Fig. S1 Global geographical distribution of diploids and polyploids of endemic occurrence data at different altitude gradient ranges. (a) > 2,500 m.a.s.l.; (b) 1,500-2,500 m.a.s.l.; (c) 500-1,500 m.a.s.l.; (d) < 500 m.a.s.l. The gradient color in each map corresponds to the altitude range. Red points indicate polyploids and blue points indicate diploids. The basemaps were created based on the altitude dataset with WorldClim (http://www.worldclim.org/) at 2.5 minutes resolution.
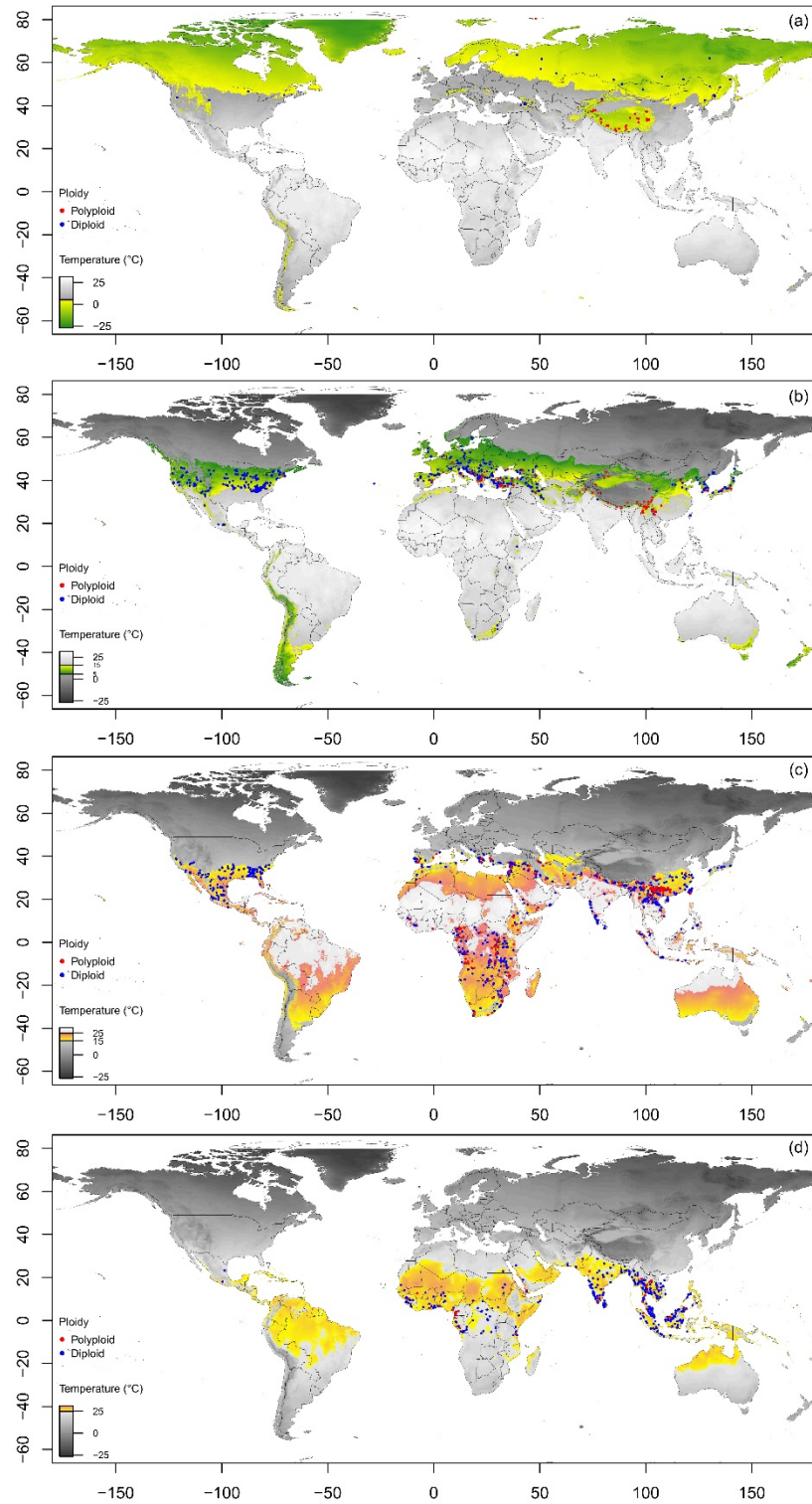
Fig. S2 Global geographical distribution of diploids and polyploids of endemic occurrence data at different mean annual temperature gradient ranges. (a) < 5 ºC; (b) 5-15 ºC; (c) 15-25 ºC; (d) > 25 ºC. The gradient color in each map corresponds to the temperature range. Red points indicate polyploids and blue points indicate diploids. The basemaps were created based on the BIO1 dataset with WorldClim (http://www.worldclim.org/) at 2.5 minutes resolution.
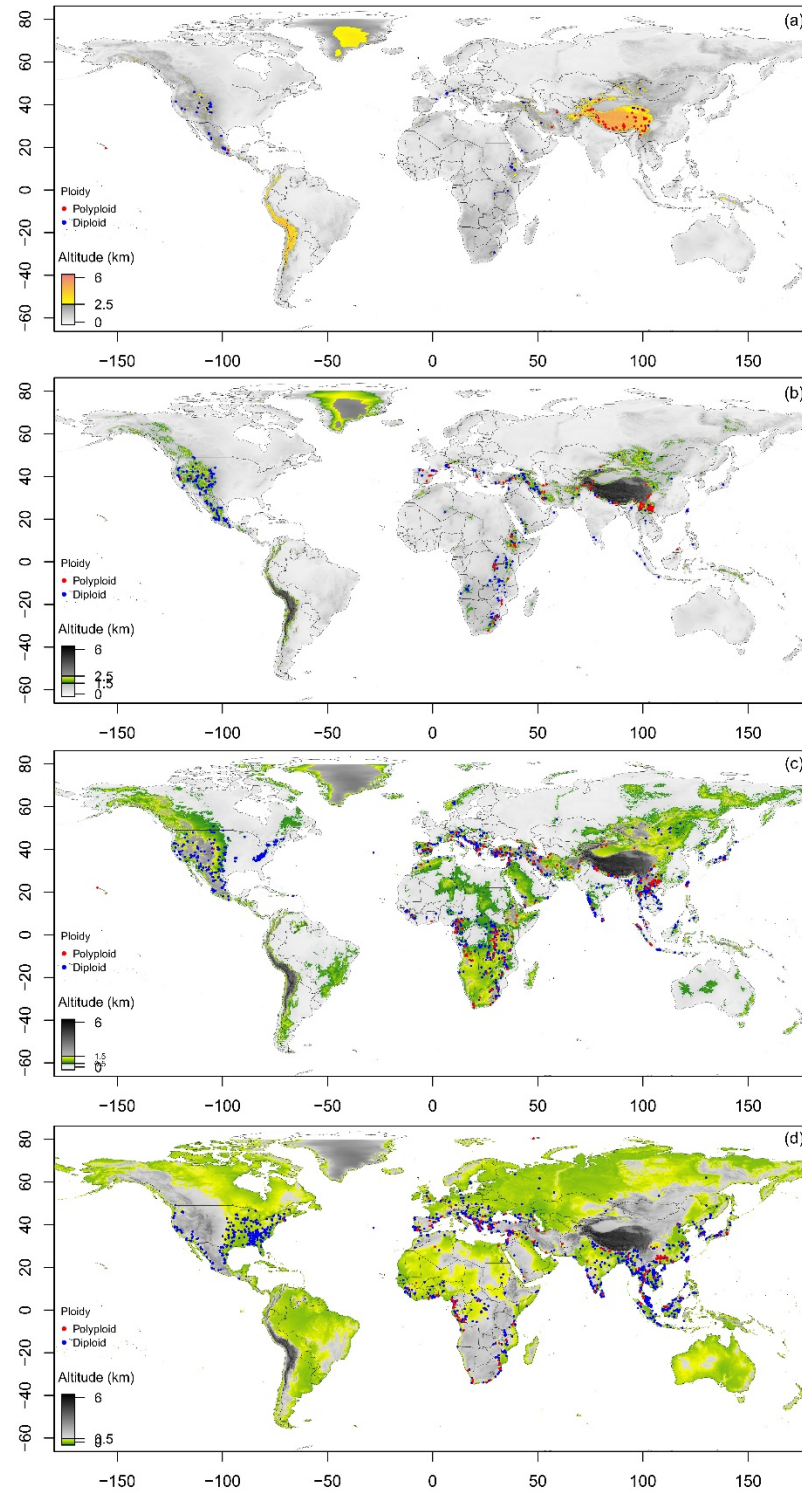
Fig. S3 Global geographical distribution of diploids and polyploids of all occurrence data at different altitude gradient ranges. (a) > 2,500 m.a.s.l.; (b) 1,500-2,500 m.a.s.l.; (c) 500-1,500 m.a.s.l.; (d) < 500 m.a.s.l. The gradient color in each map corresponds to the altitude range. Red points indicate polyploids and blue points indicate diploids. The basemaps were created based on the altitude dataset with WorldClim (http://www.worldclim.org/) at 2.5 minutes resolution.
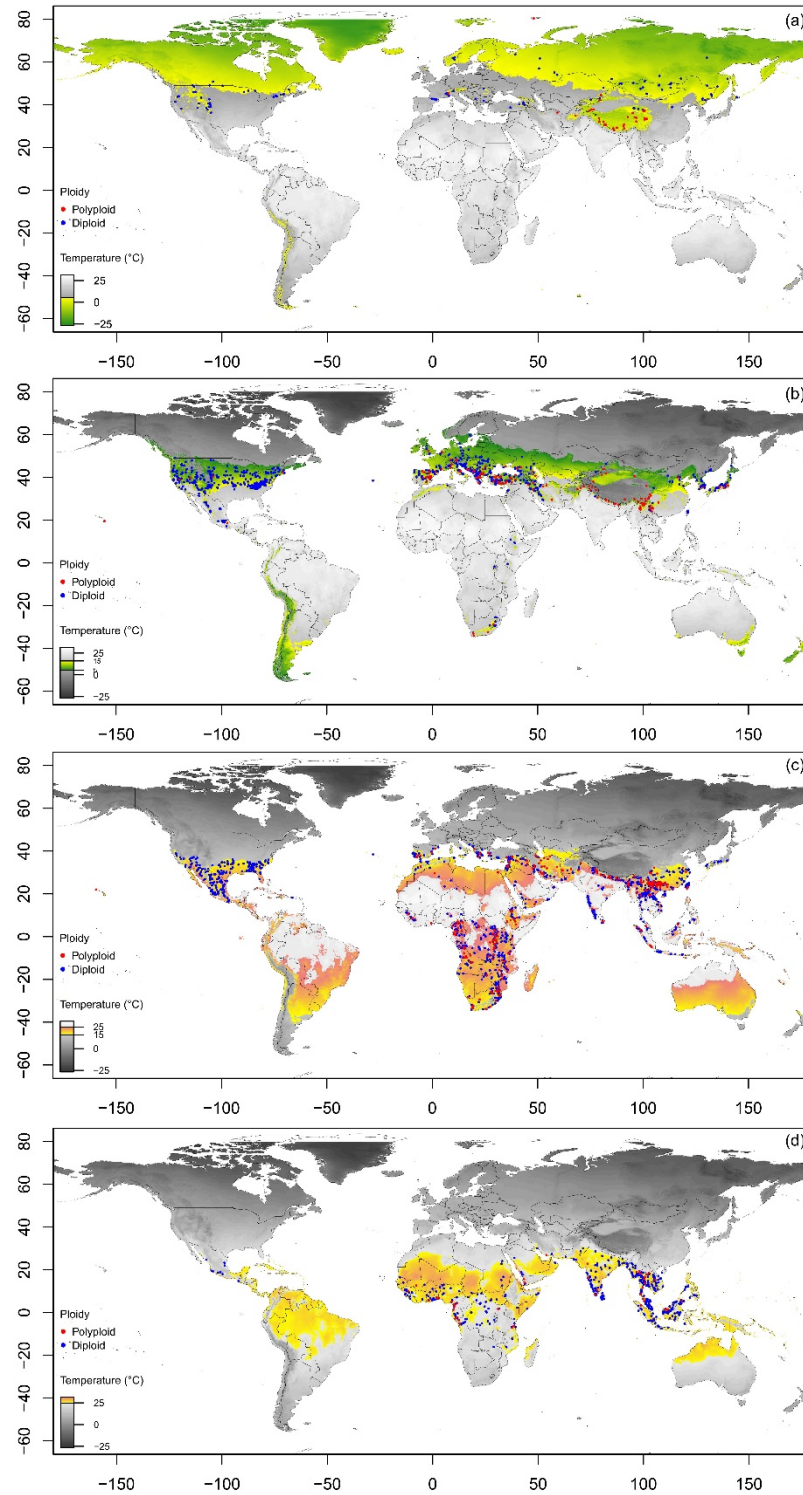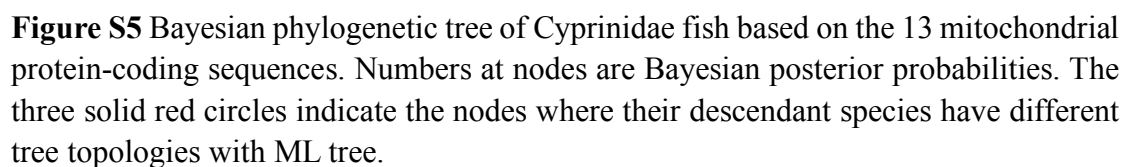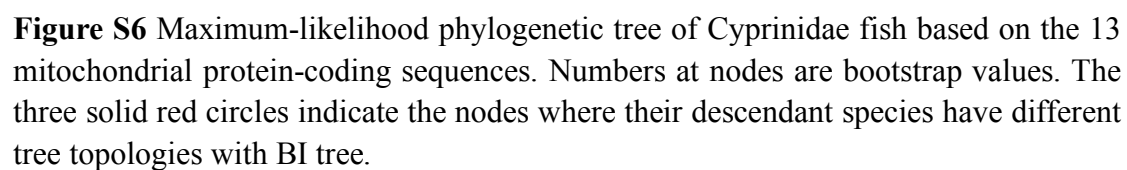
Fig. S4 Global geographical distribution of diploids and polyploids of all occurrence data at different mean annual temperature gradient ranges. (a) < 5 ºC; (b) 5-15 ºC; (c) 15-25 ºC; (d) > 25 ºC. The gradient color in each map corresponds to the temperature range. Red points indicate polyploids and blue points indicate diploids. The basemaps were created based on the BIO1 dataset with WorldClim (http://www.worldclim.org/) at 2.5 minutes resolution.

Figure S5 Bayesian phylogenetic tree of Cyprinidae fish based on the 13 mitochondrial protein-coding sequences. Numbers at nodes are Bayesian posterior probabilities. The three solid red circles indicate the nodes where their descendant species have different tree topologies with ML tree.

Figure S6 Maximum-likelihood phylogenetic tree of Cyprinidae fish based on the 13 mitochondrial protein-coding sequences. Numbers at nodes are bootstrap values. The three solid red circles indicate the nodes where their descendant species have different tree topologies with BI tree.

Cyprininae

Torini

Schizopygopsini
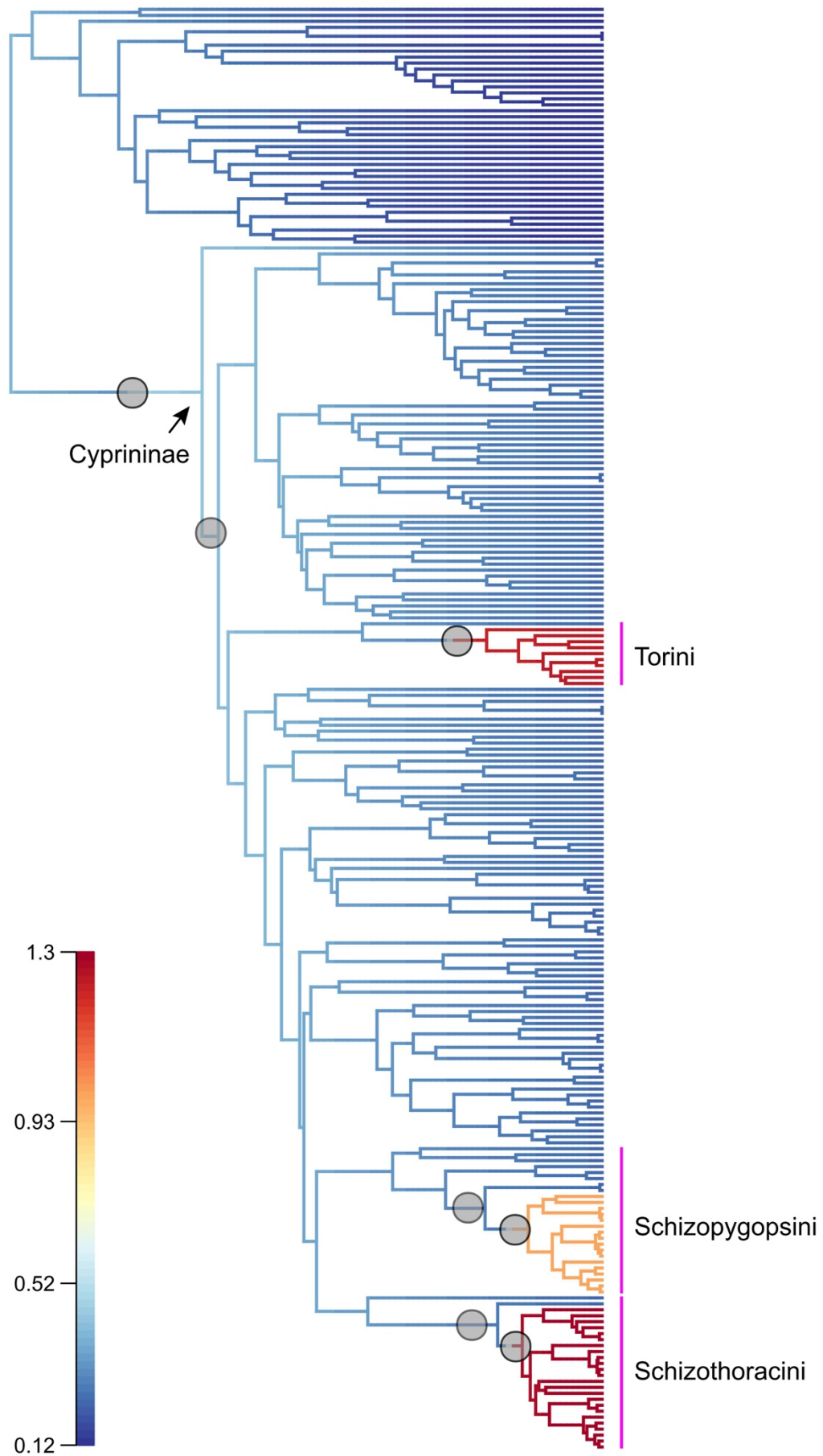
Schizothoracini

1.3

0.93

0.52

0.12

Figure S7 The plot shows the heterogeneity in net diversification rates along each branch of the Cyprinidae phylogeny. Visualization was performed using plot.credibleshiftset in BAMMtools. Warmer colours denote faster rates of diversification. Grey circles denote estimated placement of shifts based on the single configuration that has highest posterior probability (f = 0.069) in the 95% credible set of distinct shifts configurations.
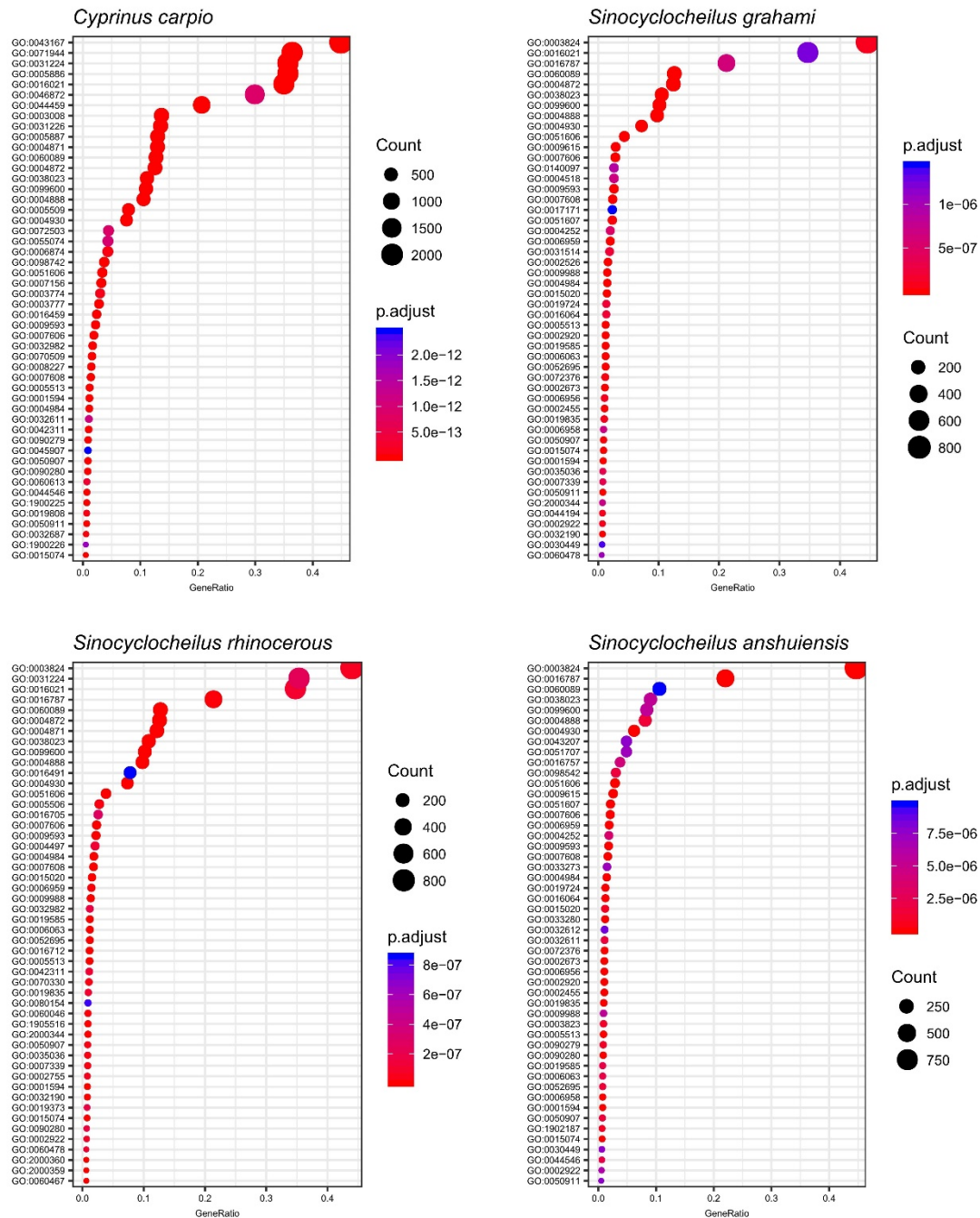
Figure S8 The Gene Ontology (GO) enrichment of pseudogenes in *Cyprinus carpio*, *Sinocyclocheilus grahami*, *Sinocyclocheilus rhinocerous* and *Sinocyclocheilus anshuiensis*, respectively.
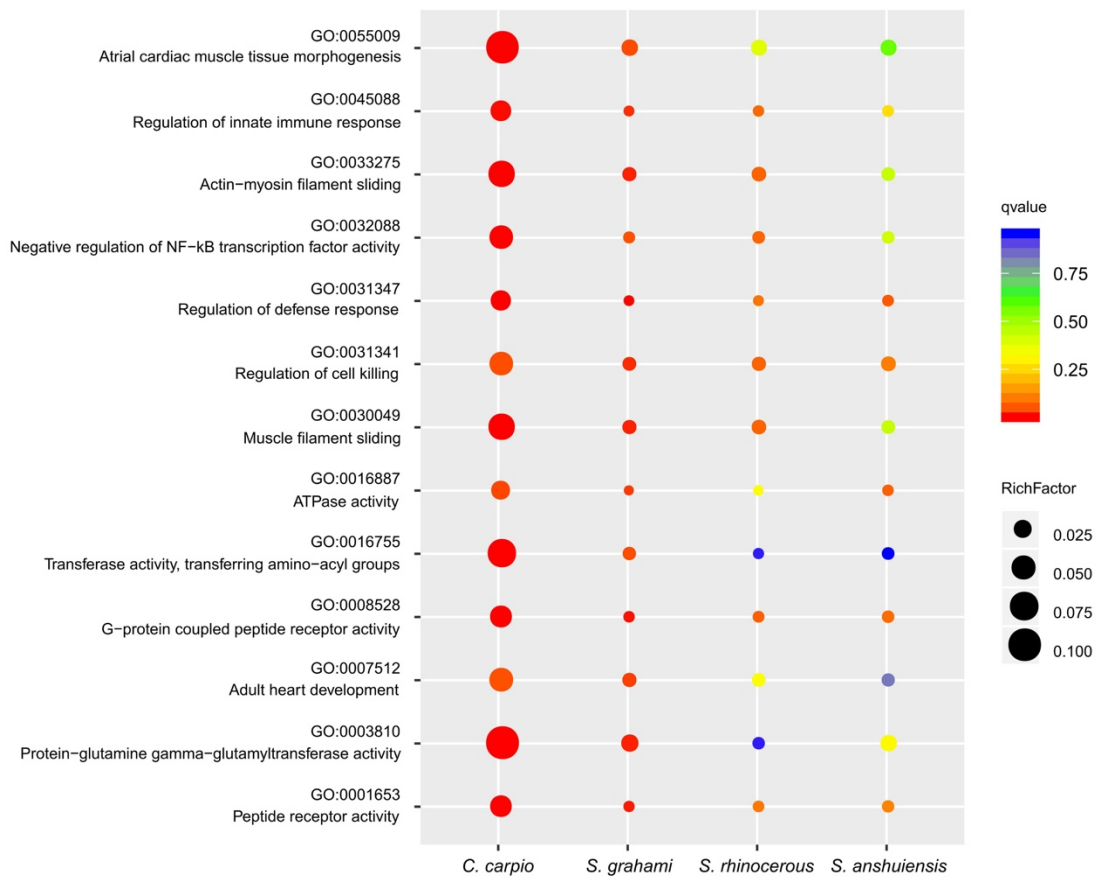
Figure S9 Differential Gene Ontology (GO) enrichment of pseudogenes between surface-dwelling polyploids (*C. carpio* and *S. grahami*) and cave-dwelling polyploids (*S. rhinocerous* and *S. anshuiensis*). Only GOs with significantly enriched pseudogenes in surface-dwelling species rather than in cave-dwelling species are depicted. The color gradient represents *q*-values. Bubble size is correlated with the RichFactor, with the greater of the Rich factor and the greater the degree of enrichment.
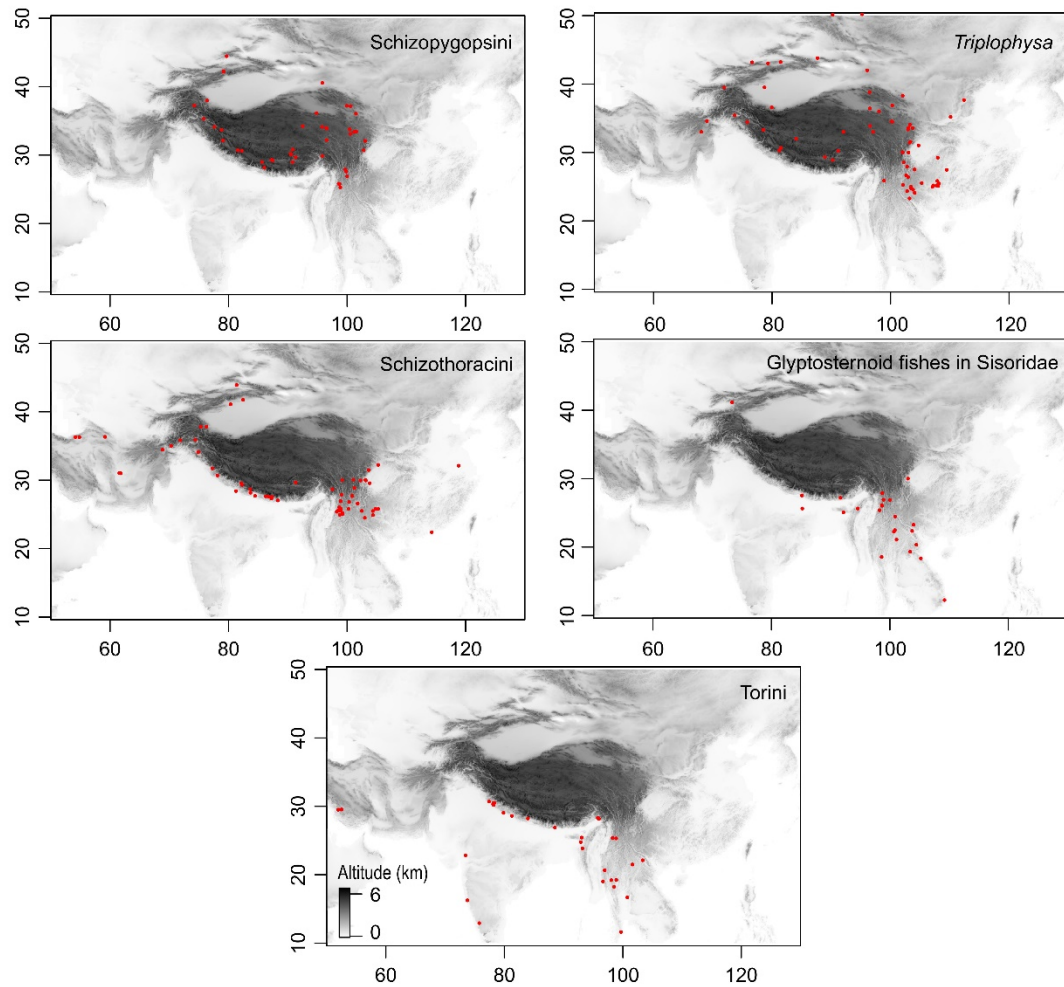
Figure S10 Global geographical distribution of the earliest occurrence record for the five groups of fishes (Schizopygopsini, Schizothoracini, and Torini in Cyprinidae, *Triplophysa* in Balitoridae, and glyptosternoid fishes in Sisoridae) endemic to QTP and its adjacent area. The basemaps were created based on the altitude dataset with WorldClim (http://www.worldclim.org/) at 2.5 minutes resolution.