

Table S20: Structure of long IGS of *Batocera* sp. and comparison with similar sequence.

Specie	Length	A+T	Position	Structure
<i>Pyrocoelia rufa</i>	1,724bp	69.5%	<i>nad2</i> , W	12 tandem repeats, 1 repeat of the beginning.
<i>Evania appendigaster</i>	534 bp	96.8%	K, D	3 types of tandem repeats (Each type has 7 copies, 12 copies, and 8 copies, respectively); 1 initial sequence; 1 terminal sequence.
<i>Metopodontus blanchardi</i>	4,051bp	65.4%	I , Q	17 tandem repeat sequences (15 copies are complete, 2 units are incomplete).
<i>Batocera</i> sp.	1,428bp	72%	W, C	18 tandem repeat sequences(17 copies are complete, 1 unit is incomplete).