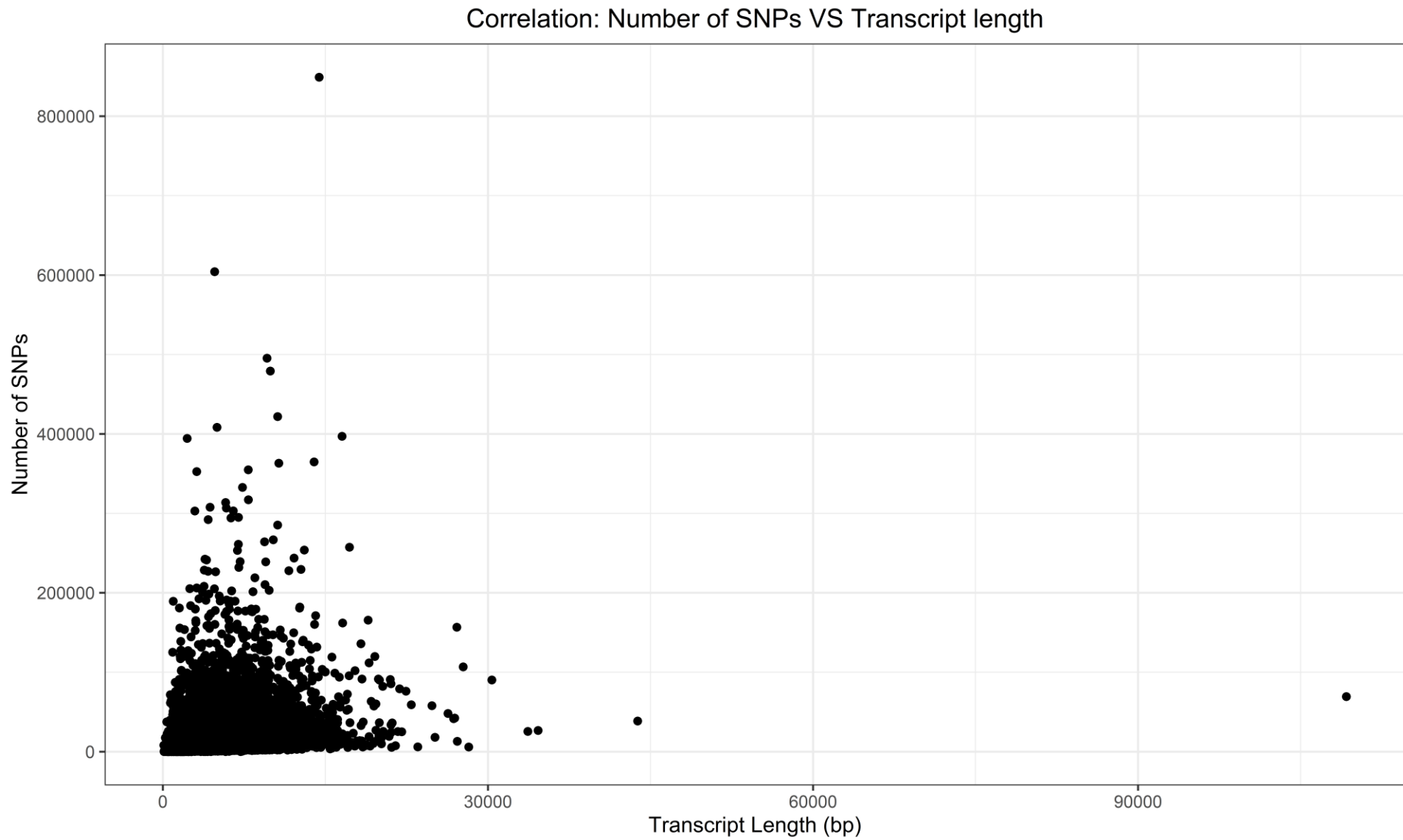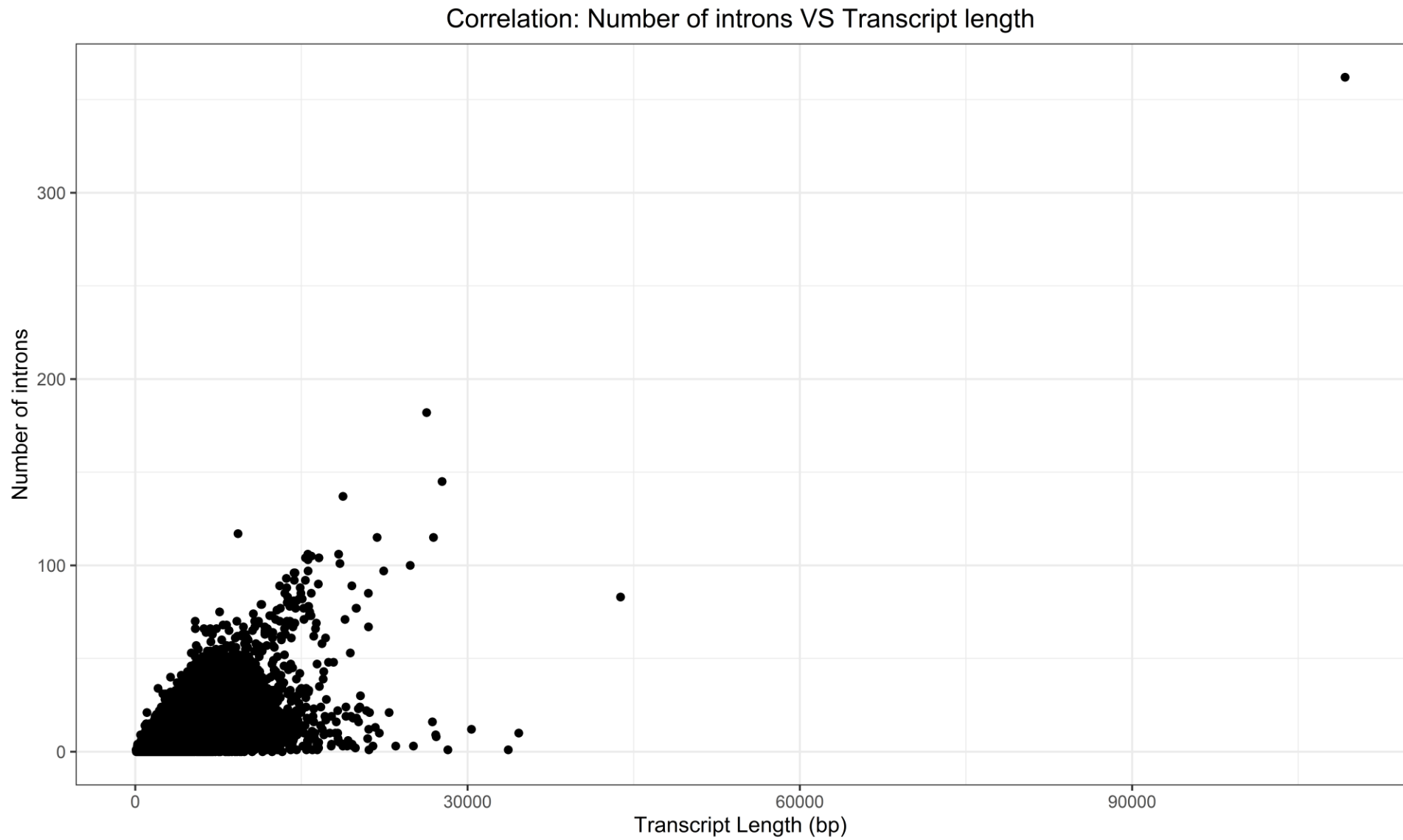**Supplementary Figure 4A.**

Correlation between the Number of SNPs per gene and Gene Length. Gene Length was obtained using the EDASeq package and the Number of SNPs was obtained using the Ensembl API.
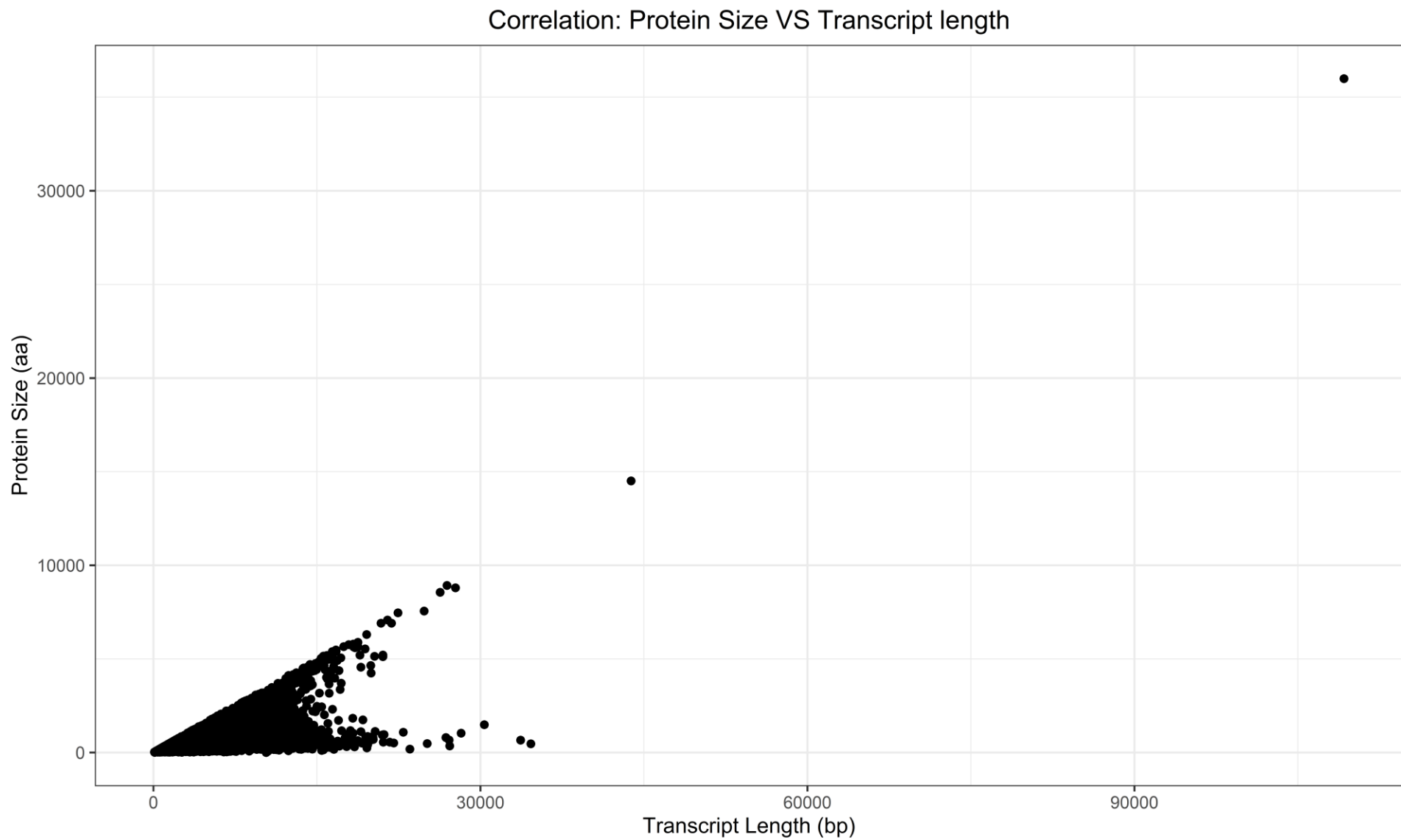
Supplementary Figure 4B.
Correlation between the Number of SNPs and Transcript Length. Number of SNPs and Transcript Length were obtained using biomart.

Correlation: Number of introns VS Transcript length

Supplementary Figure 4C.
Correlation between the number of introns and Transcript Length. Number of introns and Transcript Length were obtained using biomart.
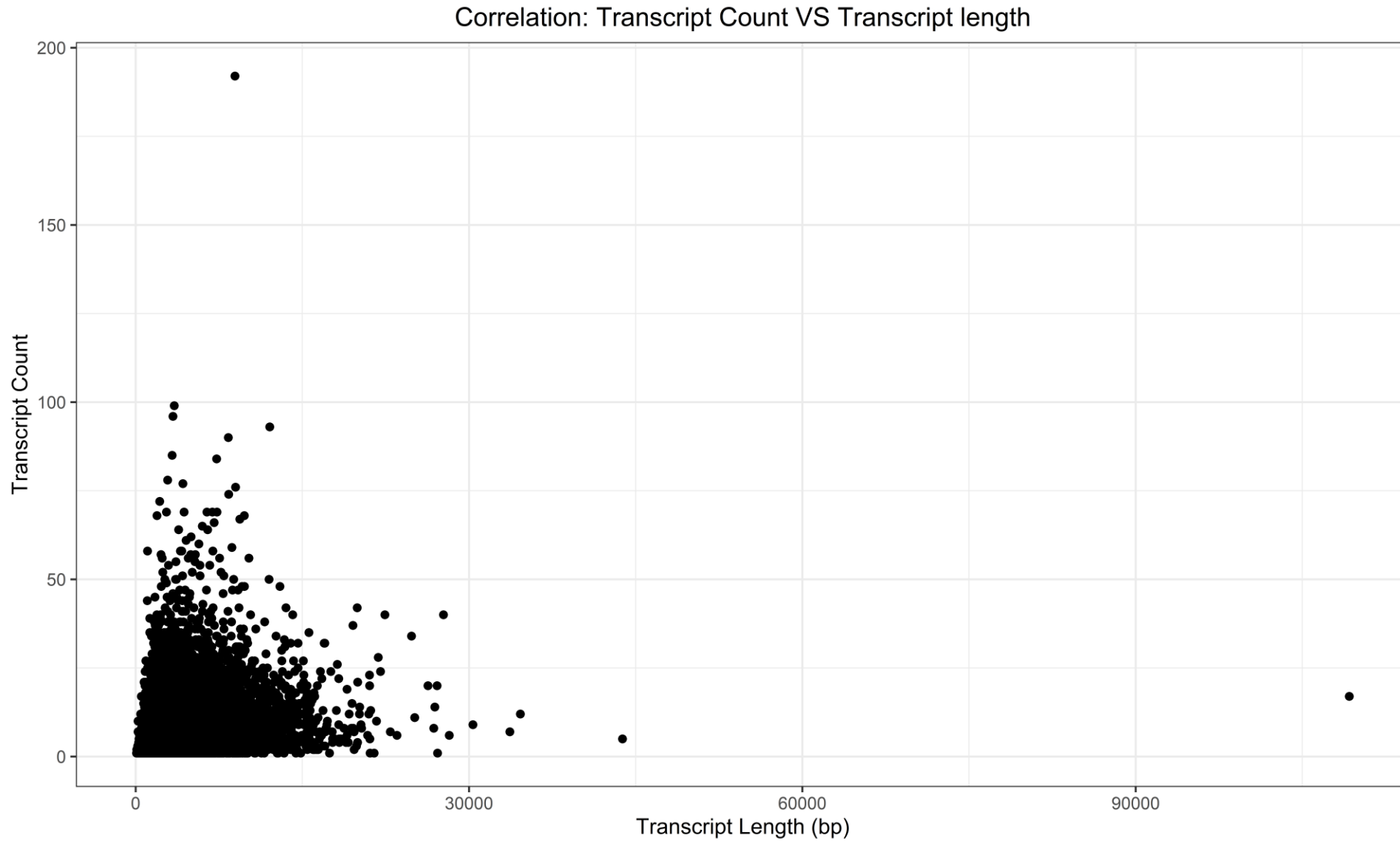
Correlation: Protein Size VS Transcript length

Supplementary Figure 4D.
Correlation between Protein size and Transcript Length. Protein size and Transcript Length were obtained using biomart.
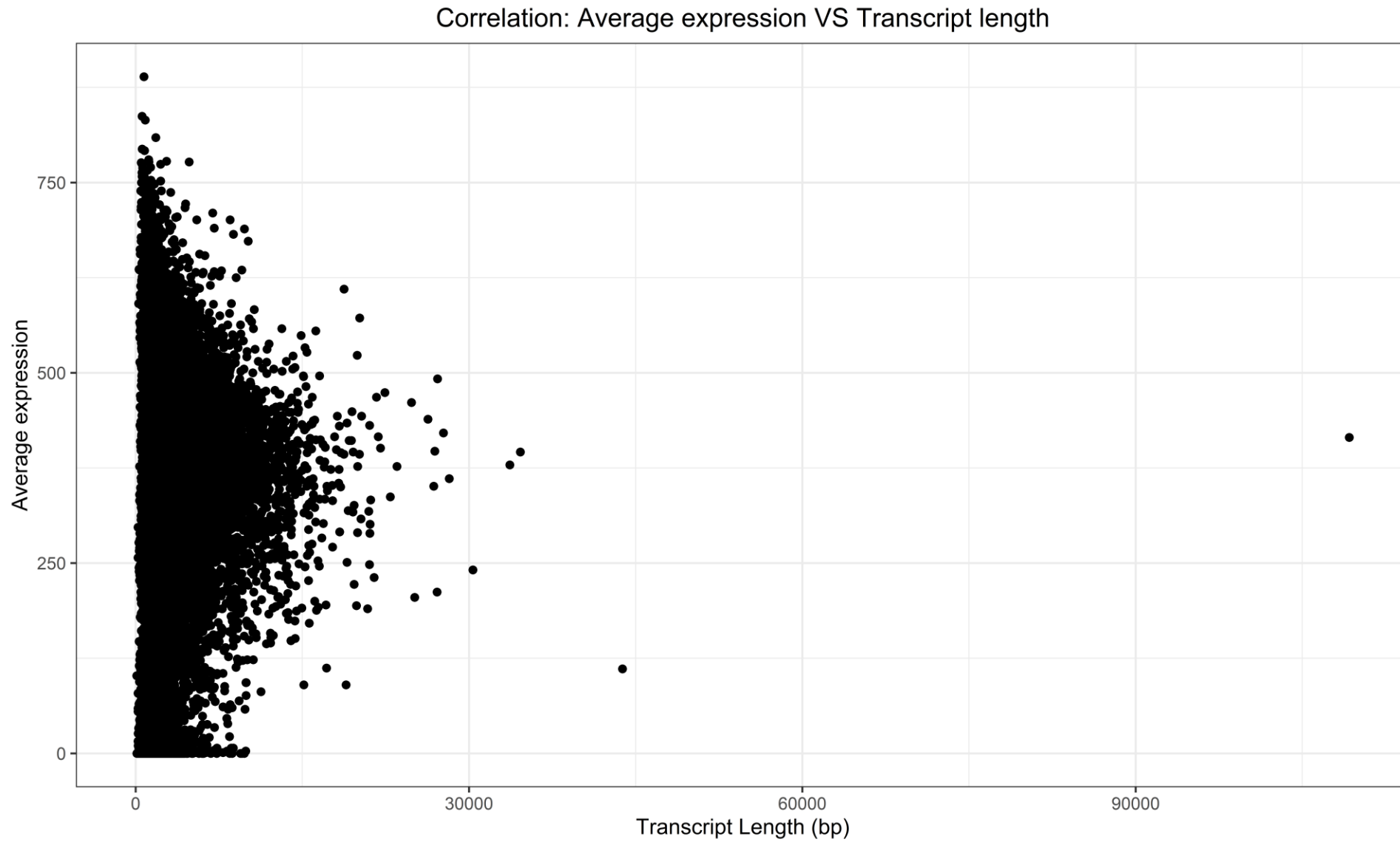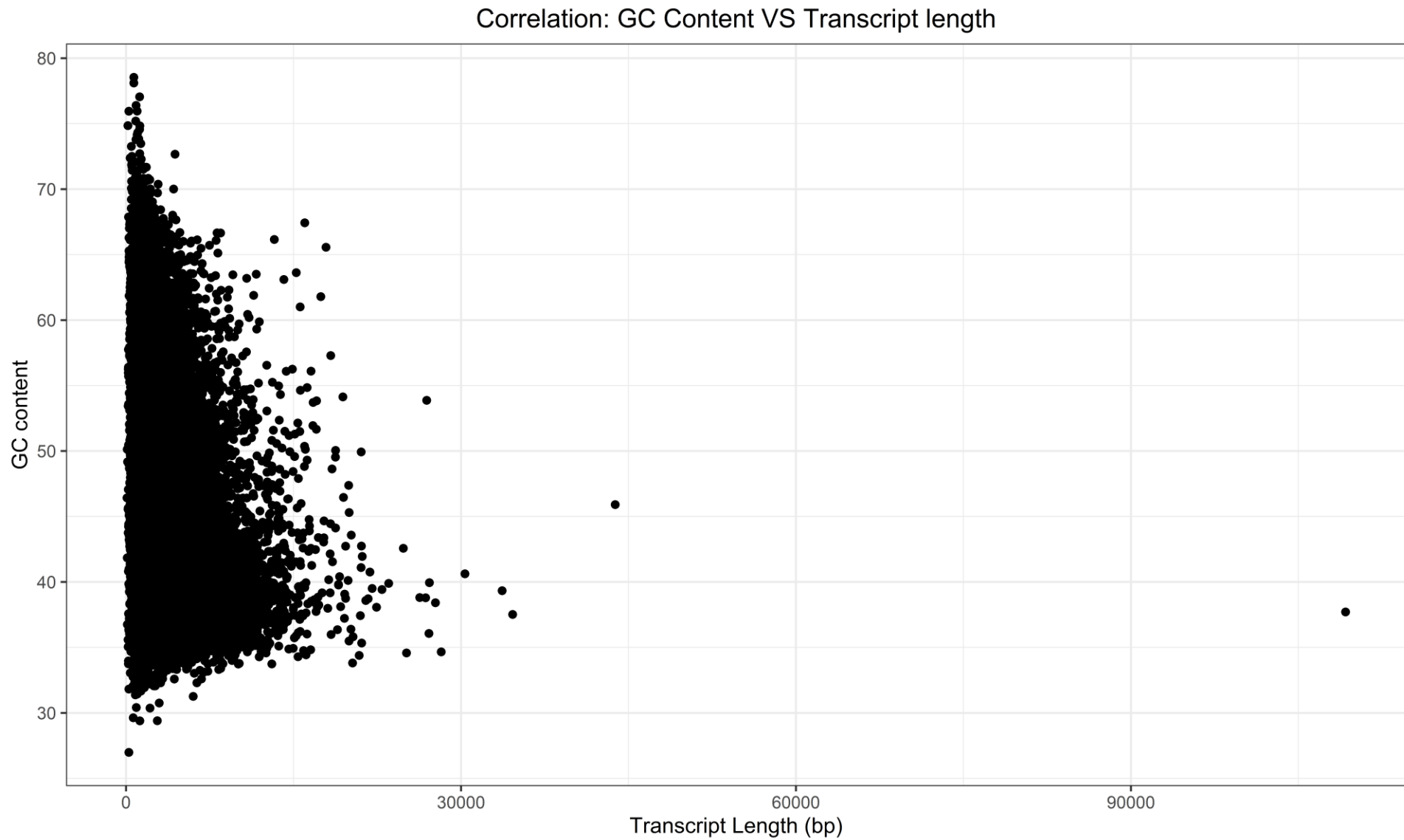
Supplementary Figure 4E.
Correlation between the Average Gene Expression and Transcript Length. Average Gene Expression was obtained from the UCSC Genome browser and Transcript Length was obtained using biomart.
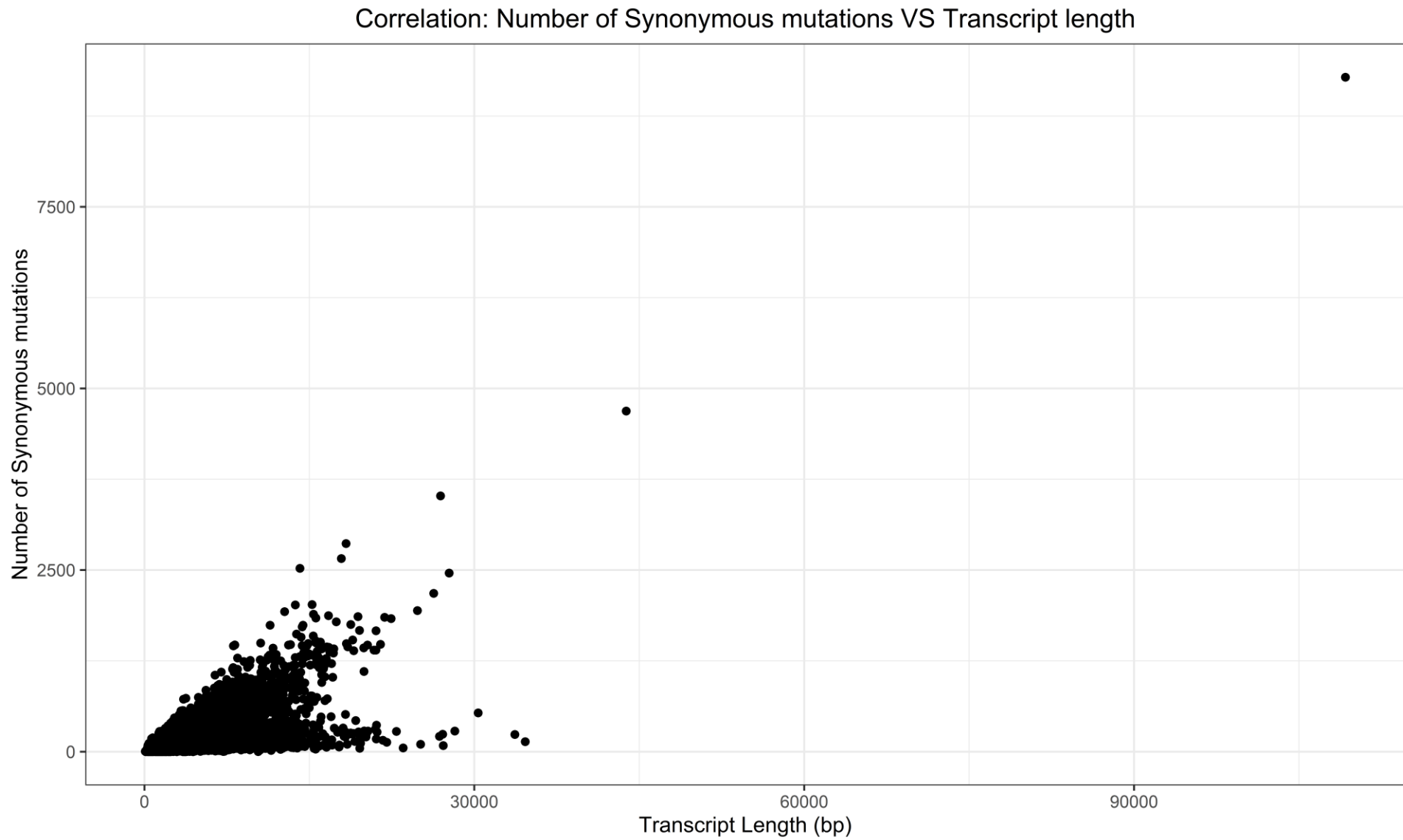
Correlation: Transcript Count VS Transcript length

Supplementary Figure 4F.
Correlation between Transcript count and Transcript Length (bp) (Kendall test, tau = 0.22, p-value < 2.20E-16).
Transcript count and Transcript Length for each transcript were obtained using biomart.

Correlation: GC Content VS Transcript length

Supplementary Figure 4G.
Correlation between the GC Content and Transcript Length (bp) (Kendall test, tau = -0.19, p-value < 2.20E-16). GC Content and Transcript Length were obtained using biomart.
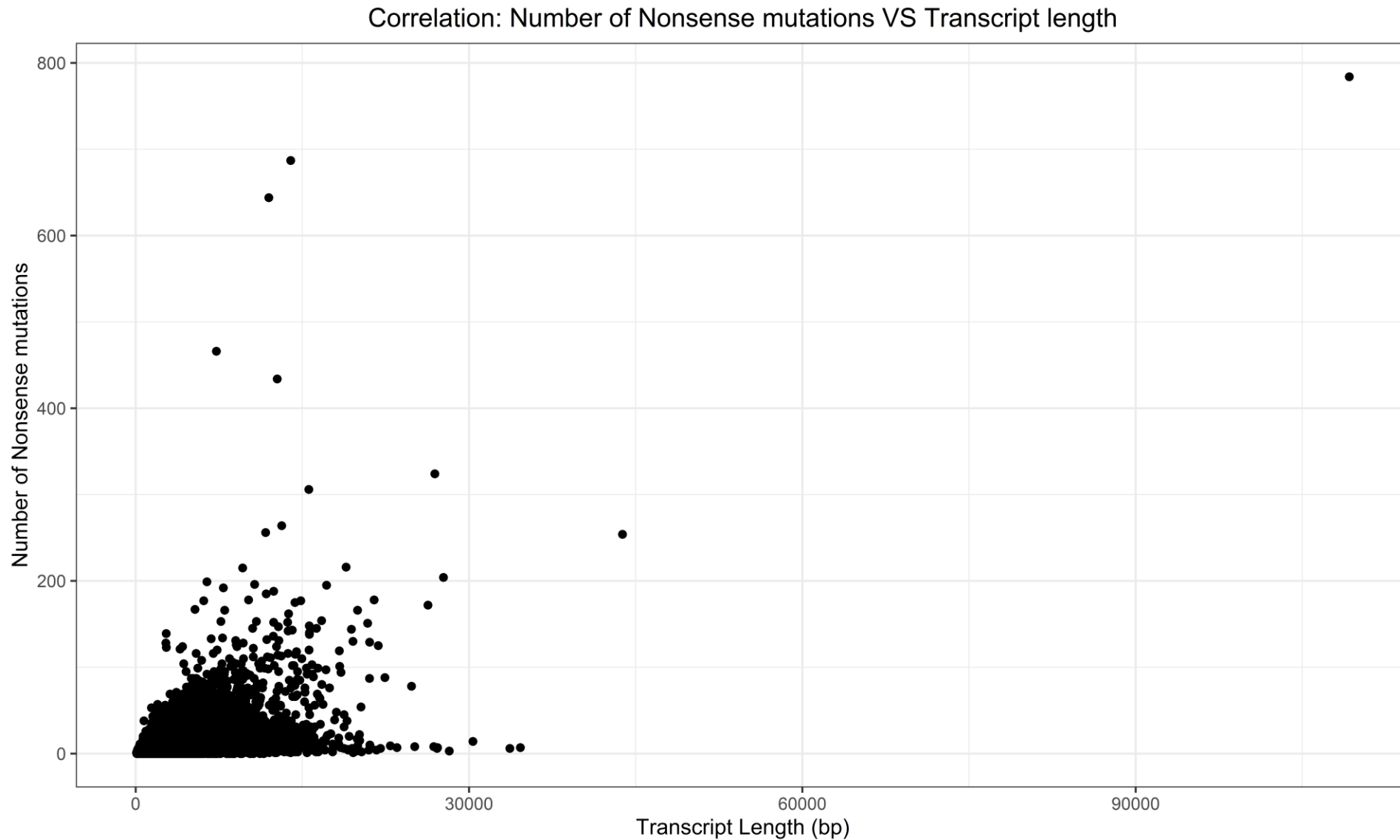
Correlation: Number of Synonymous mutations VS Transcript length

Supplementary Figure 4H.
Correlation between synonymous mutations and Transcript Length (bp) (Kendall test, tau = 0.44, p-value < 2.20E-16). The number of synonymous mutations and Transcript Length were obtained using biomart.

Correlation: Number of Missense mutations VS Transcript length

Supplementary Figure 4I.
Correlation between missense mutations and Transcript Length (bp) (Kendall test, tau = 0.42, p-value < 2.20E-16). The number of missense mutations and Transcript Length were obtained using biomart.

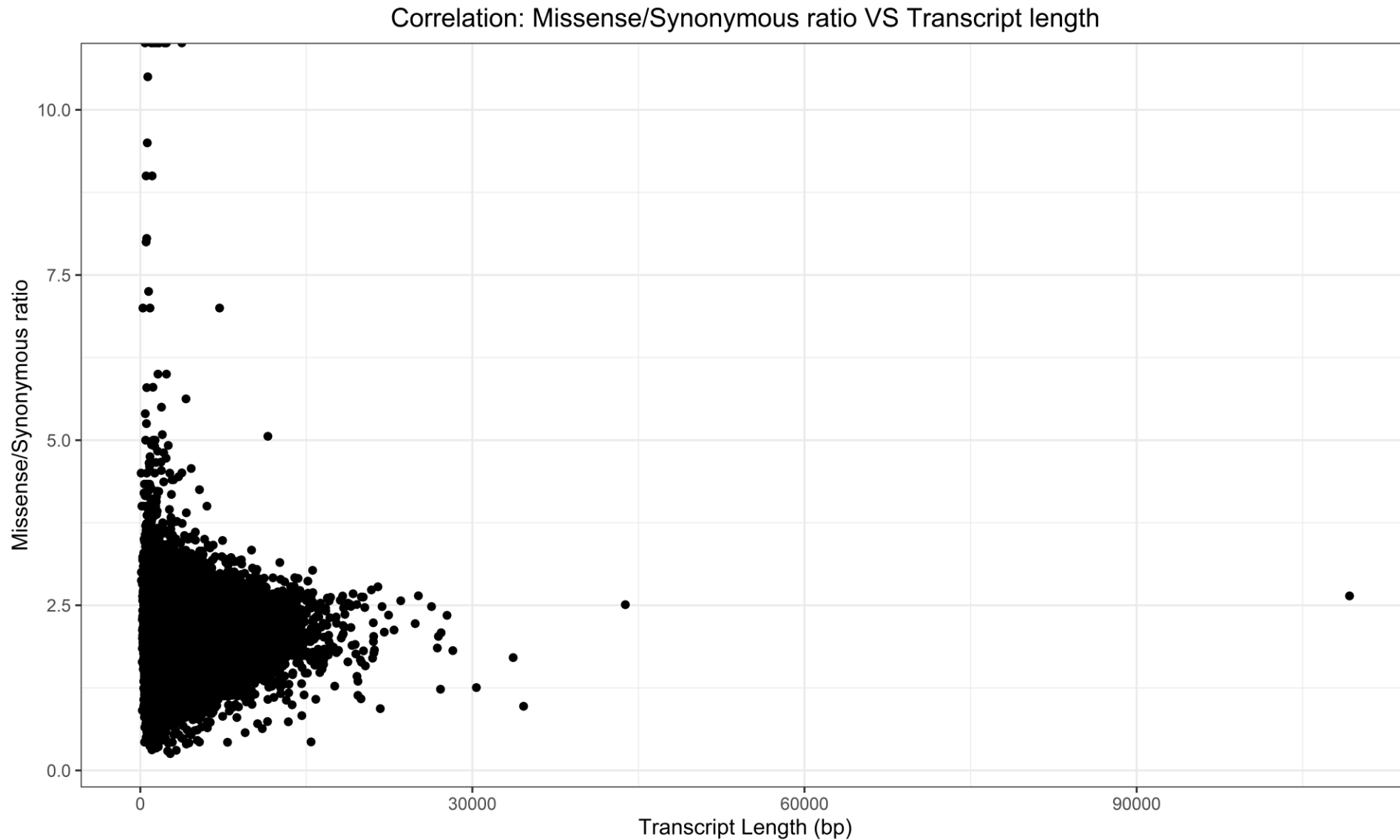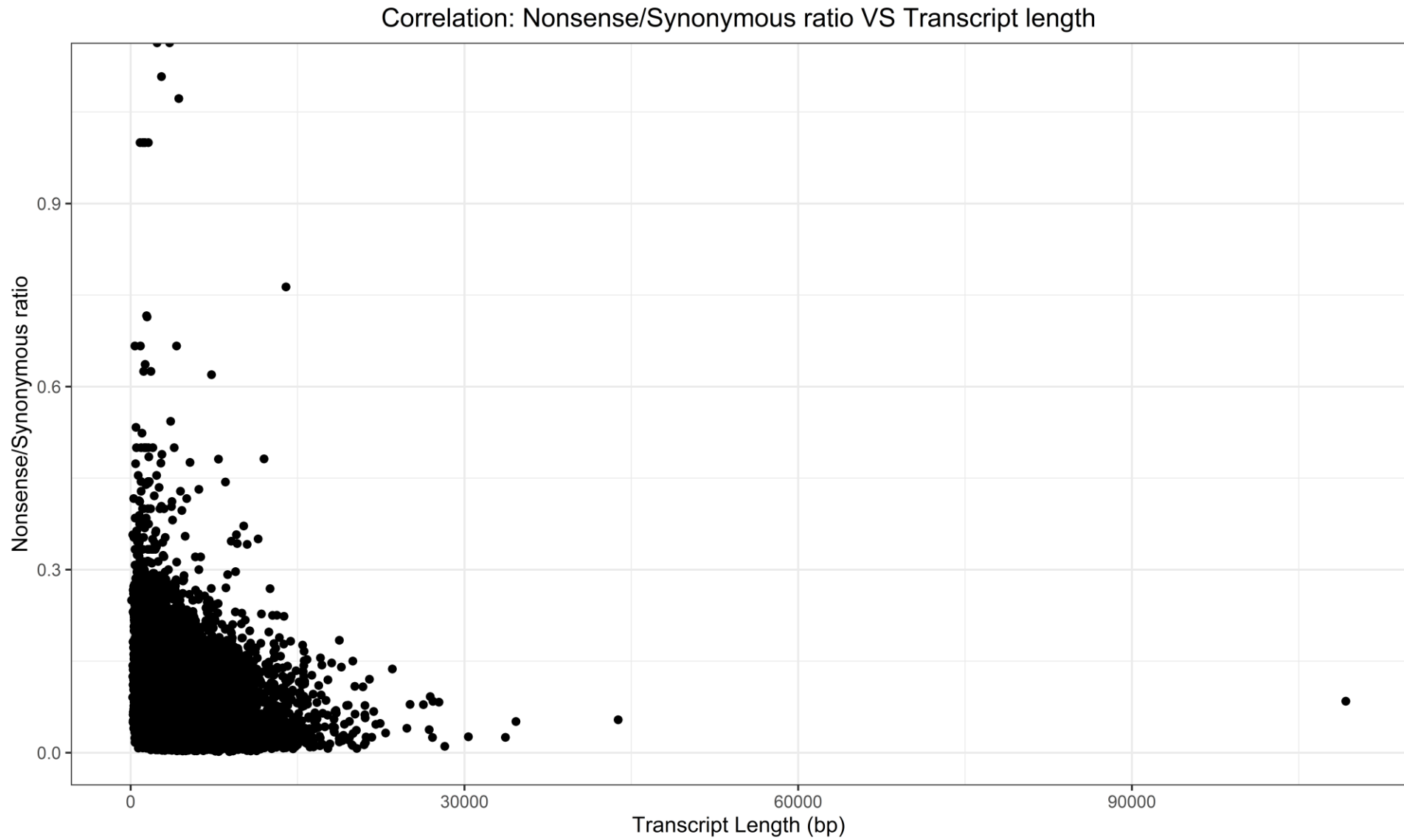**Supplementary Figure 4J.**
Correlation between nonsense mutations and Transcript Length (bp) (Kendall test, tau = 0.21, p-value < 2.20E-16). The number of nonsense mutations and Transcript Length were obtained using biomart.

Correlation: Missense/Synonymous ratio VS Transcript length

Supplementary Figure 4K.
Correlation between the missense/synonymous ratio of mutations and Transcript Length (bp) (Kendall test, tau = -0.07, p-value < 2.20E-16). The number of missense and synonymous mutations and Transcript Length were obtained using biomart.

Correlation: Nonsense/Synonymous ratio VS Transcript length

Supplementary Figure 4L.
Correlation between the nonsense/synonymous ratio of mutations and Transcript Length (bp) (Kendall test, tau = -0.19, p-value < 2.20E-16). The number of nonsense and synonymous mutations and Transcript Length were obtained using biomart.