

To trim, or not to trim: effects of read-trimming on the *de novo* genome assembly of a widespread East Asian passerine, the rufous-capped babbler (*Cyanoderma ruficeps*)

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Supplementary Figures: Figs. S1 and S2

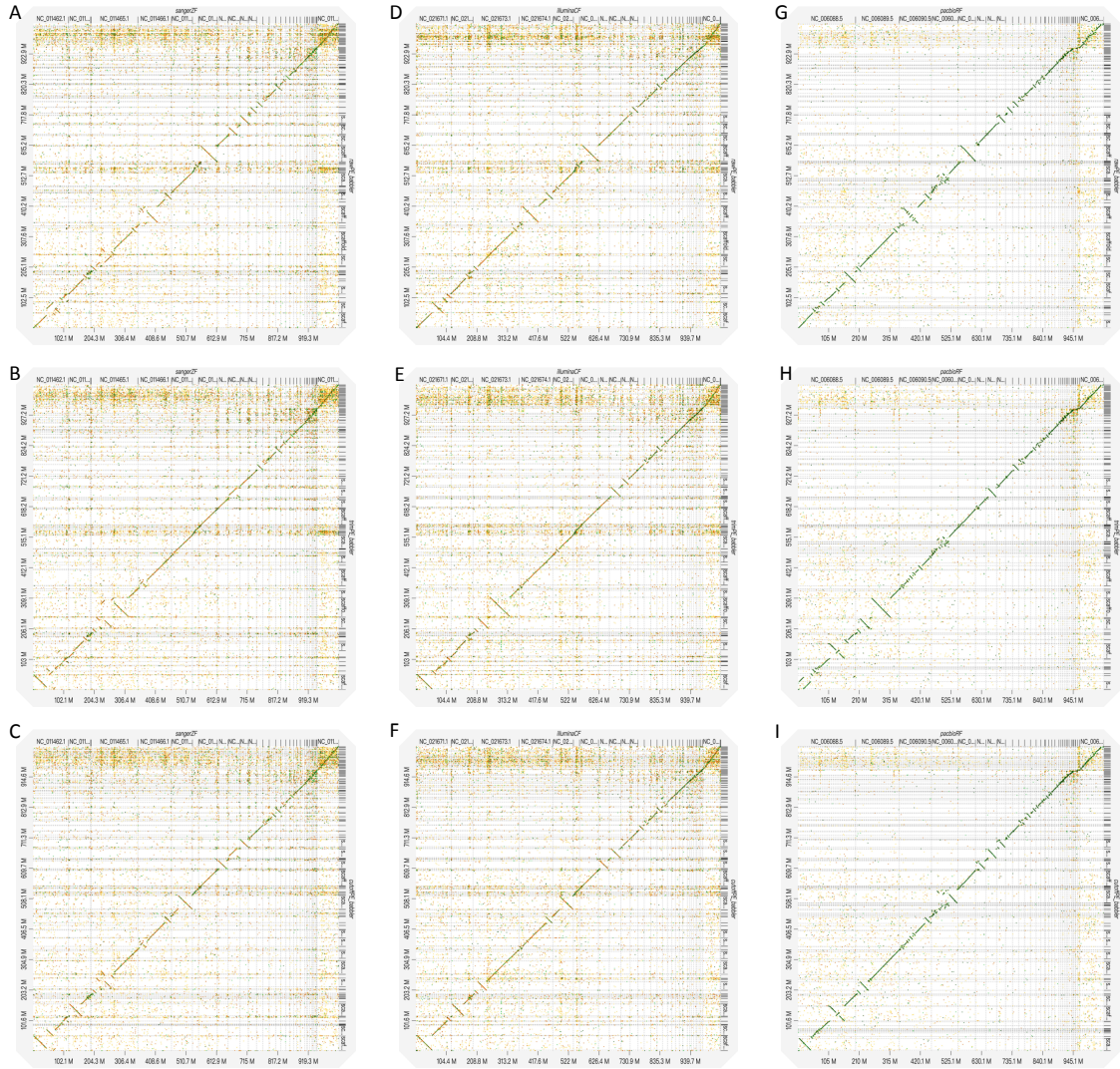


Figure S1. D-GENIES plots of alignments between the rufous-capped babbler and three avian genomes. The left panels show that the raw PE (A), trimmed (B), and cut off (C) PLATANUS-assembled genomes mapped to the zebra finch genome. The middle panels show that the raw PE (D), trimmed (E), and cut off (F) PLATANUS-assembled genome mapped to the collar flycatcher genome. The right panels show that the raw PE (G), trimmed (H), and cut off (I) PLATANUS-assembled genome are mapped to the chicken genome. Only the scaffolds of the rufous-capped babbler genomes with lengths > 5,000 bp were used. The unlocalized scaffolds of the three reference genomes were excluded from analyses.

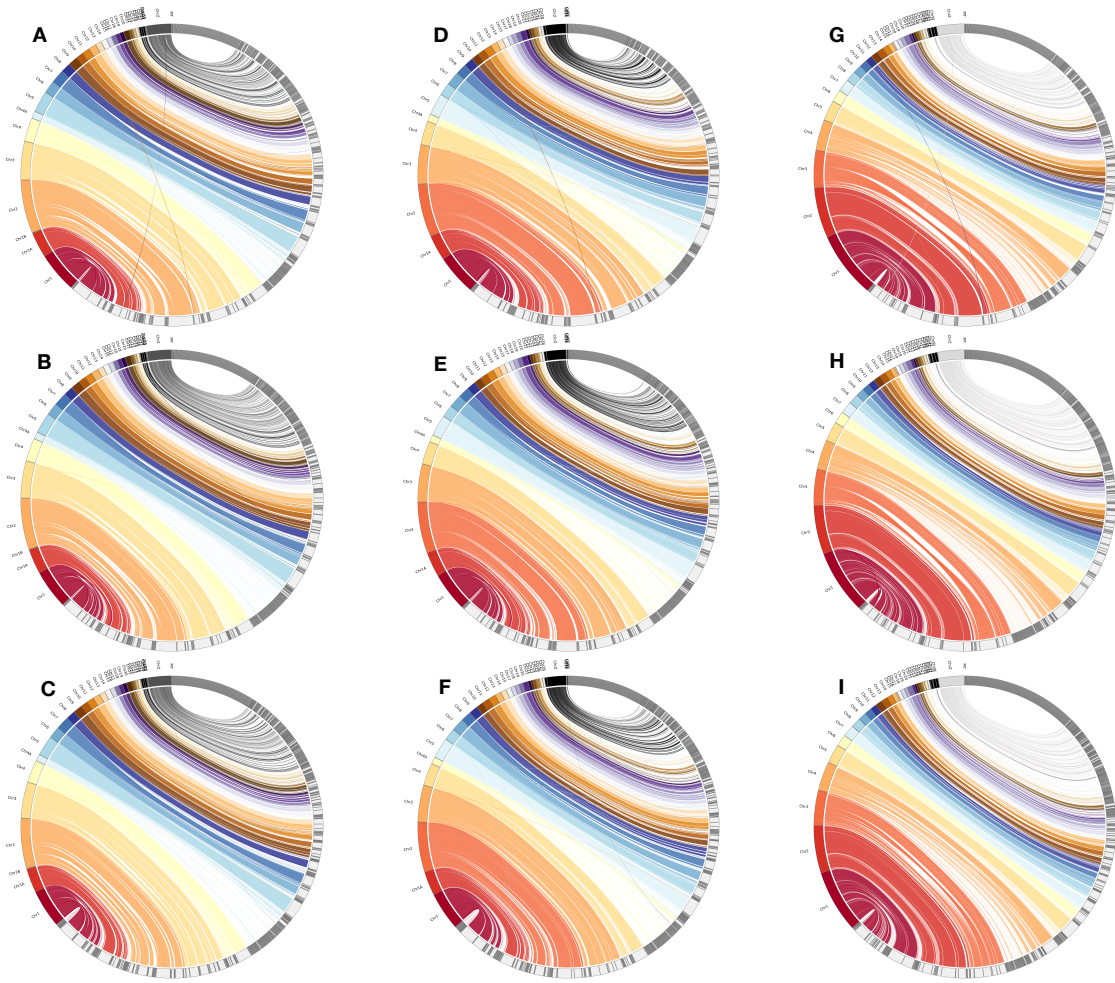


Figure S2. Jupiter plots of alignments between the rufous-capped babbler and three avian genomes. The left panels show that the raw PE (A), trimmed (B), and cut off (C) PLATANUS-assembled genomes mapped to the zebra finch genome. The middle panels show that the raw PE (D), trimmed (E), and cut off (F) PLATANUS-assembled genome mapped to the collar flycatcher genome. The right panels show that the raw PE (G), trimmed (H), and cut off (I) PLATANUS-assembled genome are mapped to the chicken genome. Only the scaffolds of the rufous-capped babbler genomes with lengths > 5,000 bp were used. The unlocalized scaffolds of the three reference genomes were excluded from analyses.