

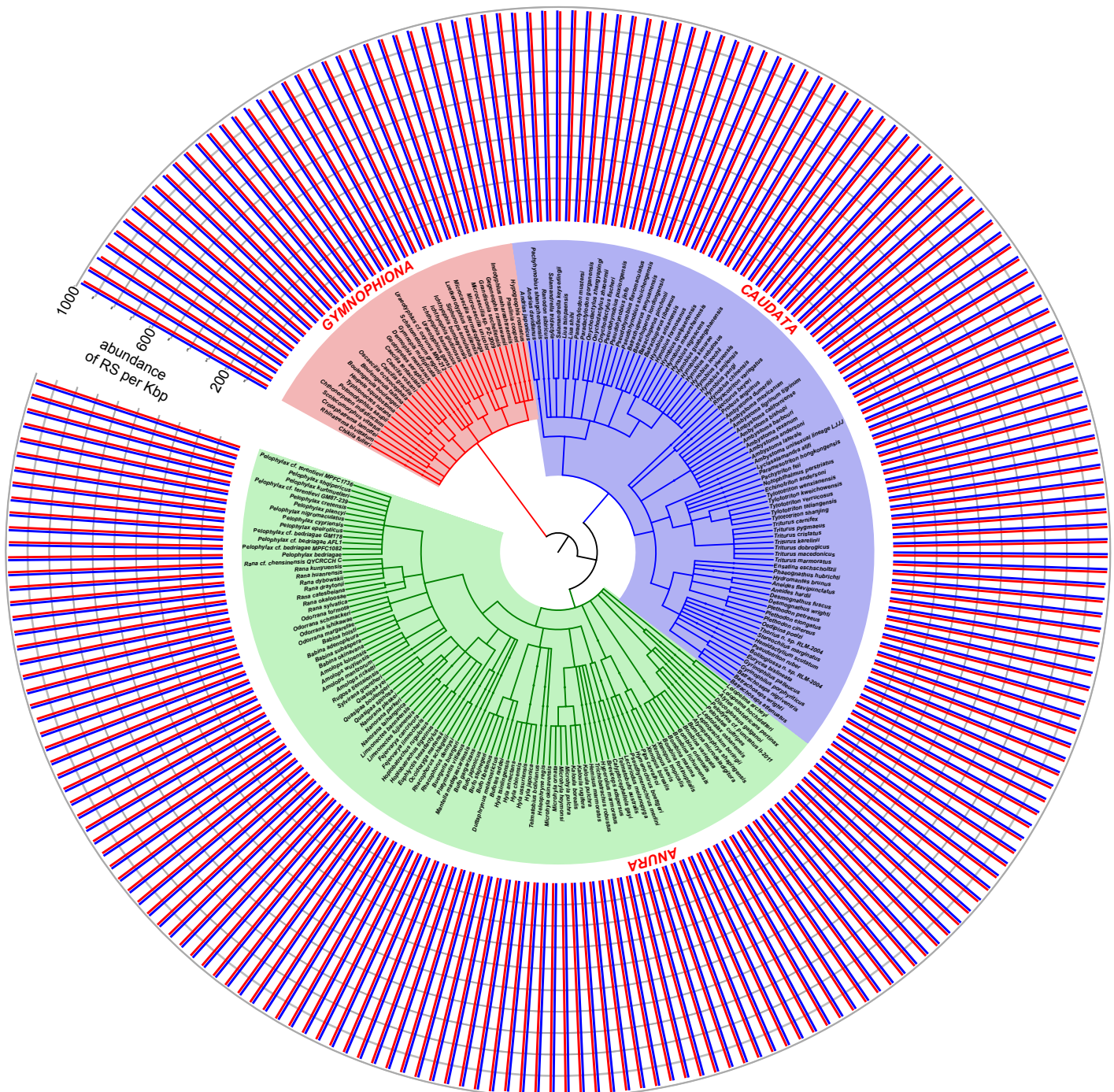
Repetitive DNA profile of the amphibian mitogenome

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These phylogenetic trees that display the abundance of repeat sequences in the amphibian mitogenomes and many others generated in this work can be visualized and exported from the iTOL webpage following this link: <https://itol.embl.de/shared/salmonellaib>

Abundance of repeat sequences of 5 bp



Anura



Caudata



Gymnophiona

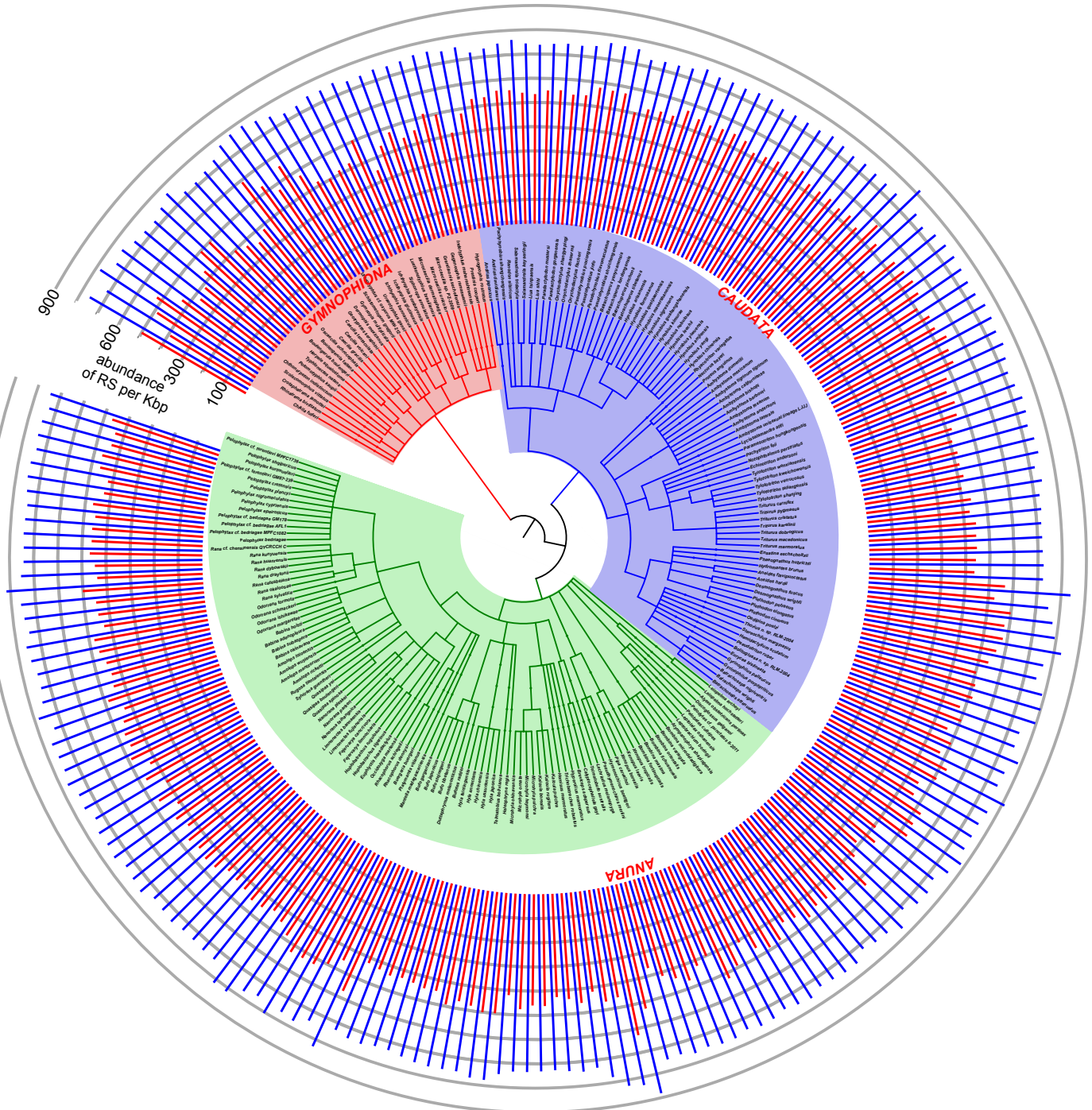


Direct



Inverted

Abundance of repeat sequences of 7 bp



Anura



Caudata



Gymnophiona

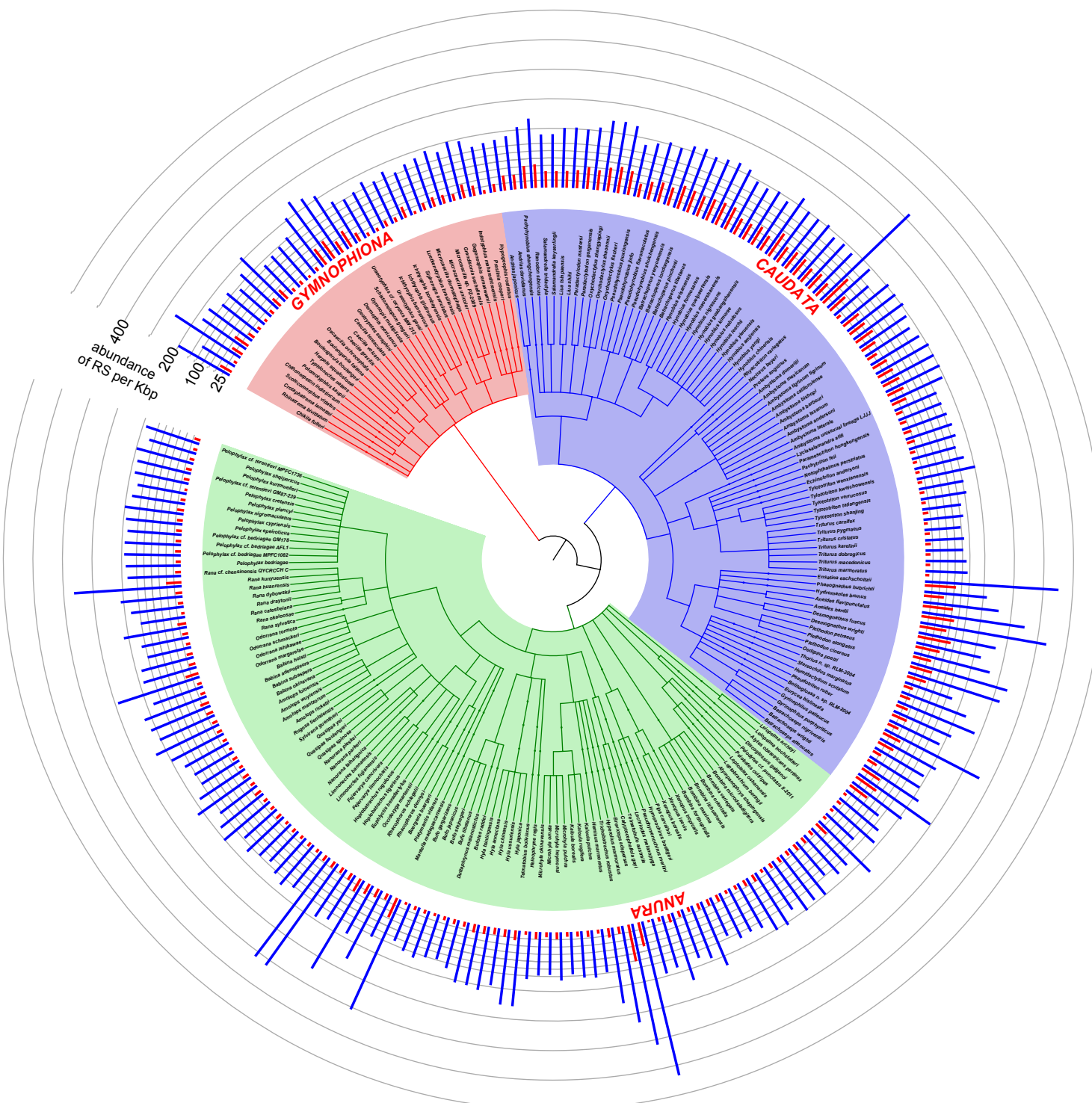


Direct



Inverted

Abundance of repeat sequences of 9 bp



Anura



Caudata



Gymnophiona

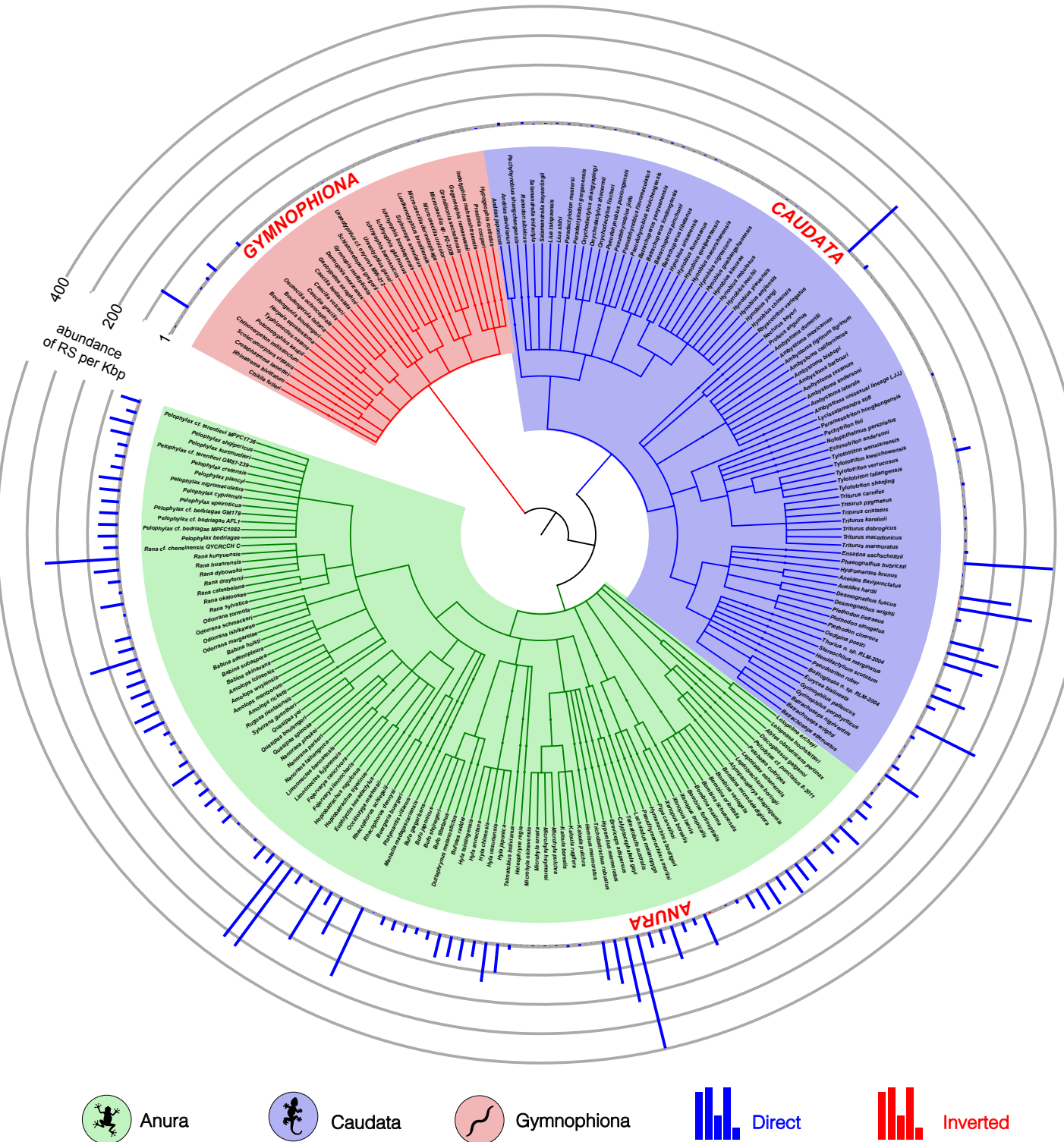


Direct



Inverted

Abundance of repeat sequences of 15 bp



Additional files 3. The abundance of repeat sequences of 5 bp, 7 bp, 9bp, and 15bp in the amphibian phylogenetic tree. These plots present the 221 amphibians classified into three orders, with their respective abundance of direct (blue bars) and inverted (red bars) repeat sequences shown as bar graphs next to each other. The scale that shows the number of repeat sequences per kilobase pairs is represented with circular gray lines. Additional distributions of other sizes of repeat sequences can be accessed online within this link: <https://itol.embl.de/shared/salmonellaib>