

**Additional File 6.** Sequence divergence of the unassigned region *nad5-trnQ* between H-type mitochondrial genomes and a closely related F-type mitochondrial genome. Alignments performed in Geneious 11.0.3 using default parameters with an IUB cost matrix.

| H-type taxa                   | F-type taxa                        | Percent<br>sequence<br>Divergence |
|-------------------------------|------------------------------------|-----------------------------------|
| <i>Anodonta cygnea</i>        | <i>Anodonta anatina</i>            | 57.5                              |
| <i>Utterbackia imbecillis</i> | <i>Utterbackia peninsularis</i>    | 60.0                              |
| <i>Margaritifera falcata</i>  | <i>Cumberlandia monodonta</i>      | 65.7                              |
| <i>Lasmigona compressa</i>    | <i>Pyganodon grandis</i>           | 56.6                              |
| <i>Toxolasma parvus</i>       | <i>Venustaconcha ellipsiformis</i> | 48.2                              |