Table S1. List of all the samples.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample ID | SRA Accession | Lab Code | Species | Identifier | Sex | Life Stage | Collectors | Collection Date | Country | Lat | Lon | Elev | Institution Storing | Reference |
| 4 | [SRR15101121](https://dataview.ncbi.nlm.nih.gov/object/SRR15101121) | I19058\_4 | *H.viteceki* | Anna E. Hjalmarsson | M | Adult | Chen, Hjalmarsson, Li | 30.7.2013 | China | 28.2934 | 99.153 | 3306 | SGN Frankfurt | This study |
| 5 | [SRR15101120](https://dataview.ncbi.nlm.nih.gov/object/SRR15101120) | I19059\_5 | *H.viteceki* | Anna E. Hjalmarsson | M | Adult | Chen, Hjalmarsson, Li | 30.7.2013 | China | 28.2934 | 99.153 | 3306 | SGN Frankfurt | This study |
| 14 | [SRR15101118](https://dataview.ncbi.nlm.nih.gov/object/SRR15101118) | I19067\_14 | *H. martynovi sensu stricto* | Anna E. Hjalmarsson | M | Adult | Saldaitis | 06.10.2010 | China | 29.8667 | 102.3 | 2100 | SGN Frankfurt | This study |
| 12 | [SRR15101117](https://dataview.ncbi.nlm.nih.gov/object/SRR15101117) | I19065\_12 | *H. martynovi sensu stricto* | Hans Malicky | M | Adult | Saldaitis | 05.7.2010 | China | 32.9167 | 103.4 | 3500 | SGN Frankfurt | This study |
| 16 | [SRR15101116](https://dataview.ncbi.nlm.nih.gov/object/SRR15101116) | I19068\_16 | *H. martynovi sensu stricto* | Hans Malicky | M | Adult | Floriani & Saldaitis | 23.8.2014 | China | 31.483210 | 102.493400 | 3400 | SGN Frankfurt | This study |
| 11 | [SRR15101115](https://dataview.ncbi.nlm.nih.gov/object/SRR15101115) | I19064\_11 | *H. cf. martynovi* | Hans Malicky | M | Adult | Floriani | 08.10.2011 | China | 30.0667 | 101.417 | 3611 | SGN Frankfurt | This study |
| 13 | SRR15101114 | I19066\_13 | *H. martynovi sensu stricto* | Anna E. Hjalmarsson | M | Adult | Floriani & Saldaitis | 27.8.2014 | China | 33.175770 | 104.321200 | 2900 | SGN Frankfurt | This study |
| \ |  | SPHIM424-17 | *H.martynovi* | Hans Malicky | M | Adult | Floriani | 08.10.2011 | China | 30.0667 | 101.417 | 3611 | Malicky, Lunz | Hjalmarsson et al. 2018 |
| \ |  | SPHIM425-17 | *H.martynovi* | Hans Malicky | M | Adult | Saldaitis | 05.7.2010 | China | 32.9167 | 103.4 | 3500 | Malicky, Lunz | Hjalmarsson et al. 2018 |
| \ |  | SPHIM427-17 | *H.martynovi* | Anna E. Hjalmarsson | M | Adult | Saldaitis | 06.10.2010 | China | 29.8667 | 102.3 | 2100 | Malicky, Lunz | Hjalmarsson et al. 2018 |
| \ |  | SPHIM428-17 | *H.martynovi* | Anna E. Hjalmarsson | M | Adult | Saldaitis | 14.7.2009 | China | 30.0667 | 101.433 | 3500 | Malicky, Lunz | Hjalmarsson et al. 2018 |
| \ |  | SPHIM429-17 | *H.martynovi* | Hans Malicky | M | Adult | Floriani & Saldaitis | 22.8.2014 | China | 30.4667 | 101.633 | 3500 | Malicky, Lunz | Hjalmarsson et al. 2018 |
| \ |  | SPHIM430-17 | *H.martynovi* | Hans Malicky | M | Adult | Floriani & Saldaitis | 23.07.2011 | China | 33.1333 | 103.717 | 3000 | Malicky, Lunz | Hjalmarsson et al. 2018 |
| 7 | [SRR15101113](https://dataview.ncbi.nlm.nih.gov/object/SRR15101113) | I19061\_7 | *H.epikur* | Hans Malicky | M | Adult | Chen, Hjalmarsson, Li | 07.8.2013 | China | 28.5389 | 99.8174 | 3609 | SGN Frankfurt | This study |
| 6 | [SRR15101112](https://dataview.ncbi.nlm.nih.gov/object/SRR15101112) | I19060\_6 | *H.epikur* | Anna E. Hjalmarsson | M | Adult | Chen, Hjalmarsson, Li | 07.8.2013 | China | 28.5389 | 99.8174 | 3609 | SGN Frankfurt | This study |
| 8 | [SRR15101111](https://dataview.ncbi.nlm.nih.gov/object/SRR15101111) | I19062\_8 | *H.epikur* | Anna E. Hjalmarsson |  | Larva | Tachamo Shah, Shah, Jaehnig | 10.2011 | China | 27.632556 | 99.368167 | 2500 | SGN Frankfurt | This study |
| \ |  | SPHIM405-17 | *H.epikur* | Hans Malicky | M | Adult | Chen, Hjalmarsson, Li | 07.8.2013 | China | 28.5389 | 99.8174 | 3609 | SGN Frankfurt | Hjalmarsson et al. 2018 |
| \ |  | HspXC0104FAH0697\_677 | *H.epikur* | Anna E. Hjalmarsson | F | Adult | Chen, Hjalmarsson, Li | 09.8.2013 | China | 29.116 | 100.033 | 4154 | SGN Frankfurt |  |
| \ |  | SPHIM415-17 | *H.epikur* | Anna E. Hjalmarsson | M | Adult | Chen, Hjalmarsson, Li | 09.8.2013 | China | 28.4095 | 99.7764 | 3040 | SGN Frankfurt | Hjalmarsson et al. 2018 |
| \ |  | SPHIM439-17 | *H.epikur* | Hans Malicky | M | Adult | Saldaitis | 10.4.2004 | China | 28.5333 | 99.8167 | 3500 | Malicky, Lunz | Hjalmarsson et al. 2018 |
| \ |  | LZ78\_F | *H.epikur* | Anna E. Hjalmarsson | F | Adult | Floriani & Saldaitis | 19.6.2015 | China | 29.2833 | 100.083 | 4050 | SGN Frankfurt |  |
| 3 | [SRR15101119](https://dataview.ncbi.nlm.nih.gov/object/SRR15101119) | I19057\_3 | *H.immodesta* | Anna E. Hjalmarsson | M | Adult | Chen, Hjalmarsson, Li | 23.7.2013 | China | 26.0218 | 99.888 | 2728 | SGN Frankfurt | This study |

\*SGN Frankfurt: Senckenberg Research Institute and Natural History Museum

Table S2. Best model selected by jModelTest2 based on the concatenated sequence.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Model | f(a) | f(c) | f(g) | f(t) | kappa | titv | Ra | Rb | Rc | Rd | Re | Rf | pInv | gamma |
| AIC | GTR+I+G | 0.31 | 0.18 | 0.19 | 0.32 | 0.00 | 0.00 | 0.902 | 2.665 | 1.261 | 0.806 | 3.465 | 1.000 | 0.86 | 0.90 |
| BIC | GTR+I+G | 0.31 | 0.18 | 0.19 | 0.32 | 0.00 | 0.00 | 0.902 | 2.665 | 1.261 | 0.806 | 3.465 | 1.000 | 0.86 | 0.90 |
| AICc | GTR+I+G | 0.31 | 0.18 | 0.19 | 0.32 | 0.00 | 0.00 | 0.902 | 2.665 | 1.261 | 0.806 | 3.465 | 1.000 | 0.86 | 0.90 |
| DT | GTR+I+G | 0.31 | 0.18 | 0.19 | 0.32 | 0.00 | 0.00 | 0.902 | 2.665 | 1.261 | 0.806 | 3.465 | 1.000 | 0.86 | 0.90 |

Table S3. Gene flow frequency classified by species.

|  |  |  |
| --- | --- | --- |
|  | Direction of gene flow | Frequency |
| 1 | *H. viteceki* / *H. viteceki* <–> *H. cf. martynovi* | 1 |
| 2 | *H. martynovi sensu stricto* / *H. martynovi sensu stricto* <–> *H. cf. martynovi* | 11 |
| 3 | *H. martynovi sensu stricto* –> *H. cf. martynovi* | 2 |
| 4 | *H. epikur* / *H. epikur* <–> *H. martynovi sensu stricto* | 10 |
| 5 | none | 1731 |

Table S4. Information of the 1–Kite transcriptomes for probe design.

|  |  |  |
| --- | --- | --- |
| **Genus** | **Species** |  |
| *Platycentropus* | *radiatus* | INSbttTARAAPEI-9 |
| *Cheumatopsyche* | *sp.* | INSbttTCRAAPEI-92 |
| *Chimarra* | *sp.* | INSbttTDRAAPEI-118 |
| *Leptocerus* | *americanus* | INSbttTERAAPEI-126 |
| *Nectopsyche* | *albida* | INSbttTFRAAPEI-171 |
| *Psychomyia* | *flavida* | INSbttTHRAAPEI-15 |
| *Ptilostomis* | *sp.* | INSbttTHRAAPEI-17 |
| *Glyphotaelius* | *pellucidus* | INSbusTBDRAAPEI-17 |
| *Phryganea* | *grandis* | INShauTBBRAAPEI-22 |
| *Hydroptilidae* | *sp.* | INSnfrTBJRAAPEI-8 |
| *Rhyacophila* | *fasciata* | INSjdsTBSRAAPEI-9 |
| *Apatania* | *incerta* | INShkeTAARAAPEI-94 |
| *Lepidostoma* | *togatum* | INShkeTACRAAPEI-8 |
| *Agapetus* | *hessi* | INShkeTADRAAPEI-9 |
| *Diplectrona* | *sp.* | INShkeTBWRAAPEI-17 |
| *Bombyx* | *mori* | Proteom |

Fig. S1. Length distribution of anchored hybrid enrichment loci after removing gaps and removing loci cover clusters less than 75% individuals. The mean sequence length was 716 bp and the standard deviation was 237 bp. The dashed orange box shows the loci with a length higher than 400 bp which were used for further analyses, in total 691 loci, 509113 bp overall, of which 65.8% were identical, GC content was 37.6%, gap (including ambiguous) percentage was 4%. The number above the bar shows the total number of loci for each length range.