**Supplementary File 1.** Summary of results from quality control of SNP genotypes for each farmed coho salmon population.

|  |  |  |  |
| --- | --- | --- | --- |
| Parameters | Populations | | |
| **POP A** | **POP B** | **POP C** |
| Minor allele frequency | 29,895 | 19,679 | 18,478 |
| Hardy-Weinberg equilibrium | 271 | 1,283 | 32 |
| Call-rate | 34 | 0 | 1 |
| Removed\* | 3,171 | 12,409 | 14,860 |
| Final number of SNPs\*\* | 102,129 | 102,129 | 102,129 |

\* Common markers selected across all populations.

\*\*From a total of 135,500 SNPs.

**Supplementary File 2** Admixture clustering of the three coho salmon population for K = 4.

Each vertical line represents an animal and the black vertical lines were used to separate different populations.

**Supplementary File 3.** Runs of homozygosity patterns for all chromosome (Okis1 to Okis30) in three coho salmon population.

Each row represents one individual and each bar a ROH segment.

**Supplementary File 4.** Scatterplots (lower panel) and Pearson correlation coefficients (upper panel) of genomic inbreeding coefficients using runs of homozygosity (ROH) for different ROH length, based on excess of homozygosity (FHOM), genomic relationship matrix (FGRM) and pedigree-based relationship matrix (FPED) for POP A.

**Supplementary File 5.** Scatterplots (lower panel) and Pearson correlation coefficients (upper panel) of genomic inbreeding coefficients using runs of homozygosity (ROH) for different ROH length, based on excess of homozygosity (FHOM), genomic relationship matrix (FGRM) and pedigree-based relationship matrix (FPED) for POP B.

**Supplementary File 6.** Scatterplots (lower panel) and Pearson correlation coefficients (upper panel) of genomic inbreeding coefficients using runs of homozygosity (ROH) for different ROH length, based on excess of homozygosity (FHOM), genomic relationship matrix (FGRM) and pedigree-based relationship matrix (FPED) for POP C.

**Supplementary File 7.** Scatterplots (lower panel) and Pearson correlation coefficients (upper panel) of genomic inbreeding coefficients using runs of homozygosity (ROH) for different ROH length, based on excess of homozygosity (FHOM), genomic relationship matrix (FGRM) and pedigree-based relationship matrix (FPED) across populations.