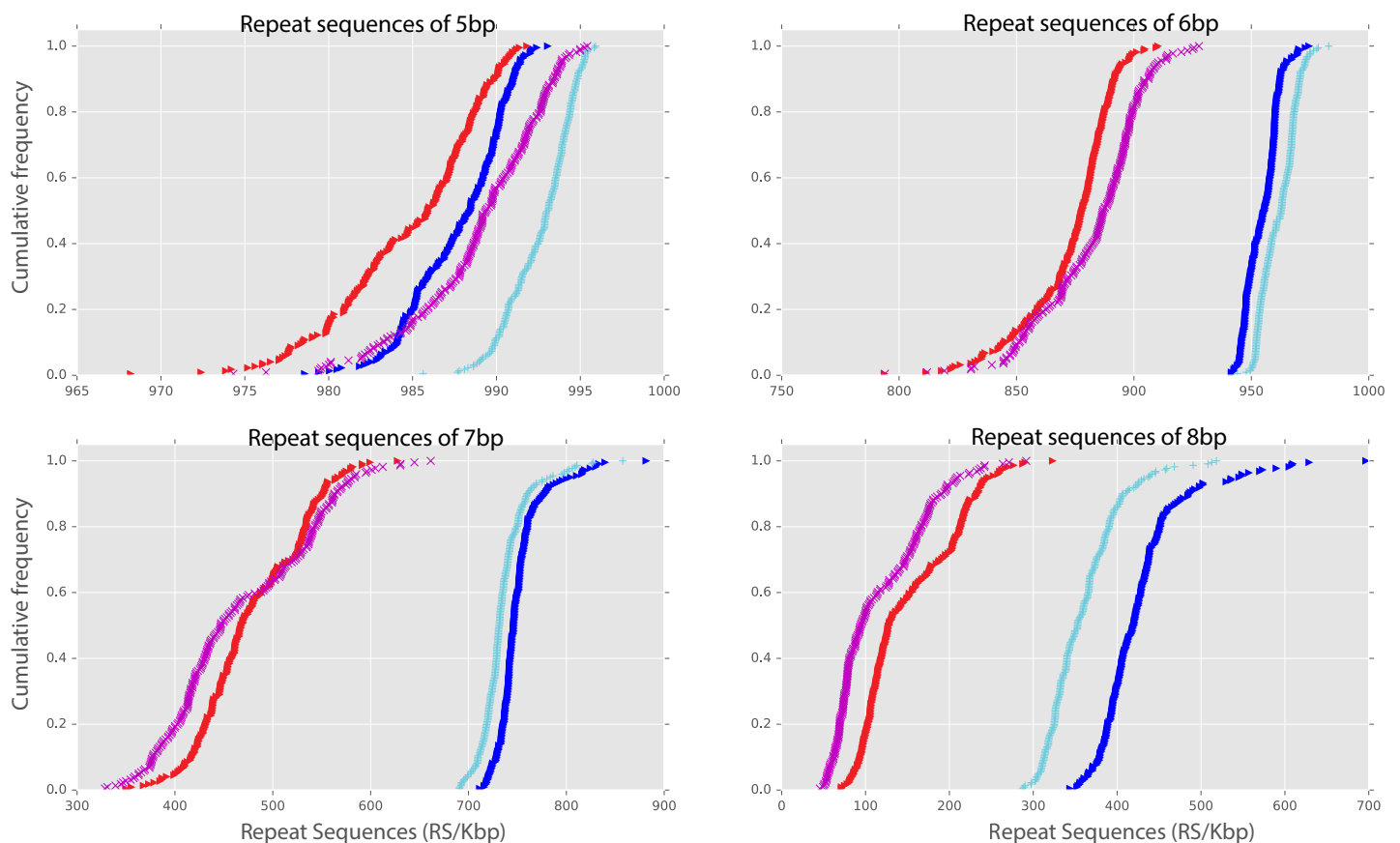


# Repetitive DNA profile of the amphibian mitogenome

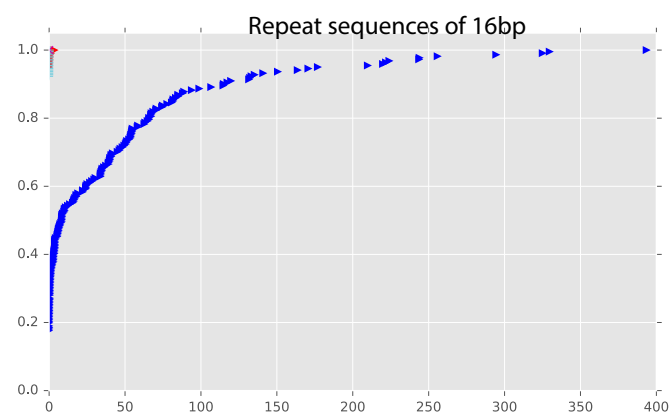
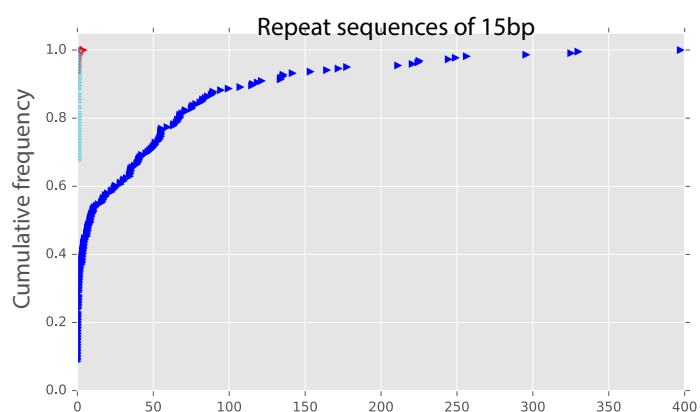
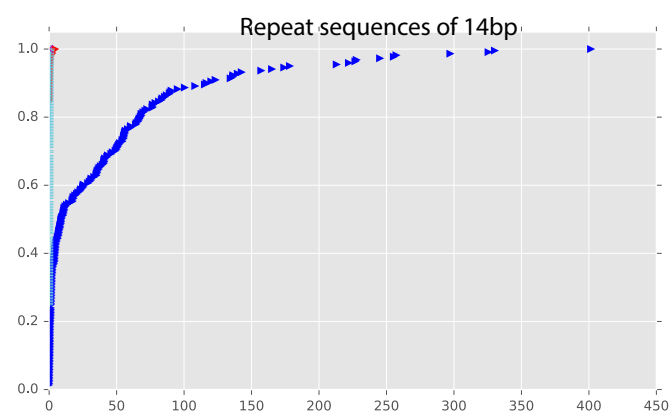
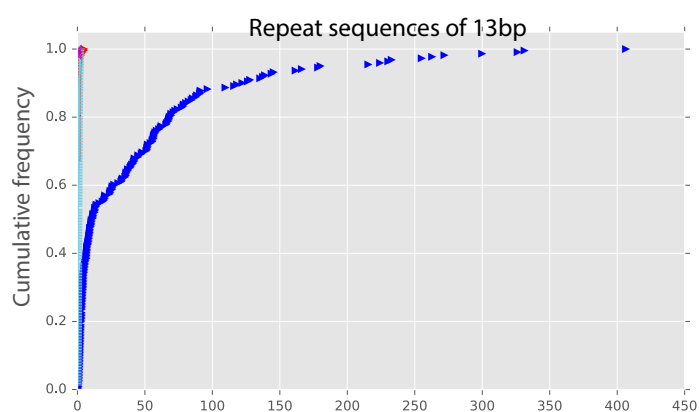
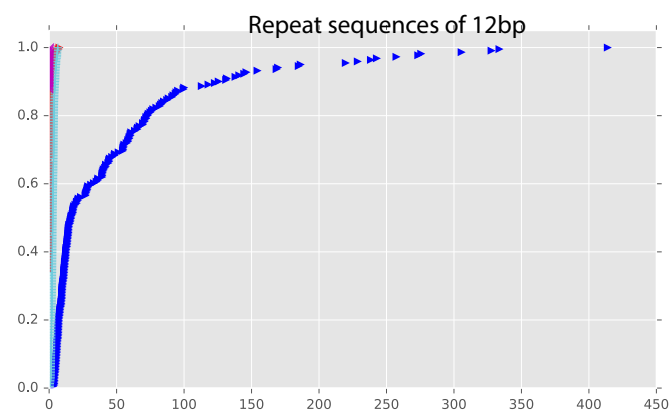
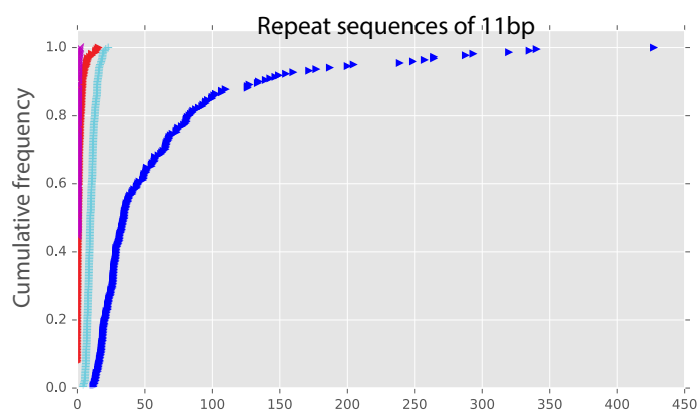
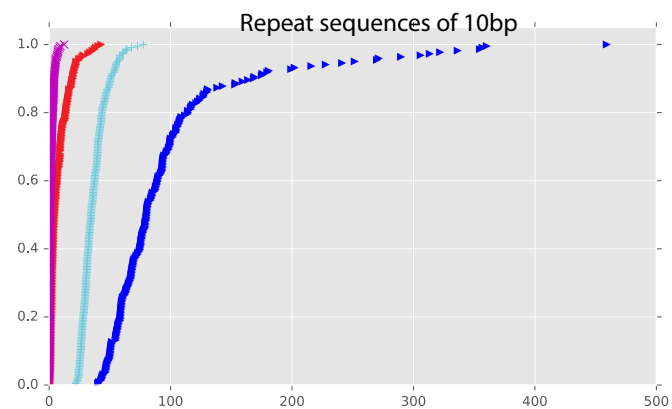
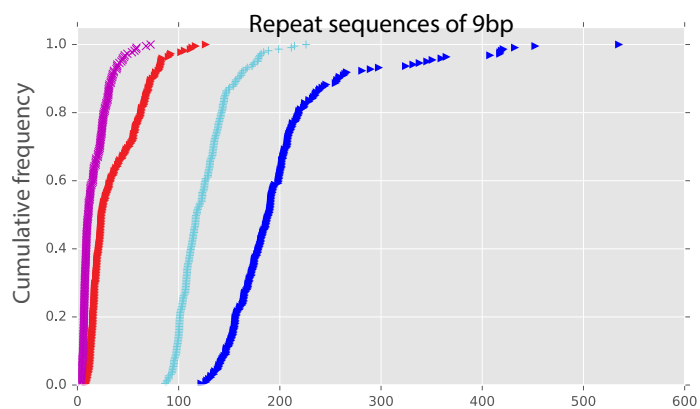
Noel Cabañas<sup>1</sup>, Arturo Becerra<sup>2</sup>, David Romero<sup>3</sup>, Tzipe Govezensky<sup>1</sup>,  
Jesús Javier Espinosa-Aguirre<sup>1</sup>, and Rafael Camacho-Carranza<sup>1,2\*</sup>

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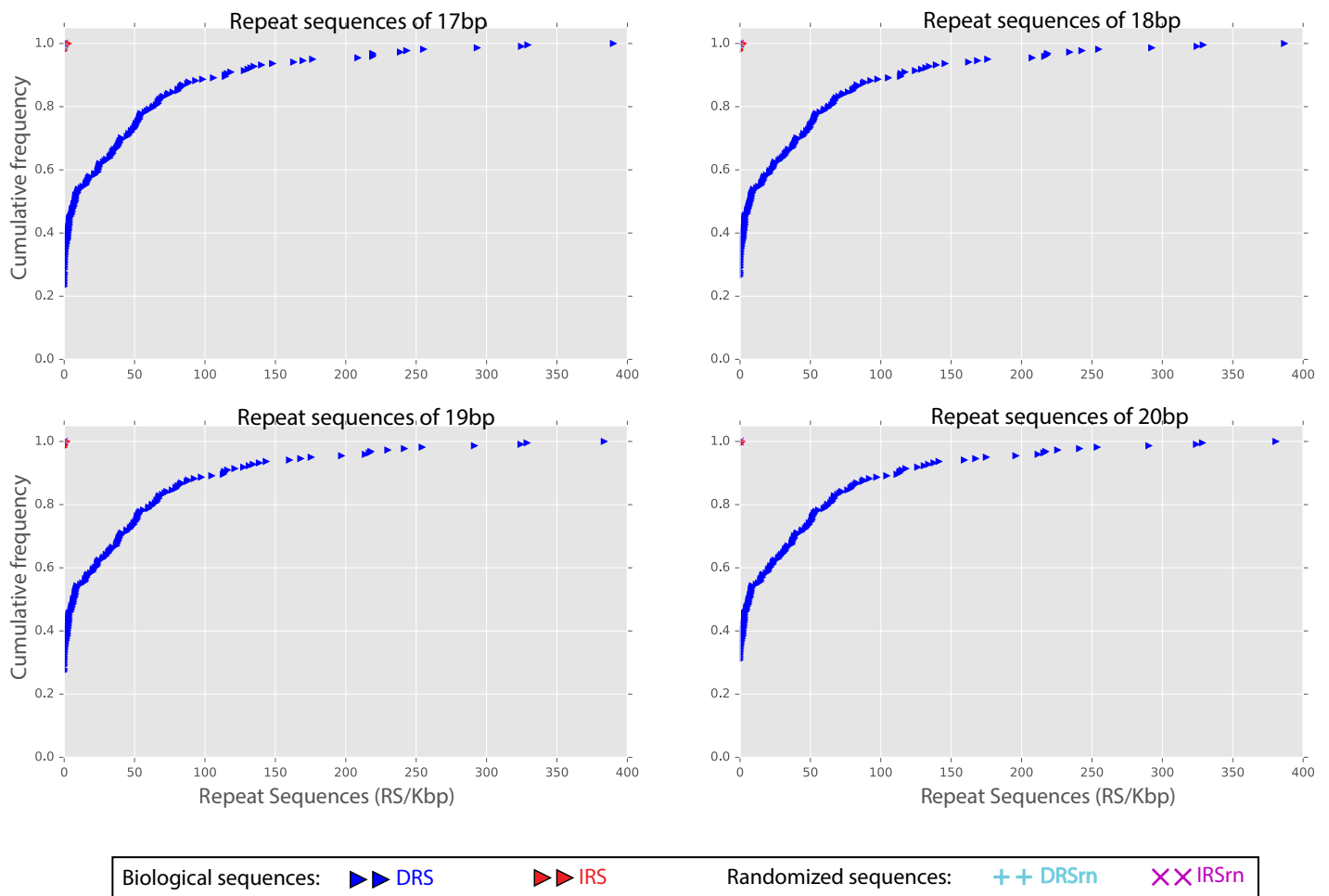
This file includes data that complement the information and enhance the interpretation of the main text.



Biological sequences: ►► DRS ►► IRS Randomized sequences: ++ DRSm ×× IRSm



Biological sequences:    ▶▶ DRS    ▶▶ IRS    Randomized sequences:    ++ DRSm    XX IRSm



**Additional files 2.** Empirical distributions (EDF) of the abundance of repeat sequences with lengths from 5bp to 20 bp. These plots show the number of DRs and IRs per kilobase pairs in the 221 amphibian mitogenomes. We additionally show and compare the abundance of repeat sequences obtained from randomized genomes. Each figure presents an independent analysis for each specific size of repeat sequence. EDF with the number of repeat sequences from 21bp to 30bp were performed, but are not included in this supplementary file since the distributions are similar to the last ones displayed.