Supplementary Material

**Unveiling a potential threat to forest ecosystems: molecular diagnosis of *Alliaria petiolata*, a newly introduced alien plant in Korea**

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# Supplementary Data

# Supplementary Information 1. Comprehensive parameters and commands employed for the ipyrad pipeline

import ipyrad.analysis as ipa

import ipyrad as ip

import ipyparallel as ipp

import pandas as pd

# ipcluster start -n 100 --cluster-id="ipyrad2" --daemonize

# After the cluster is running you can attach to it with ipyparallel

ipyclient = ipp.Client(cluster\_id="ipyrad2")

data = ip.Assembly("France")

data.set\_params("sorted\_fastq\_path", "./sample/\*.fq.gz")

data.set\_params("assembly\_method", "reference")

data.set\_params("reference\_sequence", "./reference/GCA\_020283515.1\_Apet\_EFCC3-3-20v4\_genomic.fna")

data.set\_params("datatype", "pairddrad")

data.set\_params("restriction\_overhang", "'CATG', 'AATT'")

data.set\_params("clust\_threshold", "0.9")

data.set\_params("max\_alleles\_consens", "6")

data.set\_params("max\_Hs\_consens", "0.1")

data.set\_params("max\_shared\_Hs\_locus", "1")

data.run("1234567", force=True, ipyclient=ipyclient)