**Title:**The Paucity of PAR Sizes Limits our Ability to Elucidate Sex Chromosome Evolution Across the Tree of Life

**Running title:** PAR

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# ABSTRACT

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# INTRODUCTION

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# METHODS

Data

The first step in our pipeline is to download reads from NCBI’s short read archive (SRA) database. Six criteria were used to select reads: (i) to be a DNA sample, (ii) to be paired-end reads, (iii) to be Illumina reads, (iv) to use the genome strategy, (v) to be of the taxon being searched for, and (vi) to be male reads. Once all of these criteria were met, a sample for each species could be selected. Short reads associated with a sample matching all of these criteria were downloaded with the fastq-dump tool from SRAToolkit v. 2.10.9 on the Texas A&M HPRC Grace Cluster. Raw FASTQ sequences from SRA were then trimmed using Trimmomatic v0.39 to remove adapter sequences and low-quality base calls. Our trimming scanned the reads with a 4-base wide sliding window and removed reads when the average quality per base dropped below 20. Additionally, we removed any reads shorter than 25 base pairs. Next, we use Parabricks v.4.0.0 to map and call variants.

# RESULTS

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# DISCUSSION

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# CONCLUSION

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