**Table S3** Results of bottleneck tests in 13 nine-spined stickleback populations form software Bottleneck under TPM mutation model with a one-tailed Wilcoxon signed-rank tests (*P* values) and from *M*-ratio tests (*M* and $M_c$ values) using 109 microsatellite markers.

| Population | TPM | *M* | $M_c$ |
|---|---|---|---|
| Hel | 1.00 | 0.693 | 0.874*/0.792*/0.755* |
| Sbol | 1.00 | 0.736 | 0.874*/0.792*/0.755* |
| Lev | 1.00 | 0.753 | 0.874*/0.792*/0.755* |
| Kro | 0.92 | 0.714 | 0.874*/0.792*/0.755* |
| Ska | 0.89 | 0.847 | 0.906*/0.884*/0.861* |
| Por | 1.00 | 0.797 | 0.916*/0.893*/0.871* |
| L1 | 0.03* | 0.705 | 0.914*/0.891*/0.869* |
| Rah | 1.00 | 0.780 | 0.915*/0.893*/0.872* |
| Byn | 0.42 | 0.806 | 0.911*/0.889*/0.866* |
| Pyo | 0.96 | 0.898 | 0.896/0.872/0.849 |
| Rbol | 1.00 | 0.735 | 0.874*/0.791*/0.755* |
| Ryt | 0.69 | 0.772 | 0.911*/0.889*/0.867* |
| Mat | 0.47 | 0.670 | 0.874*/0.792*/0.755* |

*$P < 0.05$. The three $M_c$ values from left to right correspond to the tests of a pre-bottleneck $N_e$ of 1,000, 5,000, 10,000 for the three marine (Hel, Sbol, Lev) and three coastal freshwater (Kro, Rbol, Mat) populations, and 100, 500 and 1000 for the seven inland freshwater populations (Ska, Por, L1, Rah, Byn, Pyo, Rbol, Ryt), respectively.