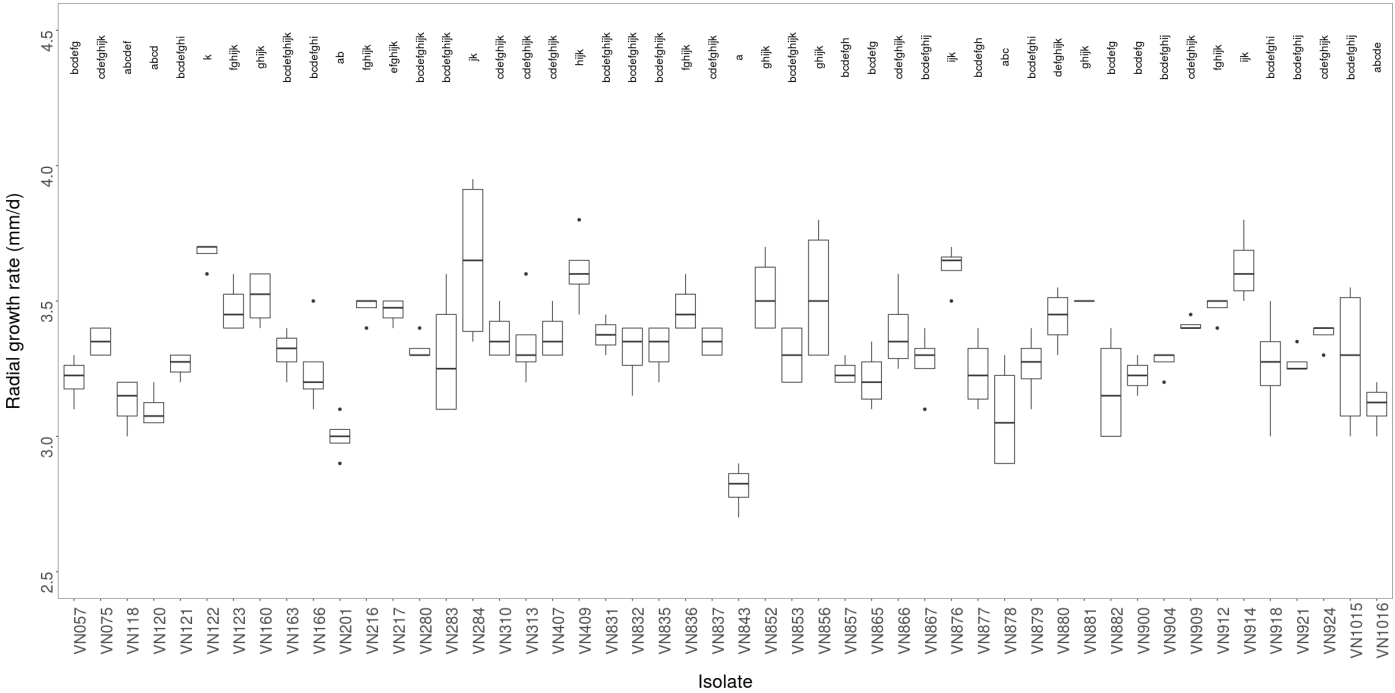
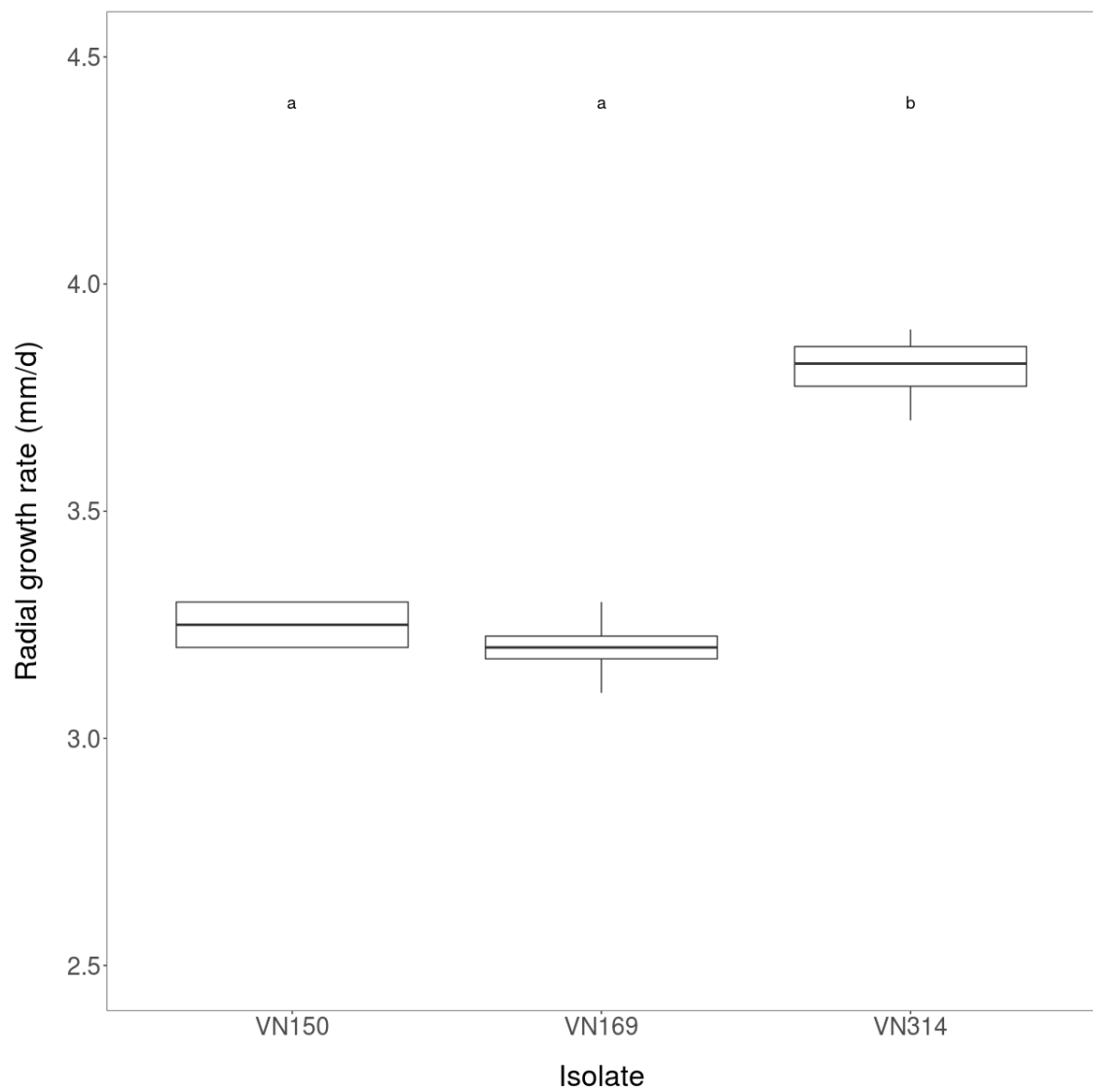


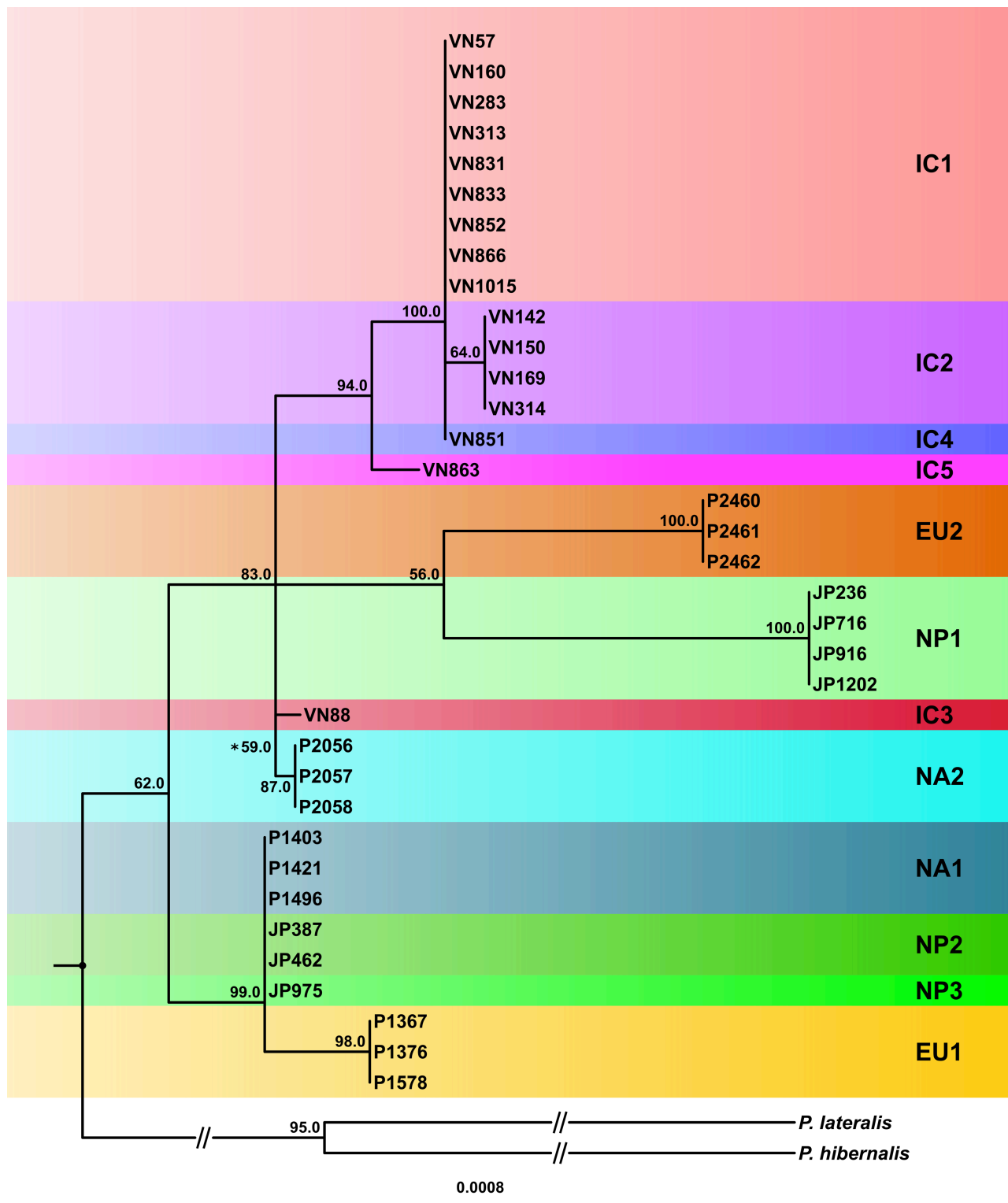
# Supplementary Figures



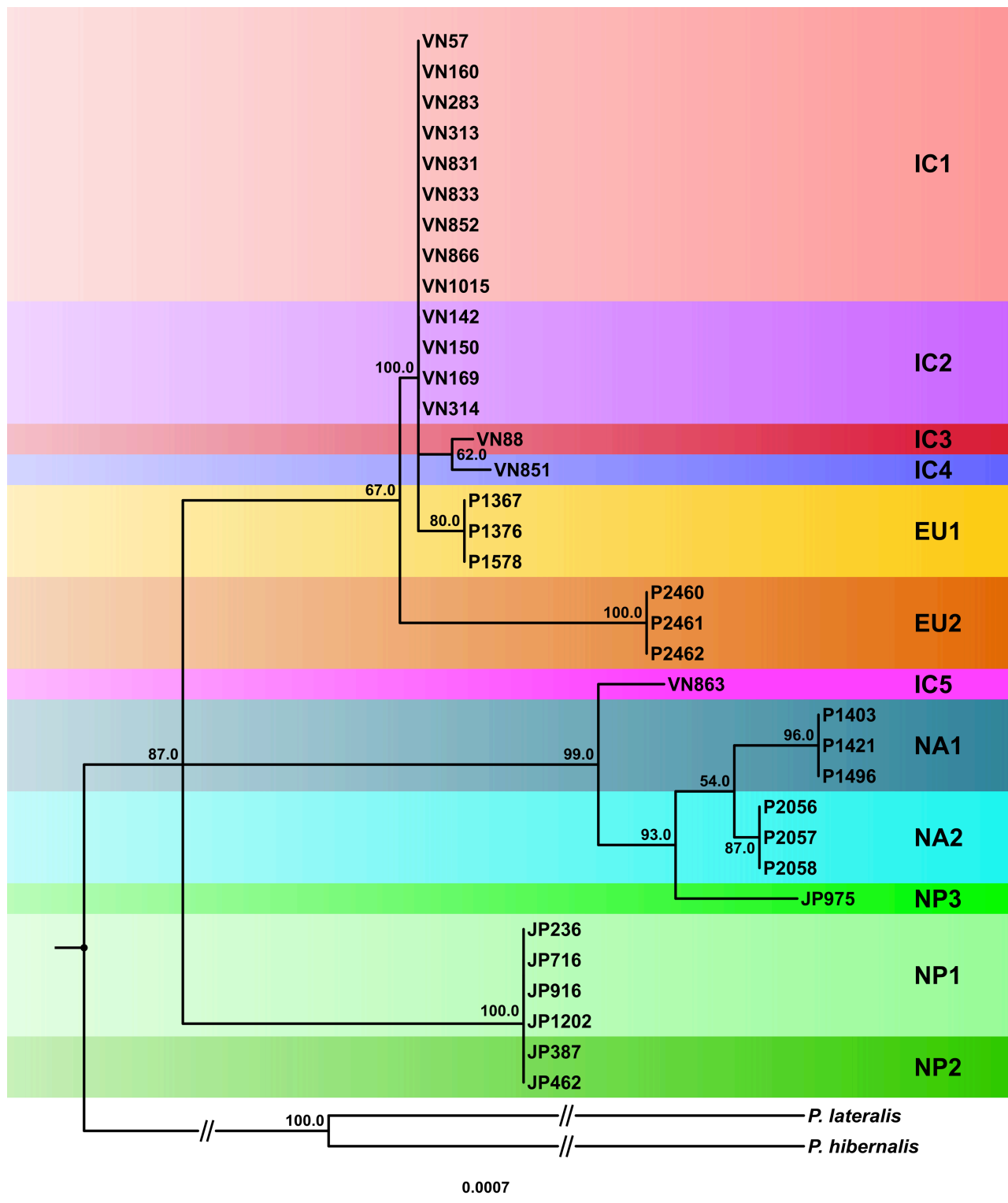
**Supplementary Figure S1.** Box and whiskers diagram showing daily radial growth rates of 50 isolates from the IC1 phenotype group of *Phytophthora ramorum* at 20 °C on carrot agar (CA). Different letters indicate statistical differences at significance level  $\alpha = 0.05$ .



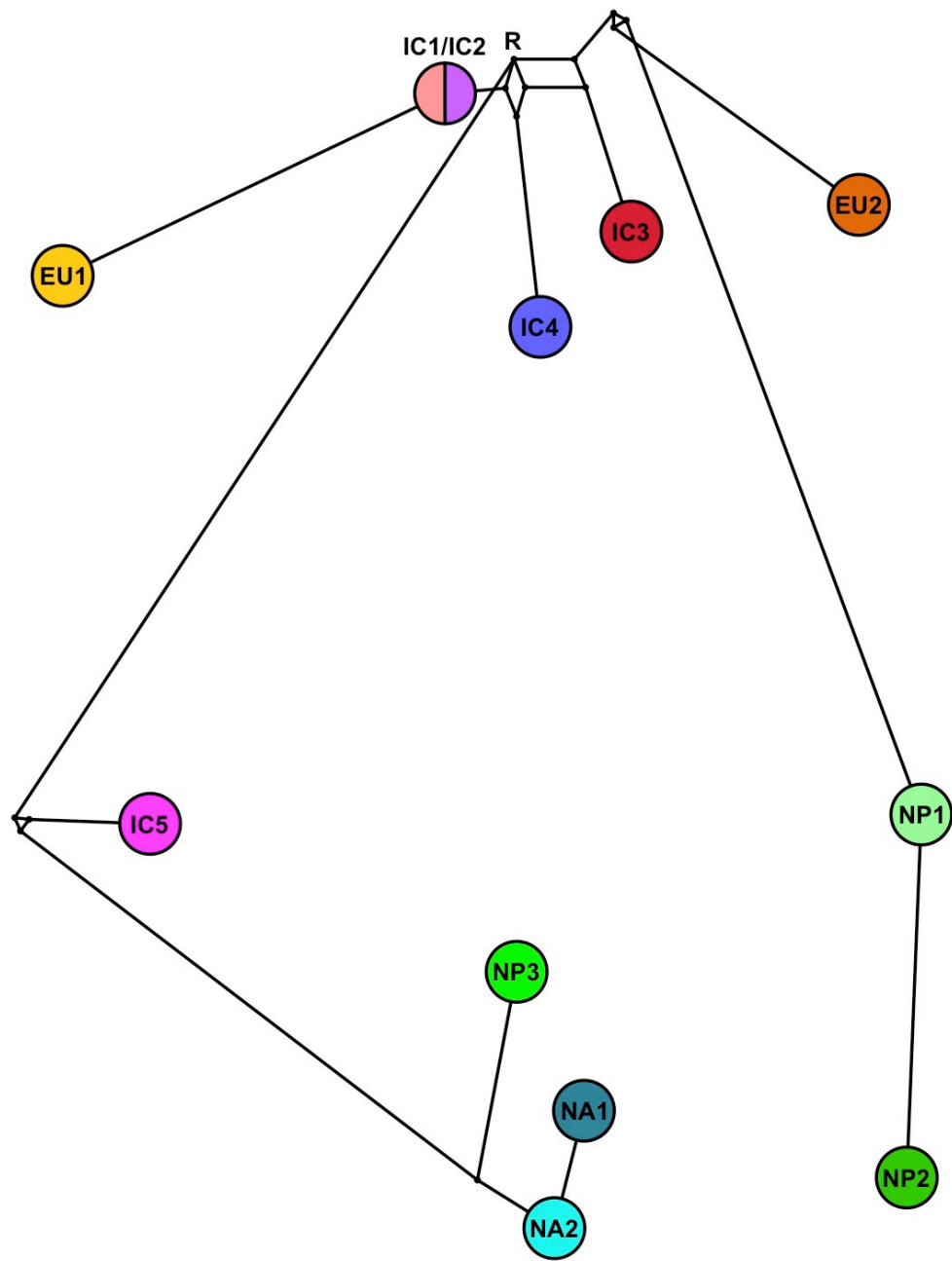
**Supplementary Figure S2.** Box and whiskers diagram showing daily radial growth rates of three isolates from the IC2 phenotype group of *Phytophthora ramorum* at 20 °C on carrot agar (CA). Different letters indicate statistical differences at significance level  $\alpha = 0.05$ .



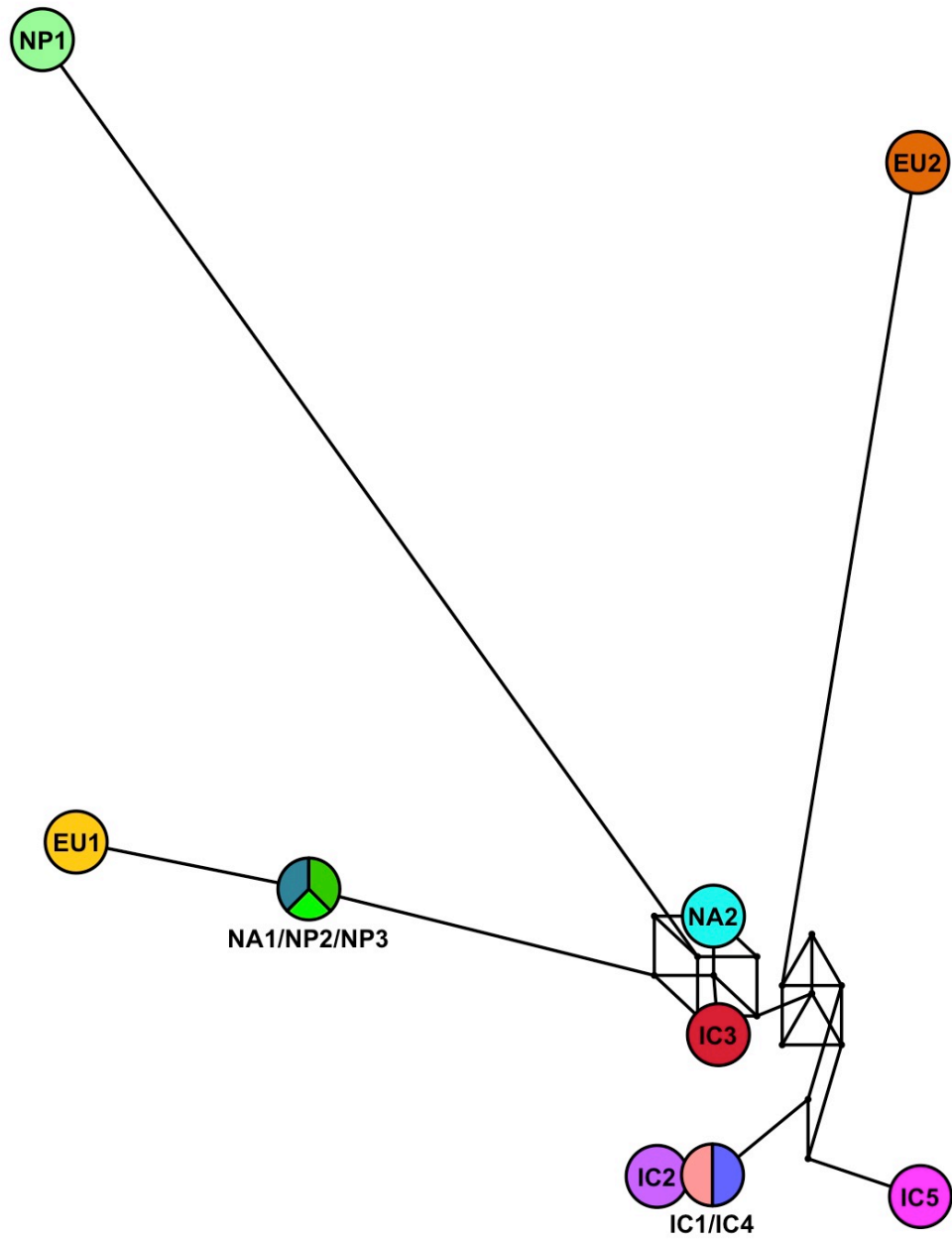
**Supplementary Figure S3.** Fifty percent majority rule consensus phylogram derived from Maximum Likelihood (ML) analysis of a mitochondrial five-loci (*cox1*, *cox2*, *nadh1*, *Prv8*, *Prv9*) dataset of the five Indochinese phenotype groups (IC1-5), the three Japanese phenotype groups (NP1-3) and the four known lineages (EU1, EU2, NA1, NA2) of *Phytophthora ramorum*. Maximum Likelihood bootstrap values (in %) are indicated above branches. *Phytophthora hibernalis* and *P. lateralis* were used as outgroup taxa. Scale bar = 0.0008 expected changes per site per branch. \* Invisible node due to extremely short branch length.



**Supplementary Figure S4.** Fifty percent majority rule consensus phylogram derived from Maximum Likelihood (ML) analysis of a nuclear seven-loci (*Avh120*, *Avh121*, *btub*, *gwEuk.30.30.1*, *hsp90*, ITS, *trp1*) dataset of the five Indochinese phenotype groups (IC1-5), the three Japanese phenotype groups (NP1-3) and the four known lineages (EU1, EU2, NA1, NA2) of *Phytophthora ramorum*. Maximum Likelihood bootstrap values (in %) are indicated above branches. *Phytophthora hibernalis* and *P. lateralis* were used as outgroup taxa. Scale bar = 0.0007 expected changes per site per branch.



**Supplementary Figure S5.** Median-joining network (MJN) with tolerance  $\epsilon = 10$  for the five Indochinese lineages (IC1-IC5), the three Japanese lineages (NP1-NP3) and four known introduced lineages (EU1, EU2, NA1, NA2) of *Phytophthora ramorum* based on a nuclear seven-loci (*Avh120*, *Avh121*, *btub*, *gwEuk.30.30.1*, *hsp90*, ITS, *trp1*) dataset. The node with the highest number of connections and the most central position in this network and in the MJN with  $\epsilon = 0$  (Figure 9) was designated as root (R). Compared to the nuclear MJN with  $\epsilon = 0$  this MJN shows several alternative evolutionary pathways. Missing intermediates represent extant unsampled genotypes, extinct ancestors or "false-positives". Branch lengths are proportional to the number of mutations.



**Supplementary Figure S6.** Median-joining network (MJN) with tolerance  $\varepsilon = 10$  for the five Indochinese lineages (IC1-IC5), the three Japanese lineages (NP1-NP3) and the four known lineages (EU1, EU2, NA1, NA2) of *Phytophthora ramorum* based on a mitochondrial five-loci (*cox1*, *cox2*, *nadh1*, Prv8, Prv9) dataset. Compared to the mitochondrial MJN with  $\varepsilon = 0$  this MJN contains multiple alternative evolutionary pathways and is too complex for selecting a root. Missing intermediates represent extant unsampled genotypes, extinct ancestors or "false-positives". Branch lengths are proportional to the number of mutations.