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A new genome visualization resource for exploring and visually analyzing RNA-Seq gene expression data for tardigrades (*Hypsibius exemplaris* and *Ramazzottius varieornatus*)

Nowlan Freese, Paige J. Kulzer, Ann E. Loraine
University of North Carolina at Charlotte

The tardigrade species *Hypsibius exemplaris* is an emerging model system for understanding the evolution of animal development. Its transparent embryos, rapid generation time, ease of cultivation in laboratory settings, and small genome size make this microscopic invertebrate amenable to genome-scale assays such as RNA-Seq gene expression analysis. Other tardigrade species, including *Ramazzottius varieornatus*, offer models for studying resilience in the face of extreme environmental stresses, such as ionizing radiation. However, advanced genomics visualization

resources for tardigrade species are lacking in comparison to other invertebrates important in developmental biology and stress resilience studies. To address this, we developed a new genome browser resource for tardigrades using the Integrated Genome Browser, an open-source genome browser well-suited for visual analysis of functional genomics data sets, especially data from scaffold (incomplete) genome assemblies like those currently available for tardigrades. This new resource contains published RNA-Seq datasets downloaded from public archives as original sequence data and then re-aligned to tardigrade genome assemblies downloaded from Genbank. The re-processed data includes sequence alignments, useful for comparing genetic differences across species, and scaled coverage graphs, useful for observing differentially expressed genes between experimental samples. In addition, researchers can use the browser to visualize their own data alongside the public, re-processed data, making it easier to interpret their work and understand its significance and impact. The Integrated Genome Browser is freely-available from bioviz.org. An award from NIH NIGMS (R35GM139609) provided funding.

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Society for Developmental Biology
6120 Executive Blvd, Suite 725
Rockville, MD 20852, USA
T: (301) 634-7815
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