



**Figure 3—figure supplement 2.** Maximum likelihood tree under the empirical LG+G substitution model and accession numbers of 447 eukaryotic intermediate filament proteins and the placement of the IF protein genes of the tardigrade *Hypsibius dujardini* (highlighted in red). Lamins of onychophorans are highlighted in orange, copepods in purple, collembolans in green, nematodes in light brown and cytoplasmic IF proteins of nematodes in dark brown. Note the position of isom of the collembolan *Isotomurus maculatus*, which has been interpreted as a putative cytoplasmic IF protein (Mencarelli et al. 2011, BMC Biol. 9, 17), within a group of collembolan lamins (asterisk). The domain structure of each protein is depicted on the right. Note the absence of a nuclear localization signal (NLS) in cytotardin of *H. dujardini* as well as in the colored sequences of copepods (purple) and collembolans (green). Bootstrap values from 1,000 pseudoreplicates > 50% are given at the nodes. Scale bar indicates the number of substitutions per site. Abbreviations: CaaX, isoprenylation motif at the carboxyl terminus; LTD, lamin tail domain; NLS, nuclear localization signal.