

Supplementary information

• The Files are attached together below and therefore the form is .pdf

Additional file 1. The respective overall base composition and length of stomatopod crustacean mitochondrial genomes.

Additional file 2. Codon usage analysis of PCGs in the mitochondrial genome of *Faughnia haani*.

Additional file 3. Tandem repeats longer than 50 bp in the CR region of crustacean mitochondrial genomes.

Additional file 4. Predicted secondary structure of the putative control region in *Faughnia haani* using the RNA structure web server.

Additional file 1. The respective overall base composition and length of stomatopod crustacean mitochondrial genomes.

Species name	A + T	A	T	G	C	G+C	Length(bp)
<i>Squilloides leptosquilla</i> (NC02178)	71.20%	37.40%	33.80%	11.30%	17.50%	28.80%	15,995 bp
<i>Oratosquilla oratoria</i> (GQ292769)	70.80%	36.90%	33.90%	12.30%	16.90%	29.20%	15,783 bp
<i>Squilla mantis</i> (AY639936)	70.20%	35.10%	35.10%	13.00%	16.80%	29.80%	15,994 bp
<i>Harpiosquilla harpax</i> (AY699271)	69.80%	35.00%	34.80%	13.10%	17.10%	30.20%	15,714 bp
<i>Chorisquilla orientalis</i> (MT672286)	69.20%	35.50%	33.70%	12.40%	18.30%	30.70%	15,880 bp
<i>Lophosquilla costata</i> (MT276143)	68.00%	35.30%	32.70%	13.60%	18.30%	31.90%	15,771 bp
<i>Gonodactylus chiragra</i> (DQ191682)	67.50%	35.10%	32.40%	12.50%	20.10%	32.60%	16,279 bp
<i>Faughnia haani</i> (MW632159)	67.20%	35.30%	31.90%	13.30%	19.50%	32.80%	16,089 bp
<i>Taku spinosocarinatus</i> (MT672285)	66.80%	34.20%	32.60%	13.40%	19.80%	33.20%	15,960 bp
<i>Gonodactylaceus randalli</i> (MW019425)	66.20%	33.20%	33.00%	14.70%	19.10%	33.80%	15,907 bp
<i>Squilla empusa</i> (DQ191684)	63.90%	32.80%	31.10%	14.70%	21.40%	36.10%	16,325 bp
<i>Lysiosquillina maculata</i> (DQ191683)	63.90%	32.80%	31.10%	14.70%	21.40%	36.10%	16,325 bp