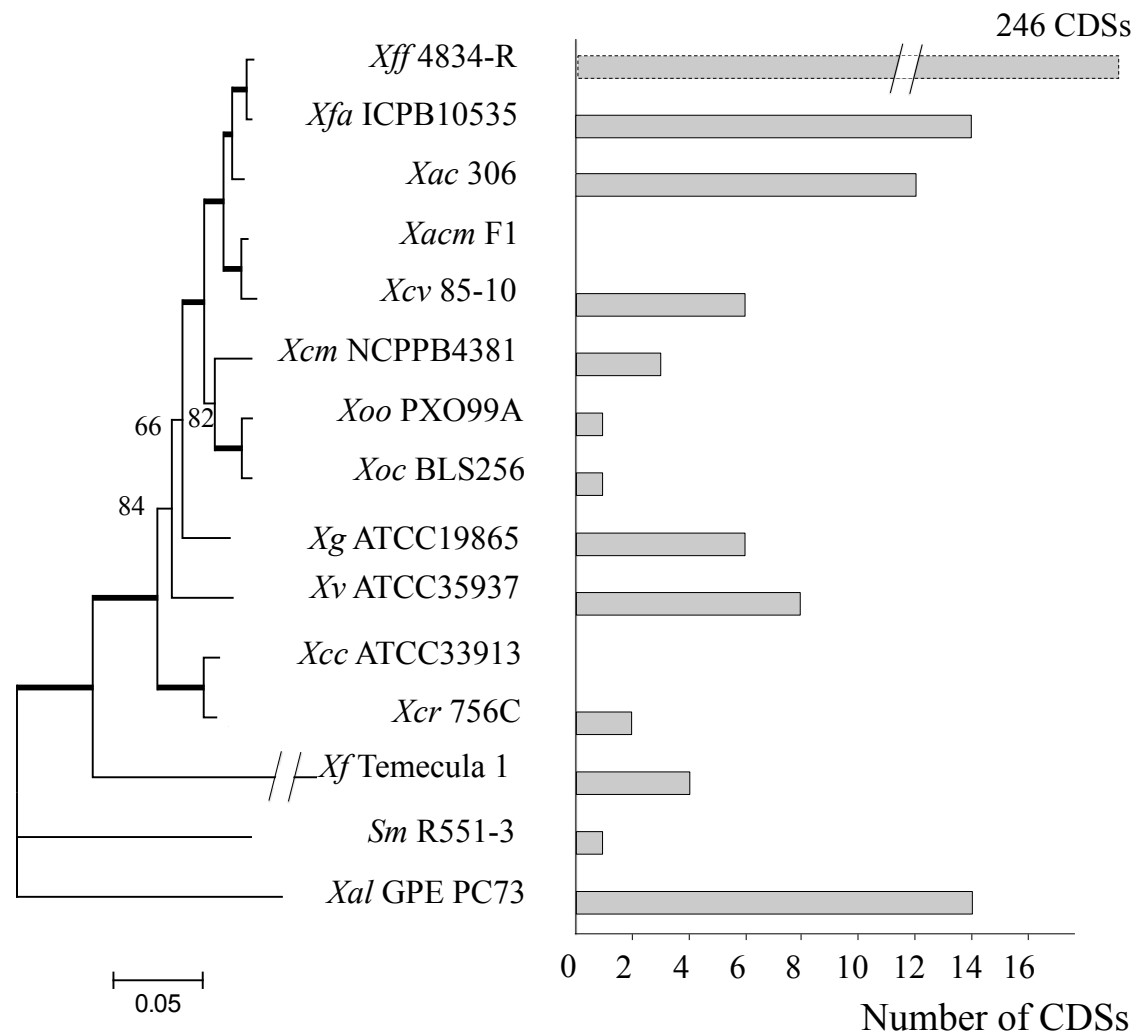




Additional file 1. Distribution of CDSs exclusively shared by *Xanthomonas fuscans* subsp. *fuscans* strain 4834-R (*Xff* 4834-R) and only one of the 15 strains used in comparative genomics. The strains, *Xff* 4834-R, *X. fuscans* subsp. *aurantifolii* strain ICPB10535 (*Xfa* ICPB10535), *X. citri* pv. *citri* strain 306 (*Xac* 306), *X. axonopodis* subsp. *citrumelonis* strain F1 (*Xacm* F1), *X. euvesicatoria* strain 85-10 (*Xcv* 85-10), *X. campestris* pv. *musacearum* strain NCPPB4381 (*Xcm* NCPPB4381), *X. oryzae* pv. *oryzae* strain PXO99A (*Xoo* PXO99A), *X. oryzae* pv. *oryzicola* strain BLS256 (*Xoc* BLS256), *X. gardneri* strain ATCC19865 (*Xg* ATCC19865), *X. vesicatoria* strain ATCC35937 (*Xv* ATCC35937), *X. campestris* pv. *campestris* strain ATCC33913 (*Xcc* ATCC33913), *X. campestris* pv. *raphani* strain 756C (*Xcr* 756C), *Xylella fastidiosa* strain Temecula1 (*Xf* Temecula1), *Stenotrophomonas maltophilia* strain R551-3 (*Sm* R551-3), and *X. albilineans* strain GPE PC73 (*Xal* GPE PC73), are organized according to their phylogeny represented by the Maximum Likelihood phylogenetic tree based on six housekeeping gene sequences (*atpD*, *dnaK*, *efP*, *glnA*, *gyrB*, *rpoD*). Bold line indicates that bootstrap value (1000 replicates) is 100, if not, bootstrap value of the branch is indicated on the tree. Branch length for *Xf* Temecula1 is 0.6 substitution per site.