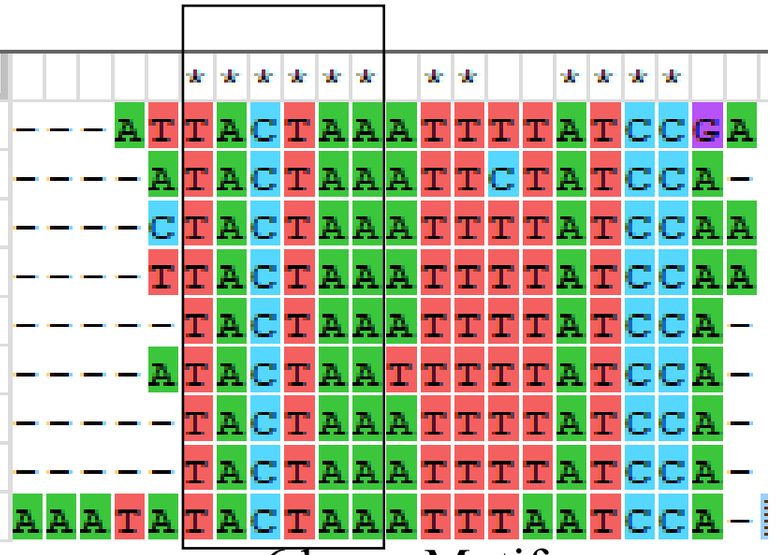
A-

Species/Abbrv	Group Name
1. Cyprolais quadrimaculata	
2. Dicronorhina derbyana	
3. Eudicella euthalia oweni	
4. Eudicella smithi	
5. Goliathus goliatus	
6. Jumnos ruckeri	
7. Mecynorhina polyphemus	
8. Mecynorhina torquata ugandens:	
9. Protaetia speciosa jousselini	



B-

Species/Abbrv	Group Name
1. Dynastes hercules hercules	
2. Megasoma elephas elephas	
3. Megasoma mars	

C-

Species/Abbrv	Group Name
1. Chalcosoma caucasus caucasus	
2. Dynastes hercules hercules	
3. Oryctes nasicornis	
4. Megasoma elephas elephas	
5. Megasoma mars	
6. Xylotrupes beckeri intermedius	
7. Xylotrupes gideon beckeri	
8. Xylotrupes gideon siamensis	
9. Xylotrupes gideon sumatrensis	

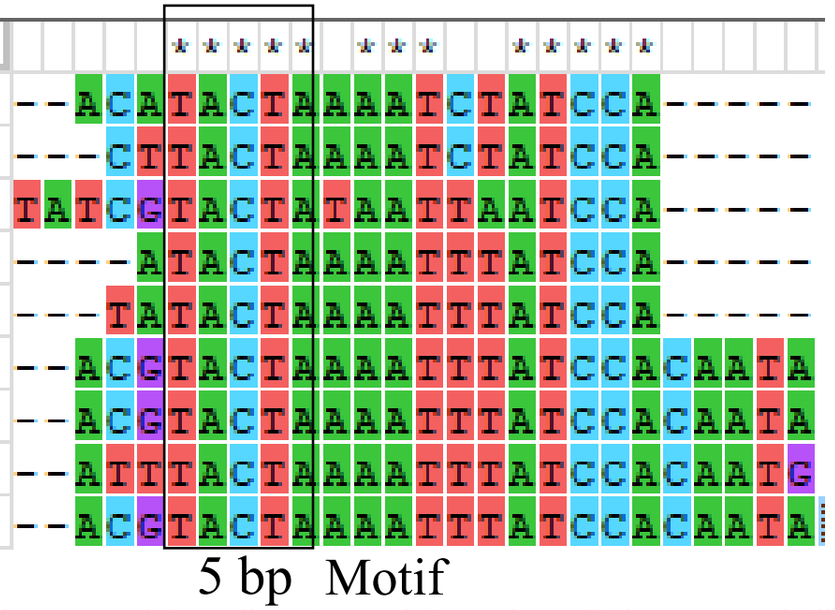


Figure S2. Alignment of the intergenic spacer region located between ND1 and tRNA Ser (UCN) from all sequenced Cetoniinae (A) and Dynastinae (C) insects. (A) indicate the conserved hexanucleotide region (TACTAA) and (C) the pentanucleotide region (TACTA) detected in all sequenced Cetoniinae and Dynastinae insects, respectively. (B) indicate the C-streches and alignment of the intergenic spacer region located between trnK and trnD from all sequenced Dynastinae (B) insects.