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Protocols for "Draft genome of the aquatic moss *Fontinalis antipyretica* (Fontinalaceae, Bryophyta)"

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ABSTRACT

Background: Mosses compose one of the three lineages that form the sister group to extant vascular plants. Having emerged from an early split in the diversification of embryophytes, mosses may offer complementary insights into the evolution of traits following the transition to and colonization of land. Here, we report the draft nuclear genome of *Fontinalis antipyretica* (Fontinalaceae, Hypnales), a charismatic aquatic moss widespread in temperate regions of the Northern Hemisphere. We sequenced and *de novo* assembled its genome using the 10 × genomics method. The genome comprises 385.2 Mbp, with a scaffold N50 of 45.8 Kbp. The assembly captured 87.2% of the 430 genes in the BUSCO viridiplantae odb10 dataset. The newly generated *F. antipyretica* genome is the third genome of mosses, and the second genome for a seedless aquatic plant.

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