

Chromosome-level analysis of the *Mauremys mutica* genome reveals adaptation of temperature-dependent sex-associated genes

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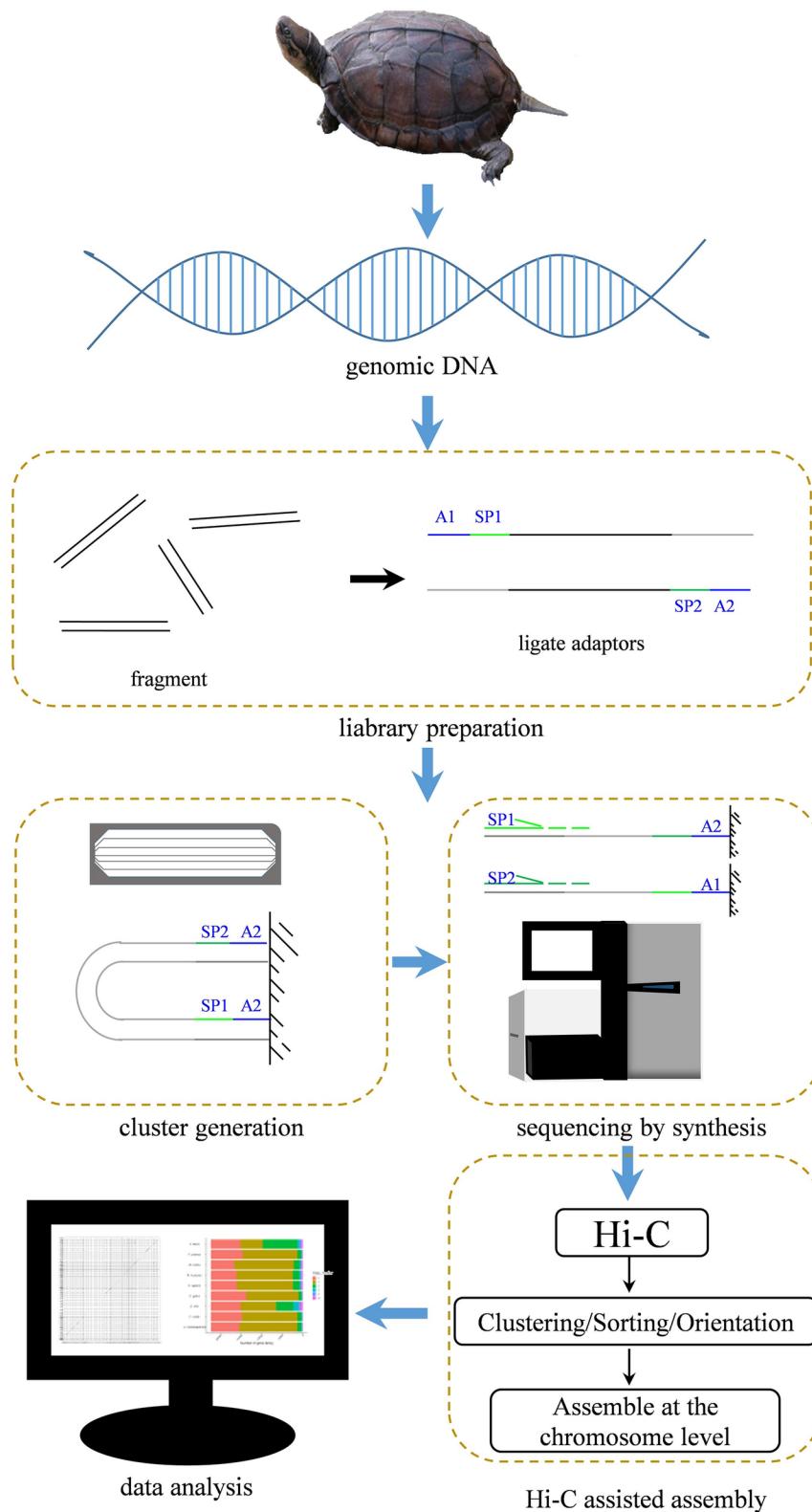
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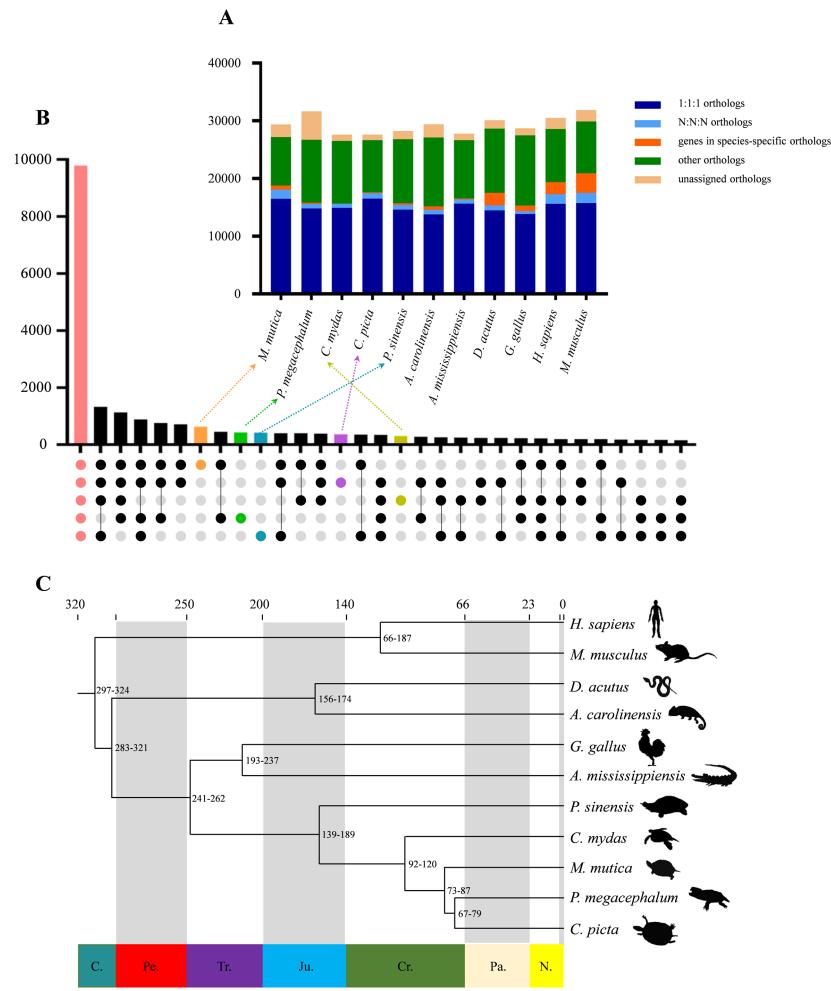
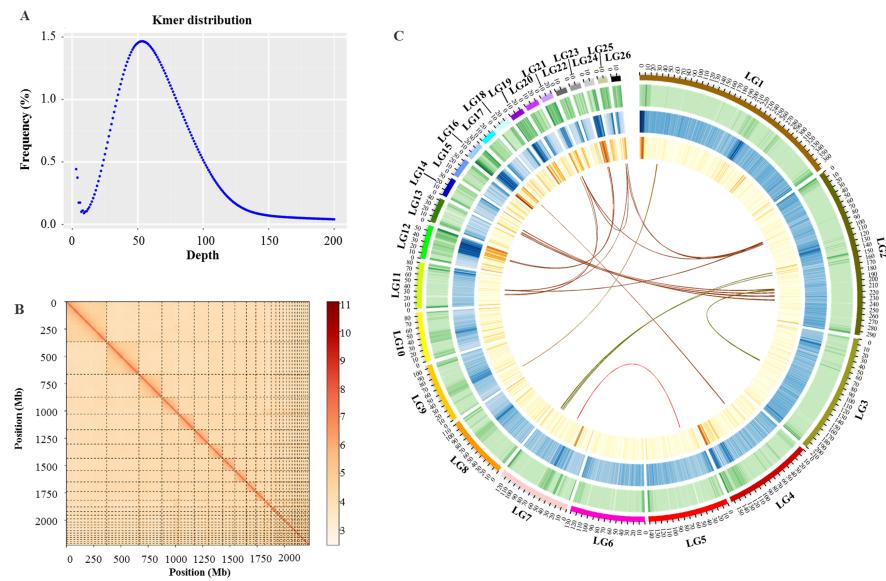
Abstract

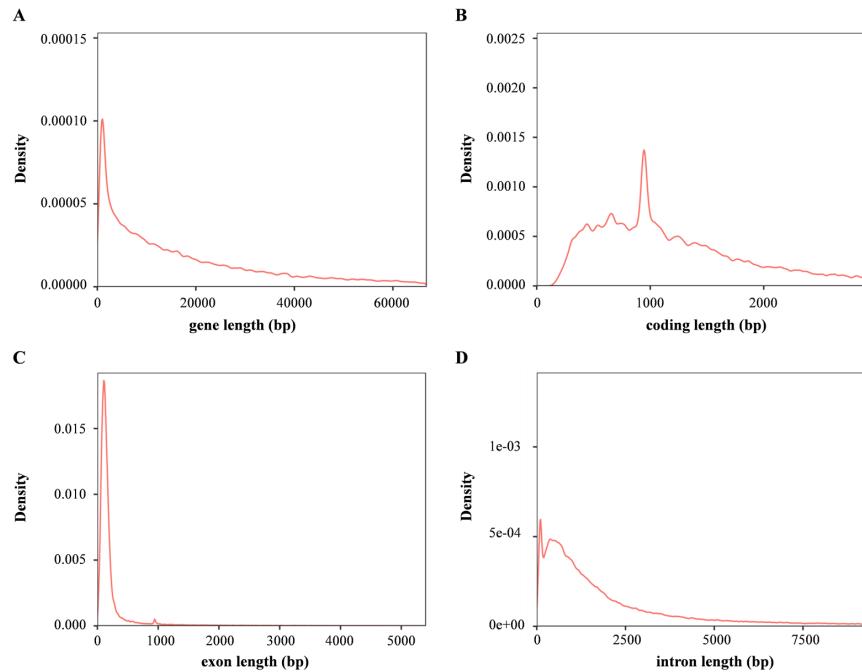
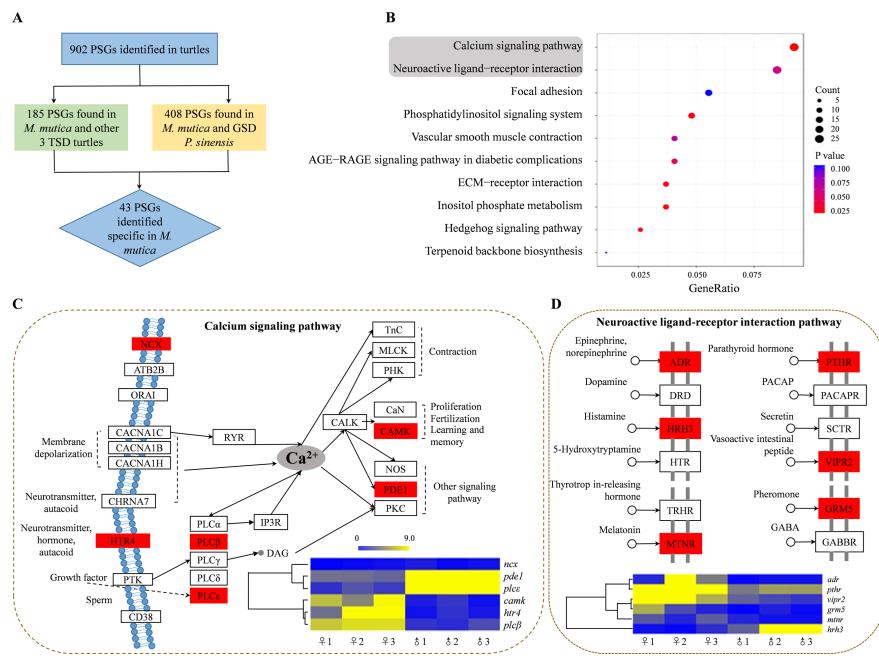
Knowledge of the sex determination system and sex-associated genes has important implications in physiology, ecology and evolution, but the mechanisms underlying sexual determination systems in turtles has not been fully elucidated, due to their remarkable variability and a lack of reference genomes in some species. In this report, we describe the first genome assembled at the chromosome scale for *Mauremys mutica* using Illumina and high-throughput chromatin conformation capture (Hi-C) technology. A total of 280.42 Gb of clean data were generated using the Pacific Biosciences platforms, which represented approximately 119× coverage of the *Mauremys mutica* genome. The assembly comprised 2.23 Gb with a contig N50 of 8.53 Mb and scaffold N50 of 141.98 Mb. Genome Hi-C scaffolding resulted in 26 pseudochromosomes containing 99.98% of the total assembly. Genome annotation predicted 24,751 protein-coding genes, and 97.23% of them were annotated. Comparative genomics analysis indicated that the lizard-snake-tuatara clade diverged from the bird-crocodilian-turtle clade at approximately 283.1-320.5 Mya. Additionally, positive selection of genes and gene families related to calcium signaling, neuroactive ligand-receptor interaction, and expansion of the hormone signaling pathway were identified, implicating their roles of sex regulation in *Mauremys mutica*. High-quality genome assembly may provide a valuable genomic resource for further research investigating gene-environment interactions in *Mauremys mutica*.

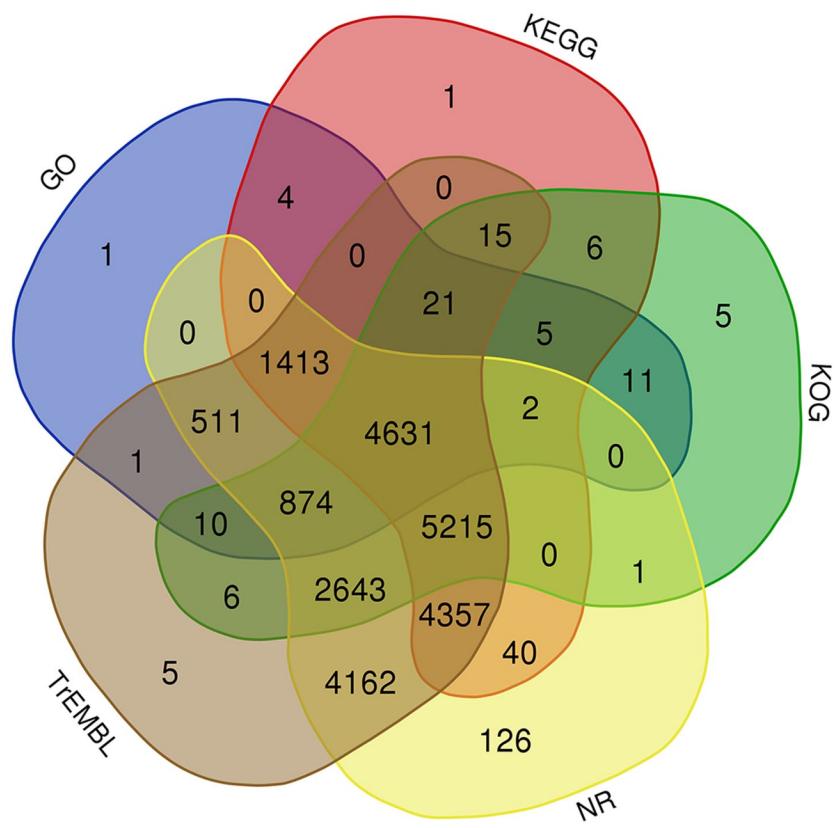
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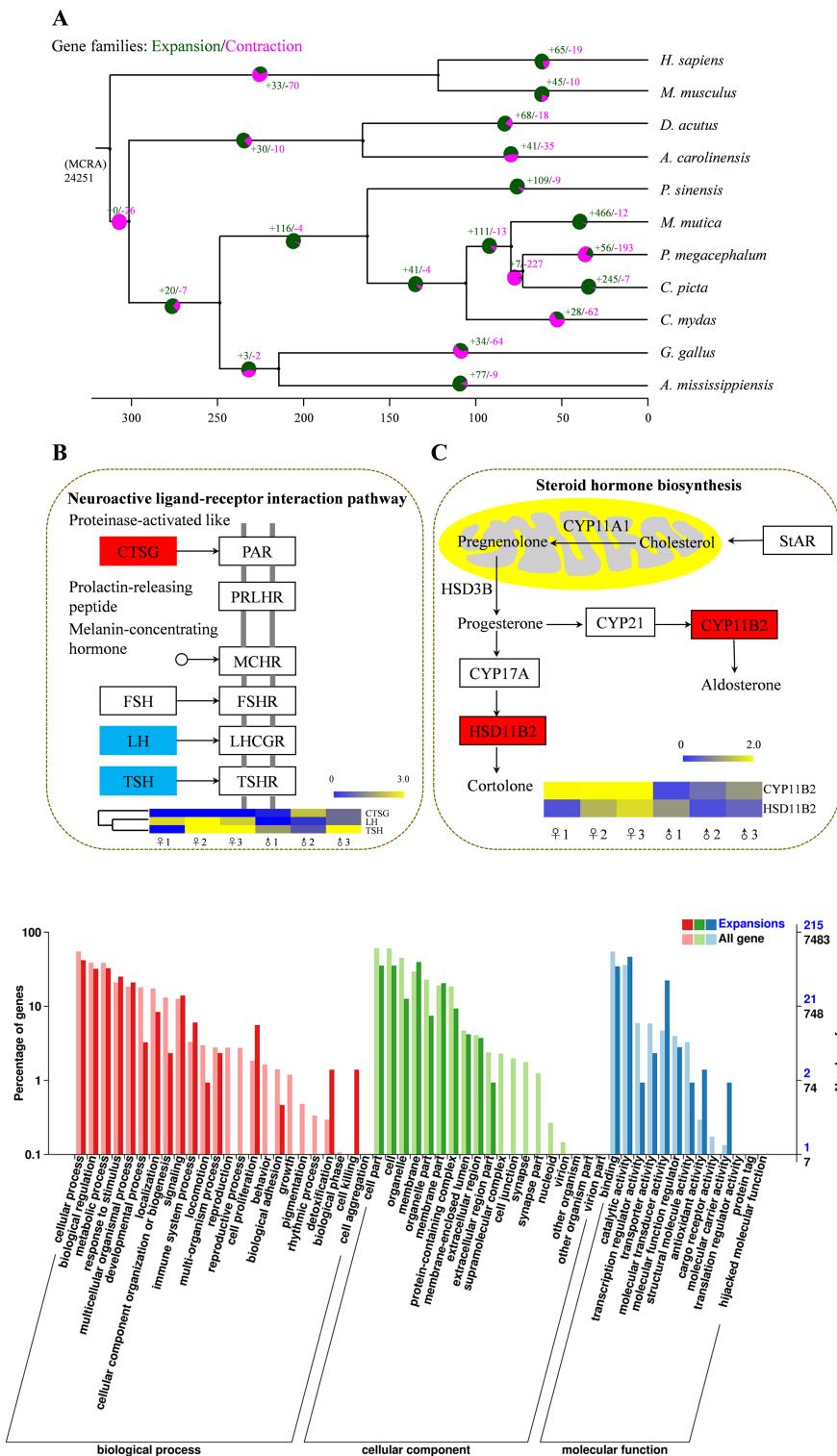
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[chromosome-level-analysis-of-the-mauremys-mutica-genome-reveals-adaptation-of-temperature-dependent-sex-associated-genes](https://doi.org/10.22541/au.163292943.37406381/v1)