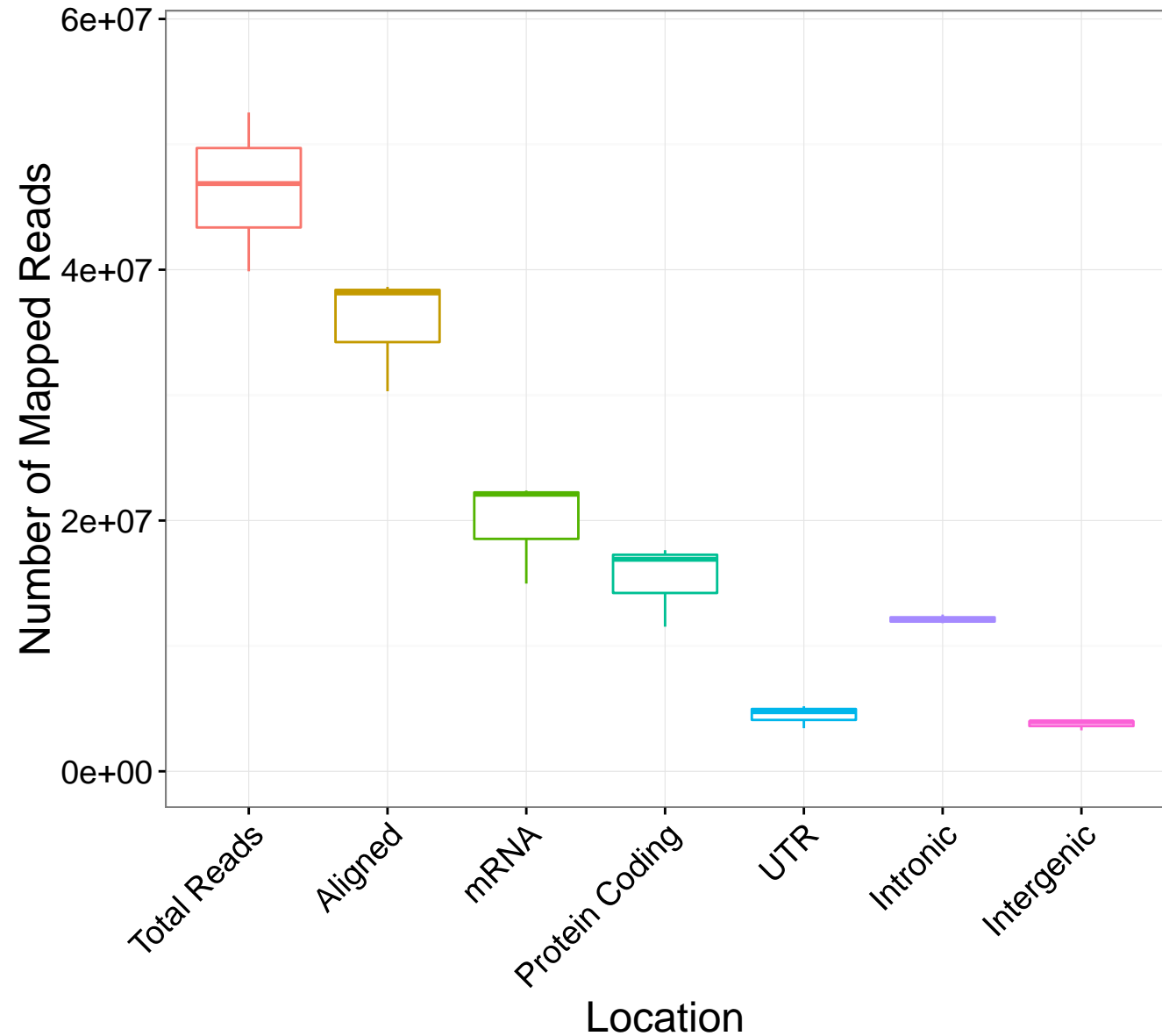


Plot_Picard_QC_Stats_HsMm.R
RNA-seq QC metrics across samples
Percent of Aligned Bases by Location



Plot_Picard_QC_Stats_HsMm.R
Number of Mapped Reads by Location



Plot_Picard_QC_Stats_HsMm.R

Percentage of Mapped Sequence Marked as Duplicate

Mean Percent Duplicate: 65.65

