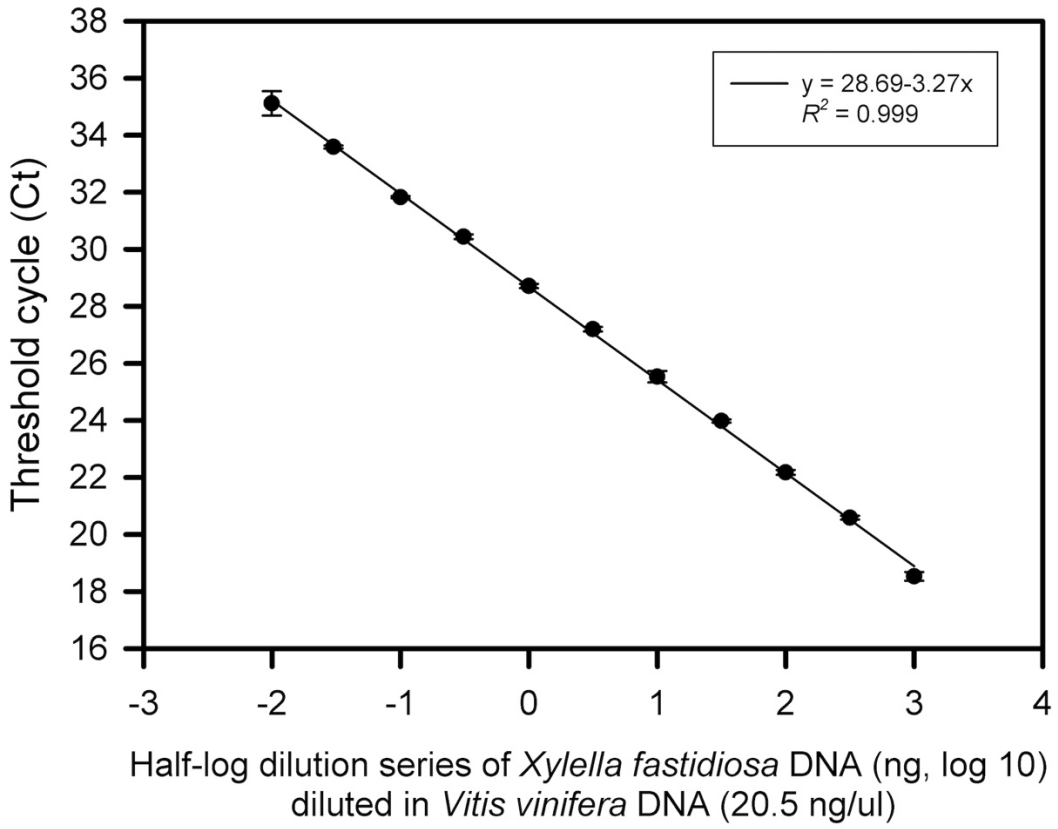


**Supplementary Figure 1.** To determine the efficiency of the *X. fastidiosa rimM* gene target simplex qPCR derived from Harper et al. [27], a standard curve was generated using *Xff* DNA (ATCC® 700964D-5™) diluted in healthy grape DNA. The dried genomic *Xff* DNA was rehydrated and re-suspended by adding 25 µl NFW and placed in a 37°C water bath for 1 hr. A half-log dilution series of the *X. fastidiosa* subsp. *fastidiosa* DNA from 1.0 ng to 0.31 fg was prepared in 20.5 ng/µl of healthy genomic *Vitis vinifera* DNA, extracted using the Isolate II Plant DNA Kit and quantified using a spectrophotometer (NanoDrop, NanoDrop, Wilmington, DE). Real-time PCR reactions were prepared with 3 replicates of each dilution series. Ct-values were applied automatically by the StepOne™ Software v. 2.1 (Life Technologies, Durham, NC). The standard curve showed a regression coefficient of 0.99 and an amplification efficiency of 102%. The *X. fastidiosa* singleplex assay reliably detected at 9.9 fg (~4 copies based on an estimated *X. fastidiosa* genome size of 2.5 MB) with an average Ct-value of 35.12 among 3 replicate samples with a SD of 0.43). Harper et al. [27] reported reliable detection (average Ct-value of 31.67, SD < 0.5) to 125 copies.