Supplementary information

A highly flexible and repeatable genotyping method for aquaculture studies based on target amplicon sequencing using next-generation sequencing technology

Mana Sato¹, Sho Hosoya^{1*}, Sota Yoshikawa^{1,2}, Shun Ohki¹, Yuki Kobayashi³, Takuya Itou³, Kiyoshi Kikuchi¹

¹Fisheries Laboratory, University of Tokyo, Hamamatsu, 431-0214, Japan.

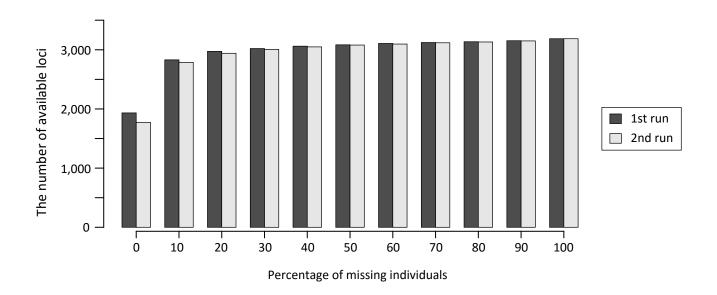
*Correspondence.

Sho Hosoya

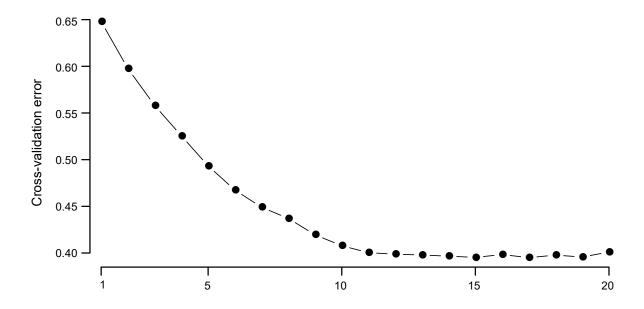
E-mail address: ahosoya@mail.ecc.u-tokyo.ac.jp

²Seed production Technology Development Center, Nagasaki Prefectural Institute of Fisheries, Nagasaki, 851-2213, Japan

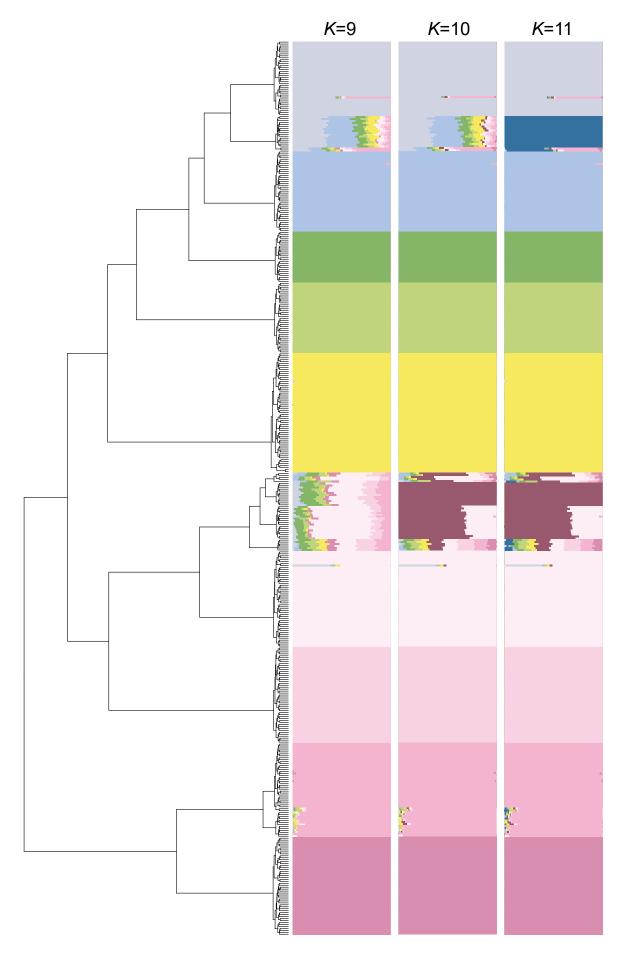
³Veterinary Research Center, Nihon University, Kanagawa, 252-0880, Japan



Supplementary Figure S1. The number of available loci with different levels of missing rates of genotyped individuals. Zero-percent indicates the number of available loci with no missing data, whreas the number of available loci with 100% missing is equivalent to the total number of targeted loci, i.e. 3,187 loci.



Supplementary Figure S2. Plot shows the error rate estimated by cross validation test for each K in the ADMIXTURE analysis from K=1 through K=20.



Supplementary Figure S3. Hierarchical clustering and population structure plots of the cultured population. The admixture proportions of individuals were estimated by ADMIXTURE software (K=9 to K=11)