Erratum

Erratum to “A De Novo Genome Assembly Algorithm for Repeats and Nonrepeats”

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(iv) in Section 3.1 in the paper titled “*A de novo genome assembly algorithm for repeats and nonrepeats*” is corrected as follows: The E-size [27] is designed to answer the question: if you choose a location (a base) in the reference genome at random, what is the expected size of the contig or scaffold containing that location?