

Patterns of DNA variation between the autosomes, the X chromosome and the Y chromosome in *Bos taurus* genome

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CONCLUSIONS

- ▶ fewer extreme variants are consistent with purging due to the homozygous state in males
- ▶ accumulation of nonsynonymous mutations on the BTY could be associated with loss of recombination
- ▶ variants in transcription regions on BTX have less severe consequences as compared to BTY and autosomes

MATERIAL

- ▶ 217 individuals of 7 Danish cattle breeds
- ▶ WGS – Illumina HiSeq 2000
- ▶ assembly: ARS-UCD1.2_Btau5.0.1Y
- ▶ Btau_5.0.1 and ARS-UCD1.2 GFFs

RESULTS

- ▶ 23,655,295 SNPs / 3,758,781 InDels
- ▶ numbers of SNPs and InDels not uniformly distributed across 100kb non-overlapping windows ($P < 0.001$)
- ▶ Ka/Ks ratio: BTA = 0.79 BTX = 0.62 BTY = 2.00

METHODS



Statistical analysis:

- variant density on each chromosome
- InDel length • Ka/Ks ratio • nucleotide divergence
- Tajima's D • SIFT score

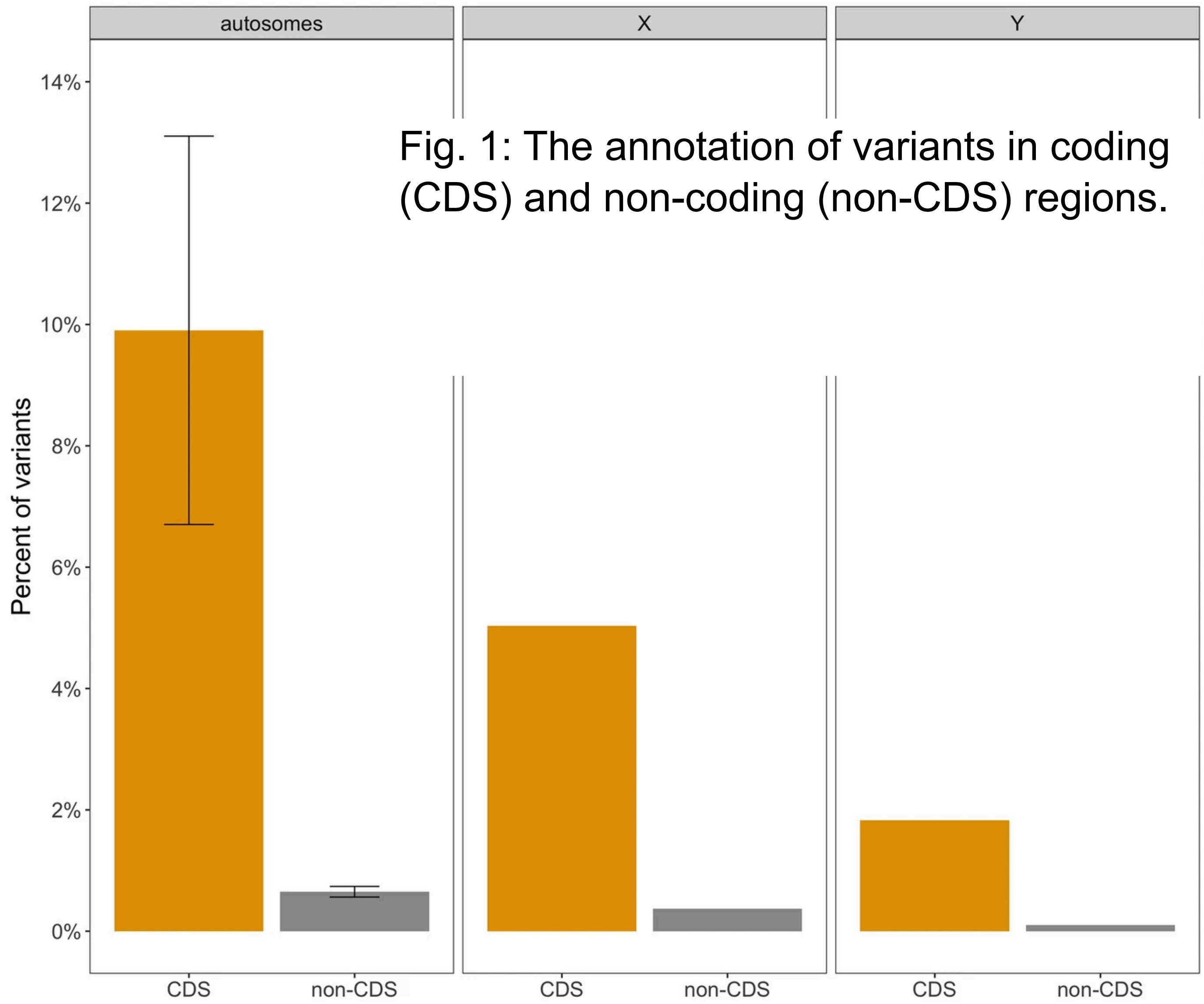


Fig. 1: The annotation of variants in coding (CDS) and non-coding (non-CDS) regions.

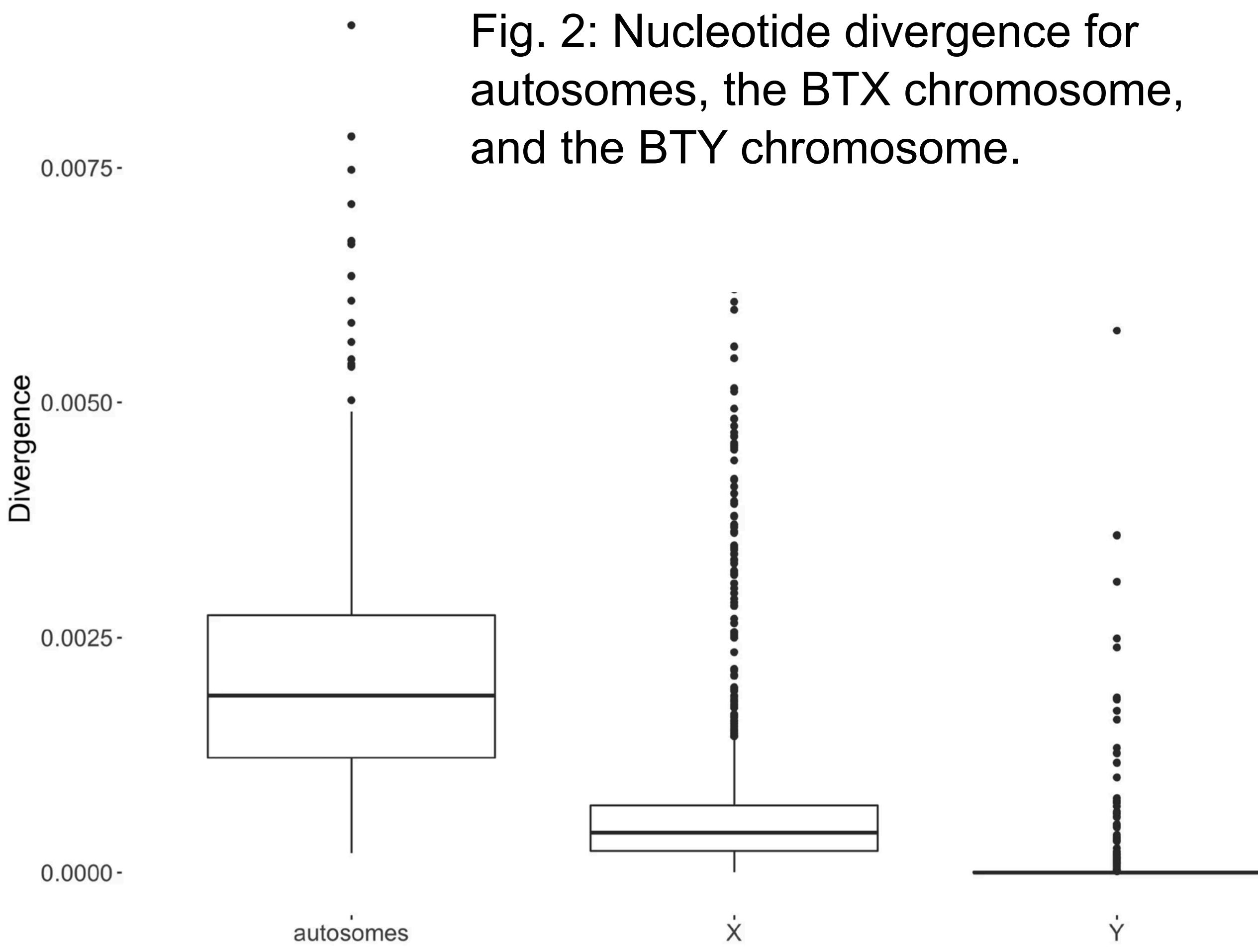


Fig. 2: Nucleotide divergence for autosomes, the BTX chromosome, and the BTY chromosome.

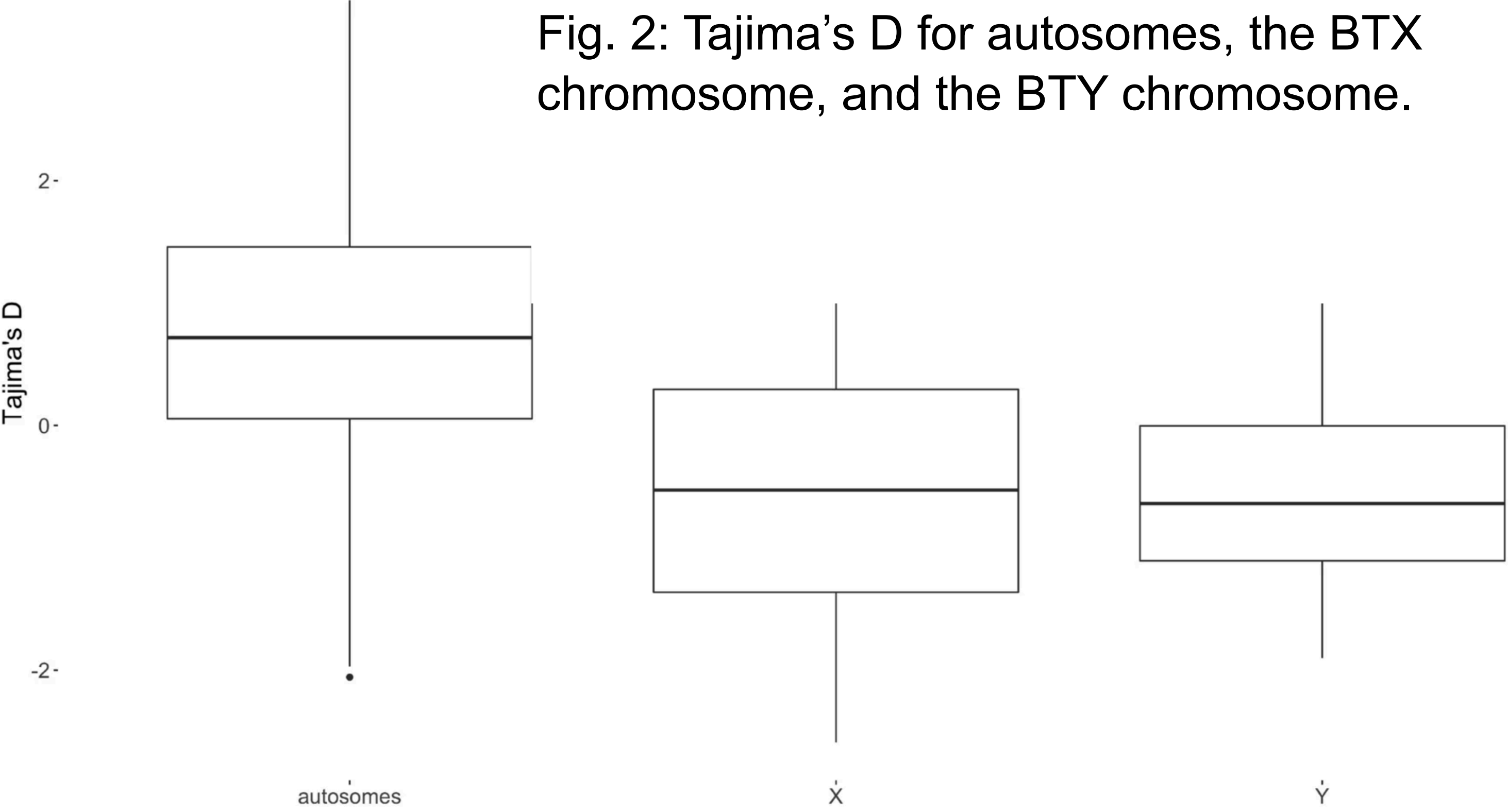


Fig. 3: Tajima's D for autosomes, the BTX chromosome, and the BTY chromosome.

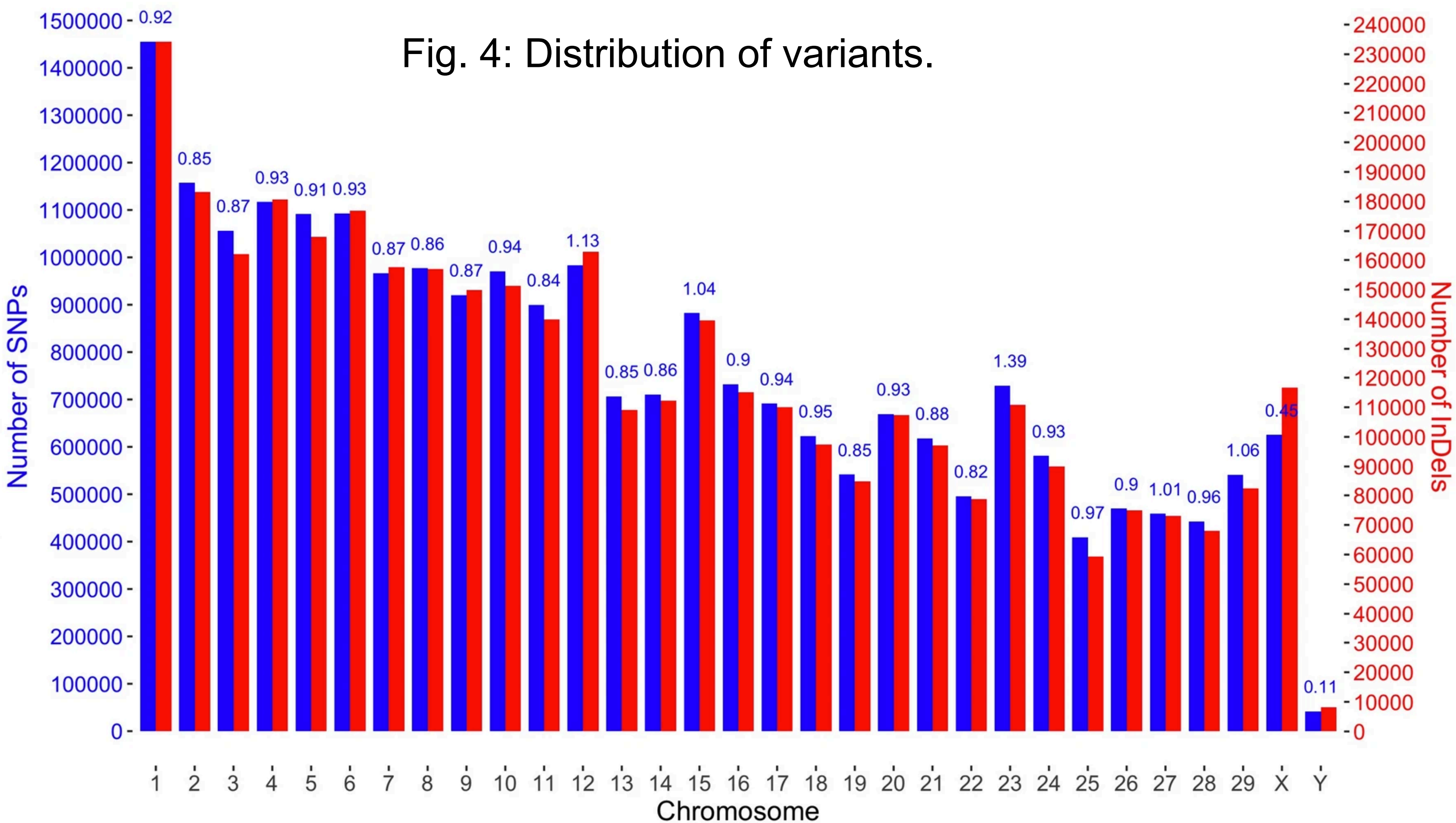


Fig. 4: Distribution of variants.