



S2 Figure. Accessory genome variation in *Xanthomonas euvesicatoria* pv. *perforans*. (A) Visualization of pangenome variation by non-metric multidimensional scaling of gene presence-absence for all 270 *X. perforans* strains by BAPS cluster. Ellipses assume a multivariate t-distribution. (B) Increase in gene count with increasing number of strains sampled. Clusters 1 and 2 were represented by the most strains, but other clusters showed similar rates of increase in the pangenome of the cluster.