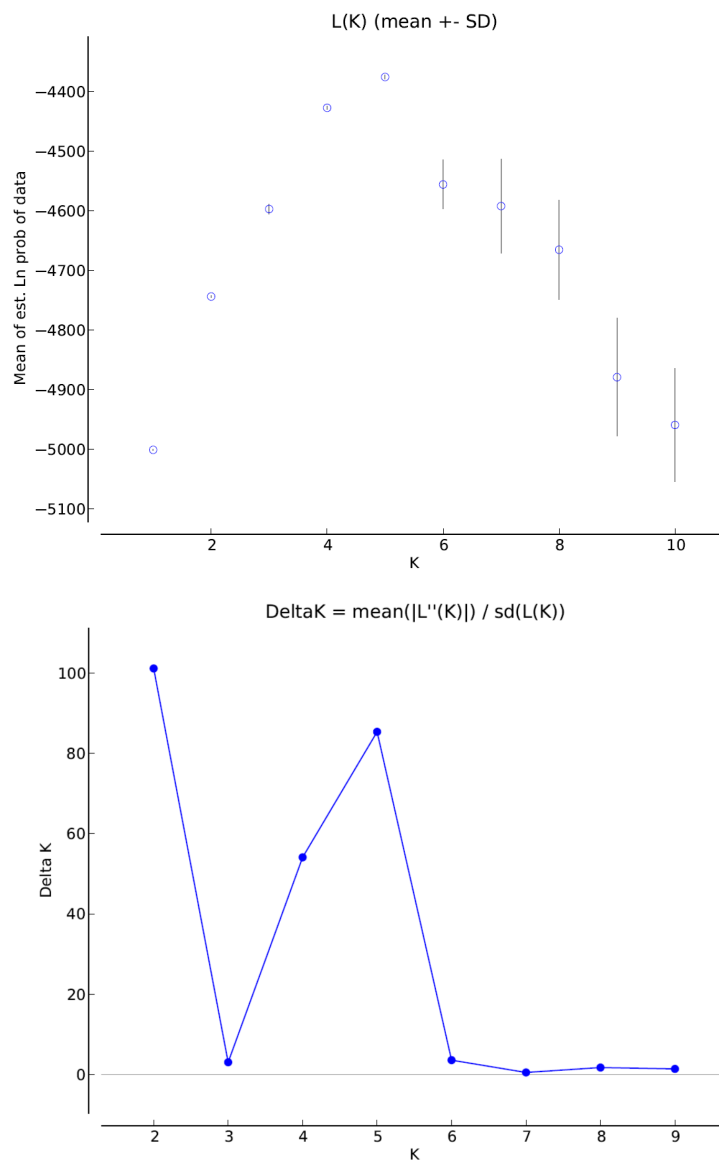


Additional file 3



| K | Reps | Mean LnP(K) | Stdev LnP(K) | Ln'(K) | Ln''(K) | Delta K |
|----|------|--------------|--------------|-------------|------------|------------|
| 1 | 40 | -5001.015000 | 0.495906 | — | — | — |
| 2 | 40 | -4743.600000 | 1.093336 | 257.415000 | 110.600000 | 101.158247 |
| 3 | 40 | -4596.785000 | 7.675287 | 146.815000 | 23.137500 | 3.014545 |
| 4 | 40 | -4426.832500 | 2.185311 | 169.952500 | 118.200000 | 54.088416 |
| 5 | 40 | -4375.080000 | 2.719559 | 51.752500 | 232.157500 | 85.365869 |
| 6 | 40 | -4555.485000 | 40.693120 | -180.405000 | 144.115000 | 3.541508 |
| 7 | 40 | -4591.775000 | 78.114314 | -36.290000 | 37.005000 | 0.473729 |
| 8 | 40 | -4665.070000 | 82.732387 | -73.295000 | 140.702500 | 1.700694 |
| 9 | 40 | -4879.067500 | 98.466327 | -213.997500 | 133.880000 | 1.359653 |
| 10 | 40 | -4959.185000 | 94.111095 | -80.117500 | — | — |

Figure S2. Excerpts of the output from STRUCTURE HARVESTER (Earl and Vonholdt 2012) employing the method of Evanno et al. (2005) to infer the most probable number of genetic clusters in the microsatellite genotypes of chub analyzed in this study. The mean likelihoods (from 40 replicate runs) show a unimodal distribution with a maximum at $K = 5$ (top panel), suggesting five as the most likely number of genetic clusters, which is also supported by a high ΔK value (bottom panel), although ΔK is even higher for $K = 2$, despite this number having the lowest likelihood of all values tested.