

SUPPORTING INFORMATION

Detection of Biomarkers of Pathogenic *Naegleria fowleri* through Mass Spectrometry and Proteomics by Hercules Moura, Fernando Izquierdo, Adrian R. Woolfitt, Glauber Wagner, Tatiana Pinto, Carmen del Aguila & John R. Barr

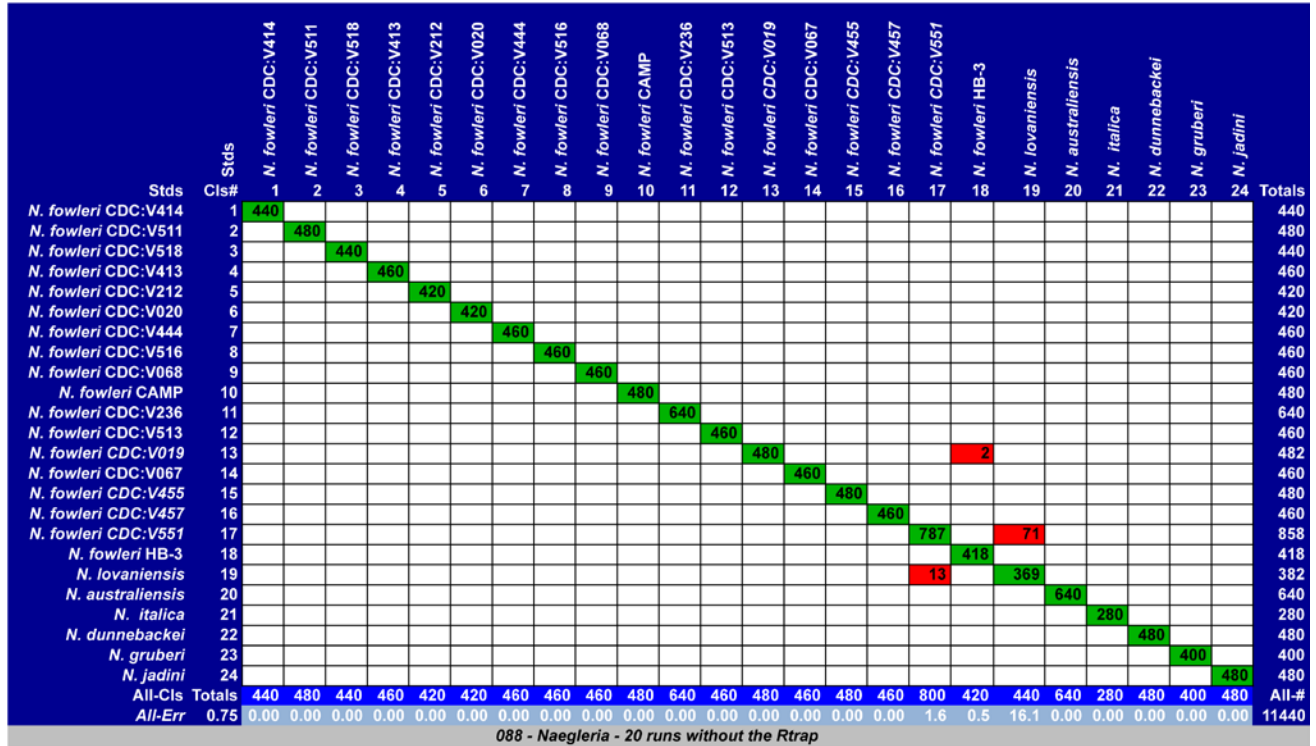


Fig.S1. Random Forest analysis of the studied *Naegleria* species and isolates. Datasets consisted of summed spectra from three harvestings of each organism as a training set (columns) and ~3 summed spectra as unknowns (rows). The estimated classification error was 0.75%, and the RF algorithm successfully classified all the *Naegleria* species and the majority of the isolates in the training set.

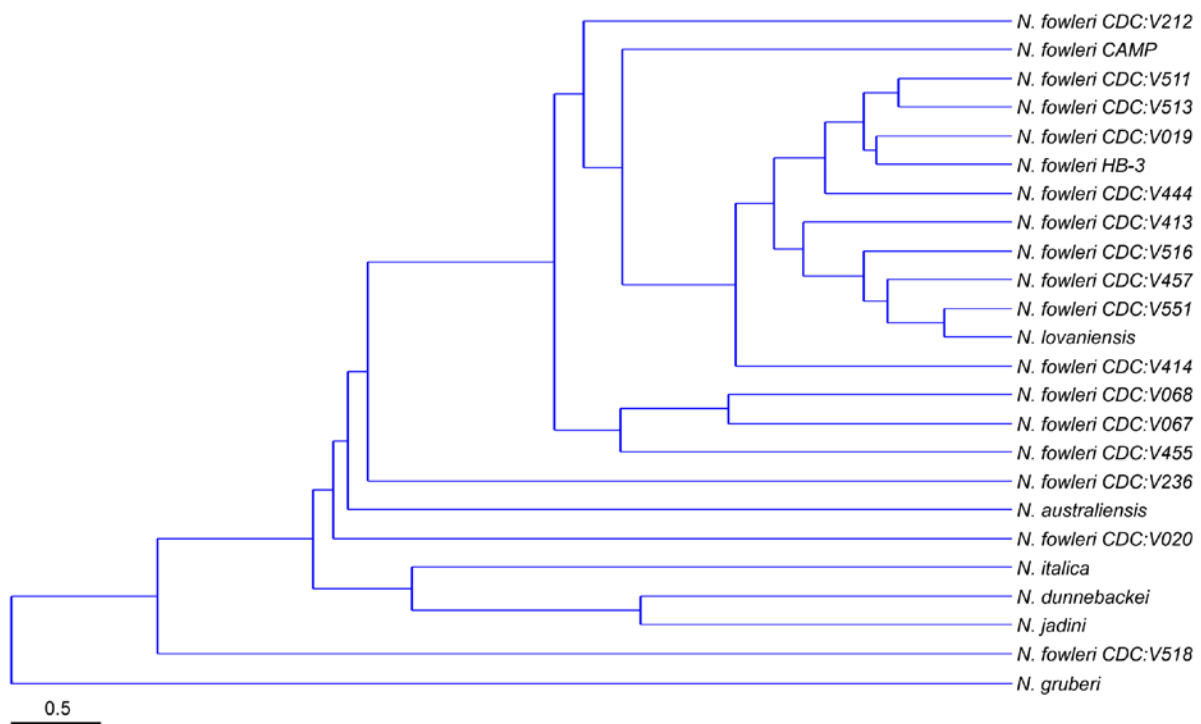


Fig.S2. Dendrogram obtained with PAST (<http://folk.uio.no/ohammer/past/index.html>). For this analysis, all spectra for each strain were summed to give one representative spectrum per organism.