



Nov 05, 2020

ND5 sequencing of *Oncorhynchus masou masou*

PLOS One

Yoko Kato-Unoki¹¹Center for Advanced Instrumental and Educational Supports, Faculty of Agriculture, Kyushu University, Fukuoka, Japan**1** Works for me dx.doi.org/10.17504/protocols.io.bmf7k3rn

Yoko Kato-Unoki

EXTERNAL LINK

<https://doi.org/10.1371/journal.pone.0240823>

THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

Kato-Unoki Y, Umemura K, Tashiro K (2020) Fingerprinting of hatchery haplotypes and acquisition of genetic information by whole-mitogenome sequencing of masu salmon, *Oncorhynchus masou masou*, in the Kase River system, Japan. PLoS ONE 15(11): e0240823. doi: [10.1371/journal.pone.0240823](https://doi.org/10.1371/journal.pone.0240823)

DOI

dx.doi.org/10.17504/protocols.io.bmf7k3rn

EXTERNAL LINK

<https://doi.org/10.1371/journal.pone.0240823>

PROTOCOL CITATION

Yoko Kato-Unoki 2020. ND5 sequencing of *Oncorhynchus masou masou*. **protocols.io**
<https://dx.doi.org/10.17504/protocols.io.bmf7k3rn>

MANUSCRIPT CITATION please remember to cite the following publication along with this protocol

Kato-Unoki Y, Umemura K, Tashiro K (2020) Fingerprinting of hatchery haplotypes and acquisition of genetic information by whole-mitogenome sequencing of masu salmon, *Oncorhynchus masou masou*, in the Kase River system, Japan. PLoS ONE 15(11): e0240823. doi: [10.1371/journal.pone.0240823](https://doi.org/10.1371/journal.pone.0240823)

EXTERNAL LINK

<https://doi.org/10.1371/journal.pone.0240823>

LICENSE

This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

CREATED

Sep 16, 2020

LAST MODIFIED

Nov 05, 2020

PROTOCOL INTEGER ID

42207

MATERIALS TEXT

MATERIALS

Phusion High-Fidelity DNA Polymerase - 100 units New England

Biolabs Catalog #M0530S

Agarose S Nippon

Gene Catalog #312-01193

- 1 Amplify the *ND5* region (1597 bp) with the following PCR mixture and program.

Component	Amount
5× Phusion HF buffer (New England BioLabs)	2 µl
Phusion DNA Polymerase (New England BioLabs)	0.1 µl
10 mM dNTPs	0.2 µl
10 µM primer ND5-F1	0.5 µl
10 µM primer ND5-R	0.5 µl
Genomic DNA	10–50 ng
Nuclease-free water	Variable
Total volume	10 µl

PCR mixture

Step	Temperature	Time	Number of cycles
1	98°C	30 sec	1
2	98°C	10 sec	40
3	64°C	20 sec	
4	72°C	60 sec	
5	72°C	2 min	1
6	8 °C	Hold	N/A

PCR program

- 2 Electrophorese 1 µl PCR product through a 1% agarose–TAE gel.
Check for the presence of non-specific amplification products and/or primer-dimers, and calculate the approximate concentration of the specific amplified DNA fragment by comparing its band intensity to that of the marker.

- 3 Sequence the PCR product with the primers ND5-F1 or ND5-F2.

Note: The PCR product can be used directly as a sequence template without purification or clean-up reagents if there is no non-specific amplification, no primer-dimer contamination, and can be diluted more than 5-fold in the sequence reaction solution.

- 4 Assemble and align the ND5 sequences by using ATGC Ver. 4.3.5 software (GENETYX Co.).