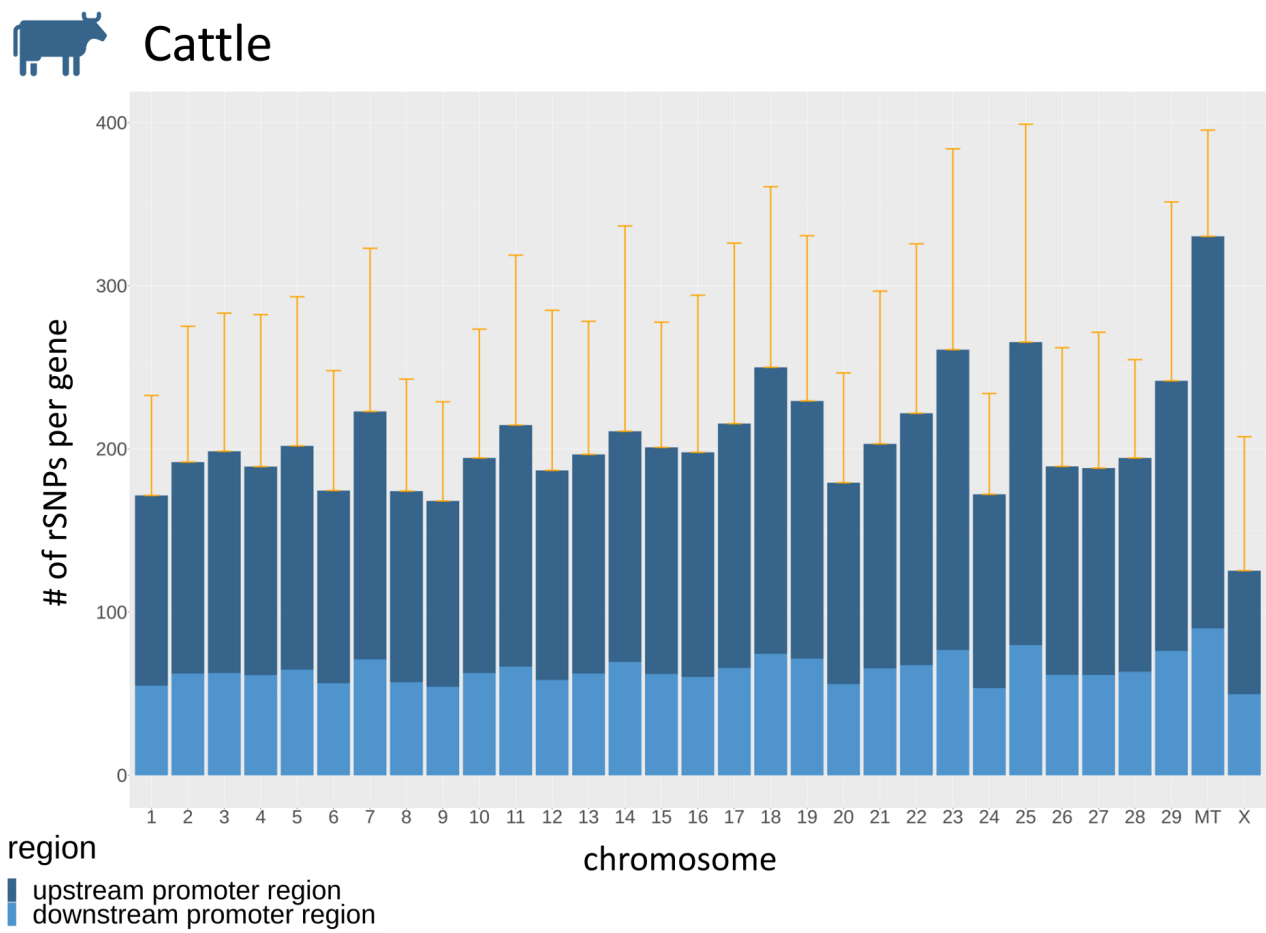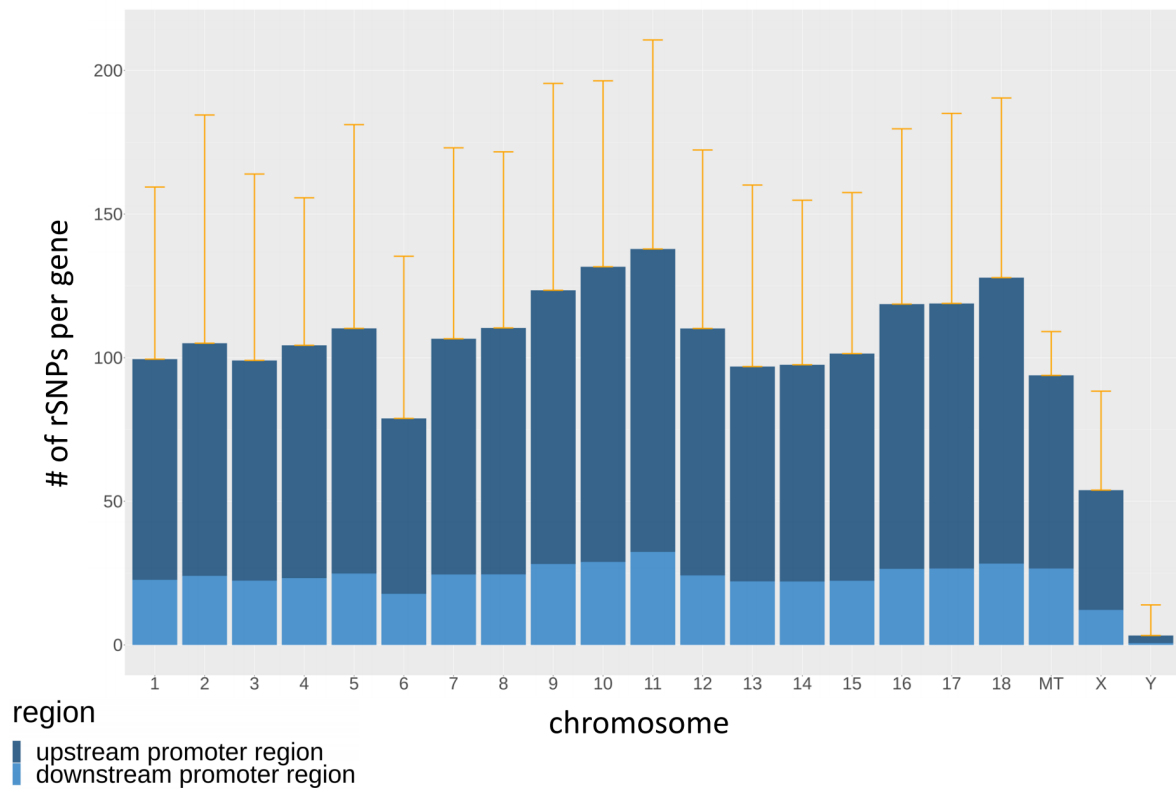**Supplementary Figures S3:** The average number of rSNPs in promoter regions per gene for each chromosome divided into upstream and downstream promoter for each animal stored in agReg-SNPdb.

Figure S3.1: The average number of rSNPs in promoter regions per gene for each chromosome of cattle, divided into upstream and downstream promoter. The orange whiskers denote the mean plus one standard deviation.
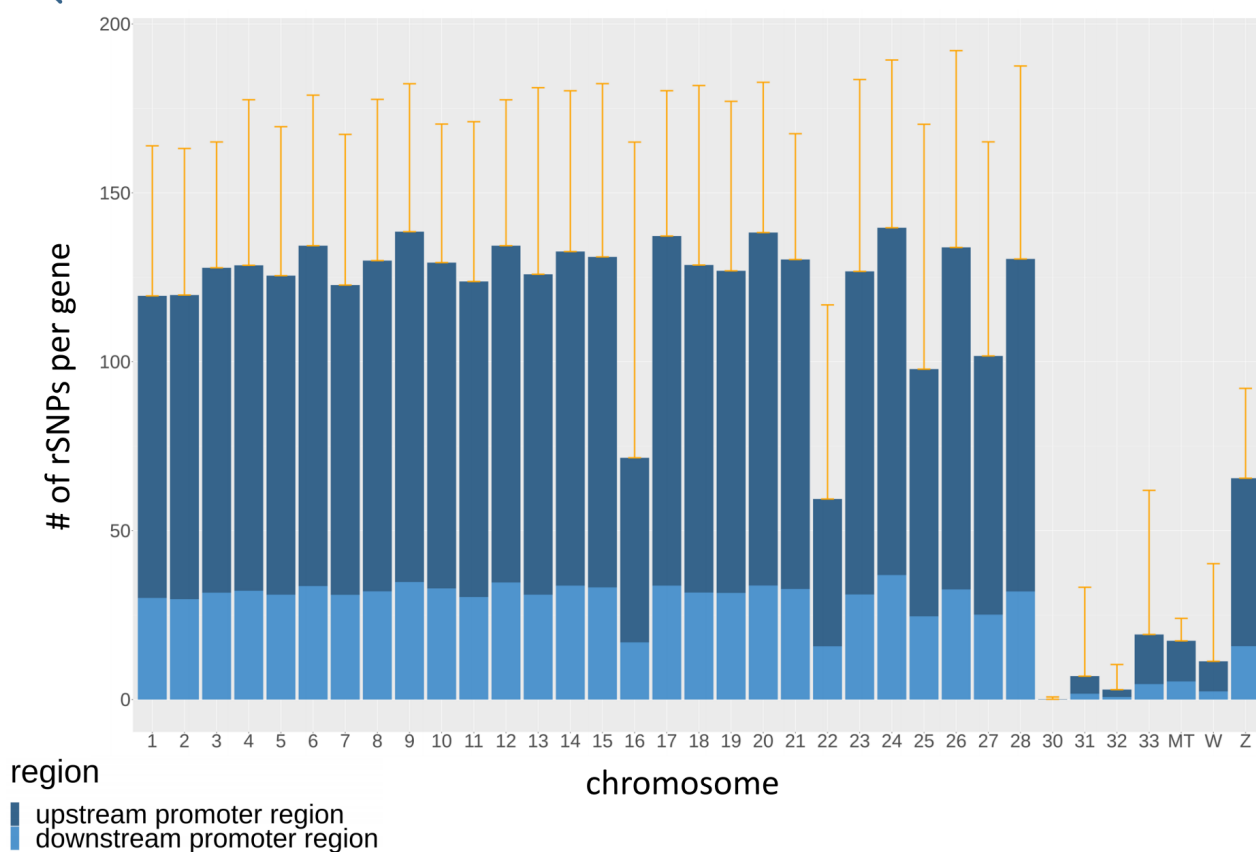
Figure S3.2: The average number of rSNPs in promoter regions per gene for each chromosome of pig, divided into upstream and downstream promoter. The orange whiskers denote the mean plus one standard deviation.
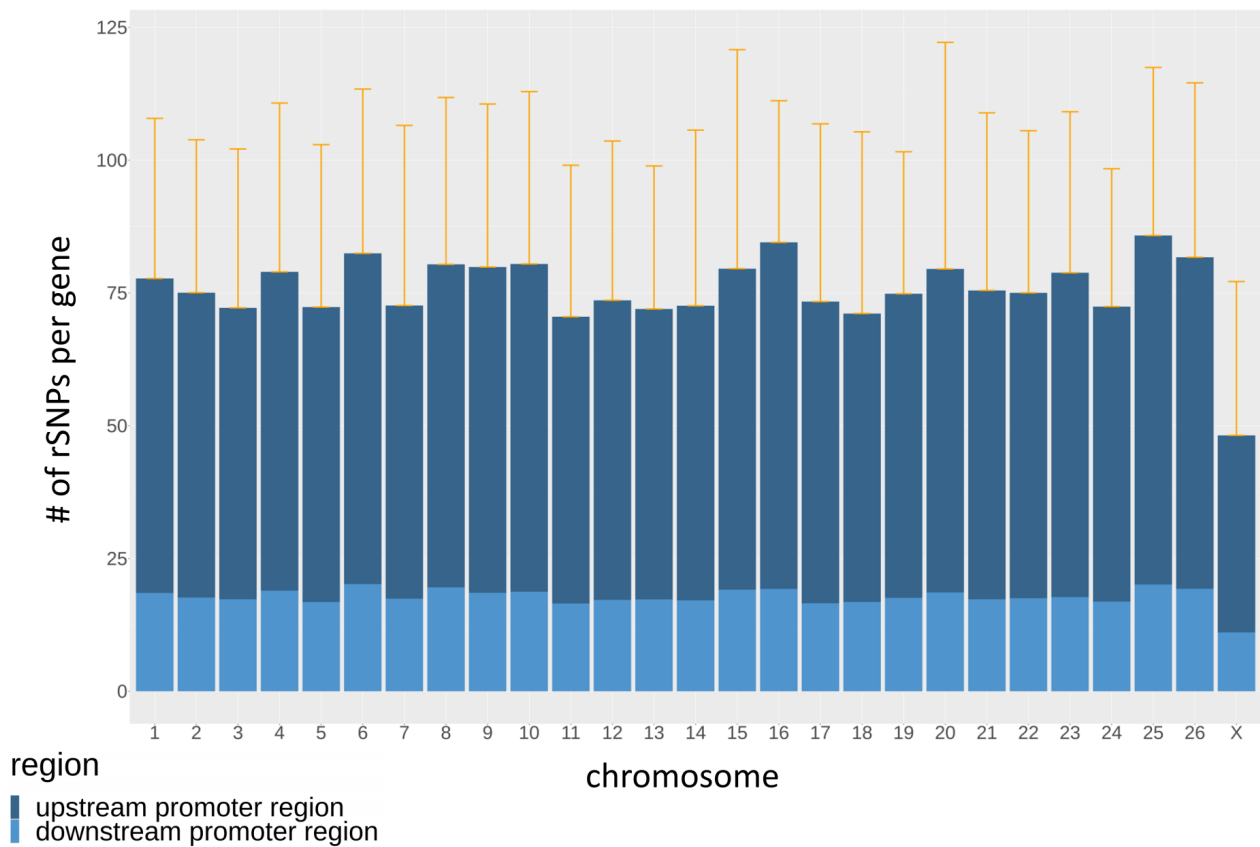
Figure S3.3: The average number of rSNPs in promoter regions per gene for each chromosome of chicken, divided into upstream and downstream promoter. The orange whiskers denote the mean plus one standard deviation.

Figure S3.4: The average number of rSNPs in promoter regions per gene for each chromosome of sheep, divided into upstream and downstream promoter. The orange whiskers denote the mean plus one standard deviation.
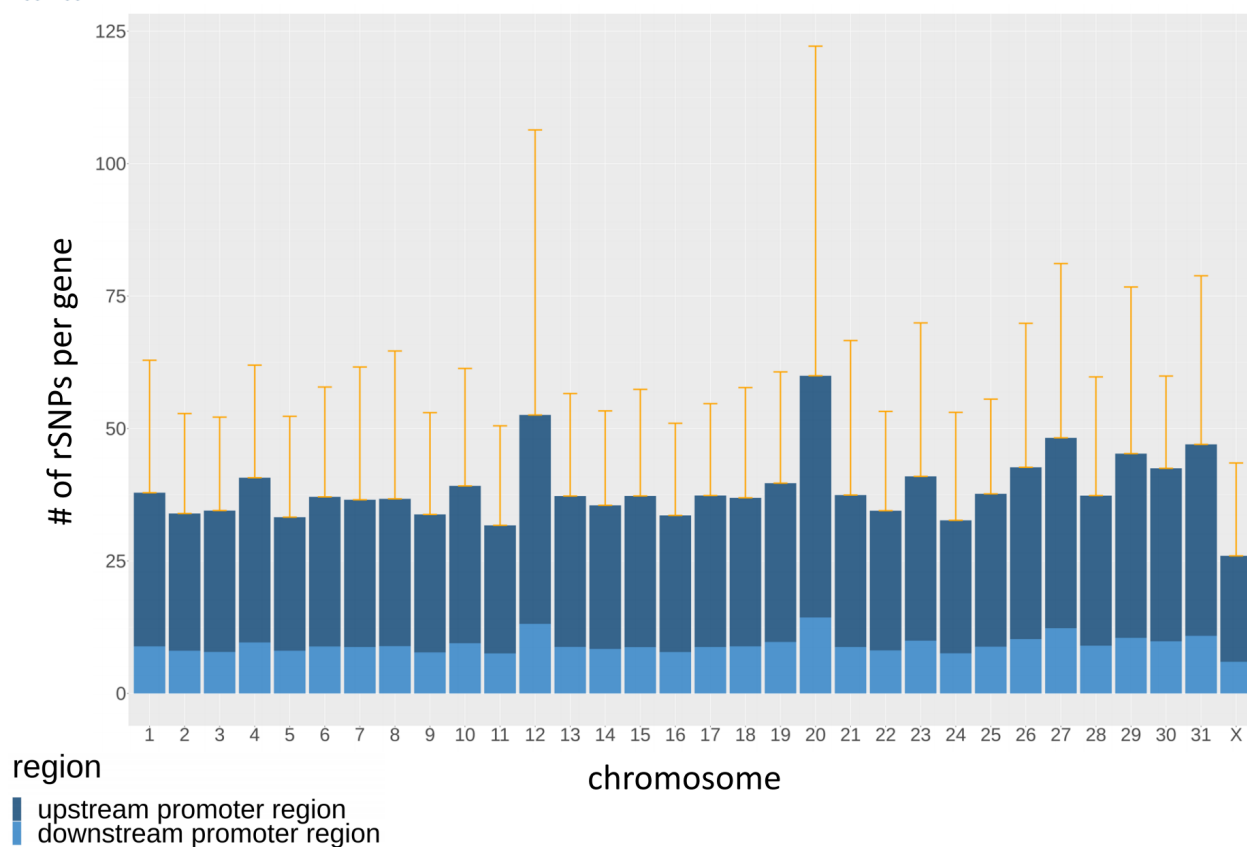
Figure S3.5: The average number of rSNPs in promoter regions per gene for each chromosome of horse, divided into upstream and downstream promoter. The orange whiskers denote the mean plus one standard deviation.
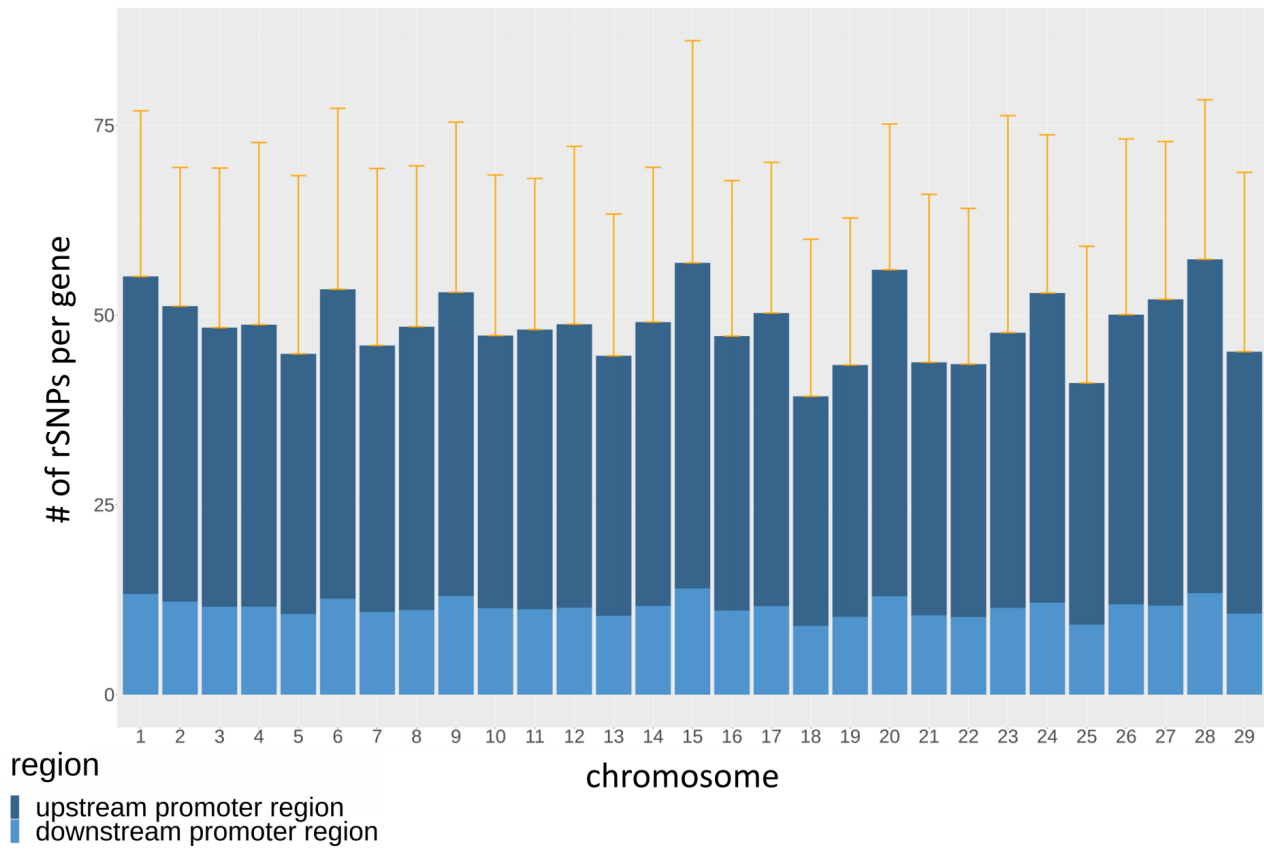
Figure S3.6: The average number of rSNPs in promoter regions per gene for each chromosome of goat, divided into upstream and downstream promoter. The orange whiskers denote the mean plus one standard deviation.
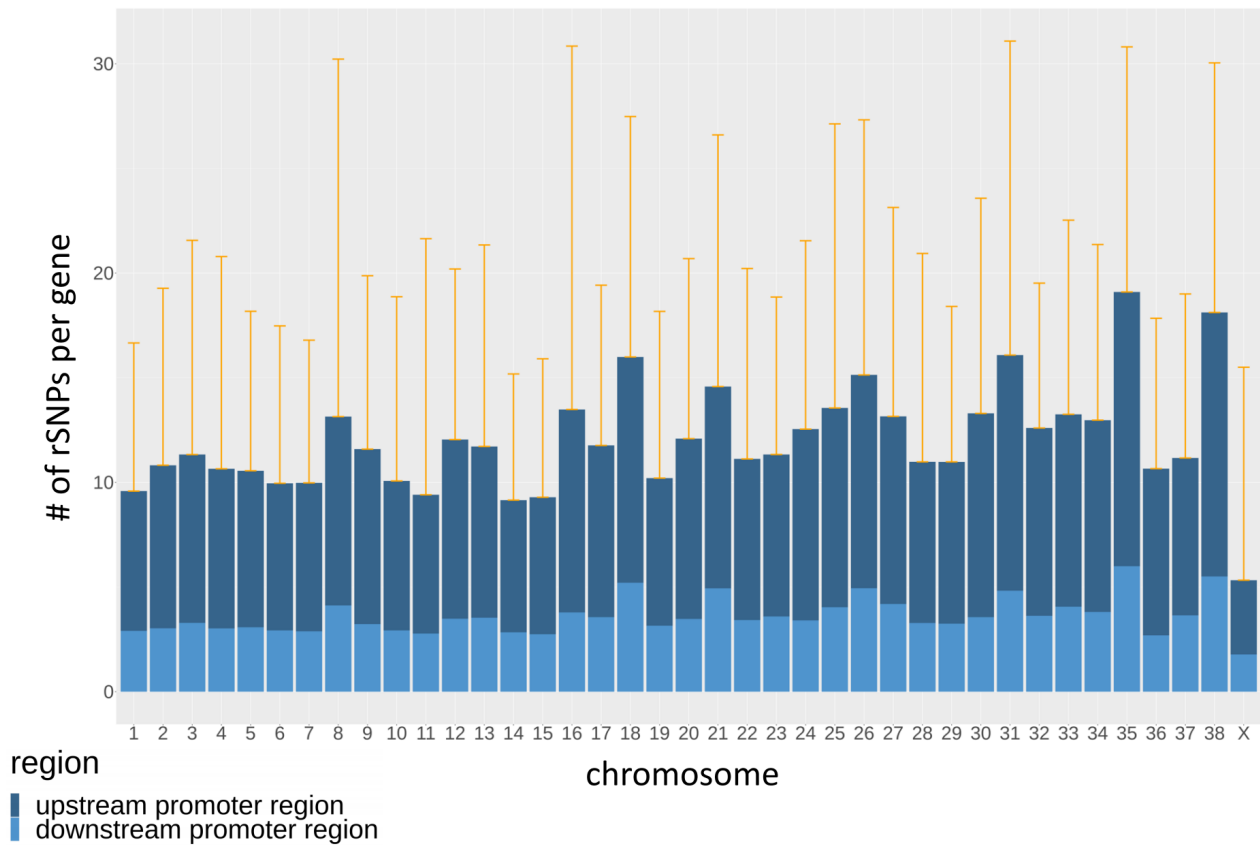
Figure S3.7: The average number of rSNPs in promoter regions per gene for each chromosome of dog, divided into upstream and downstream promoter. The orange whiskers denote the mean plus one standard deviation.