

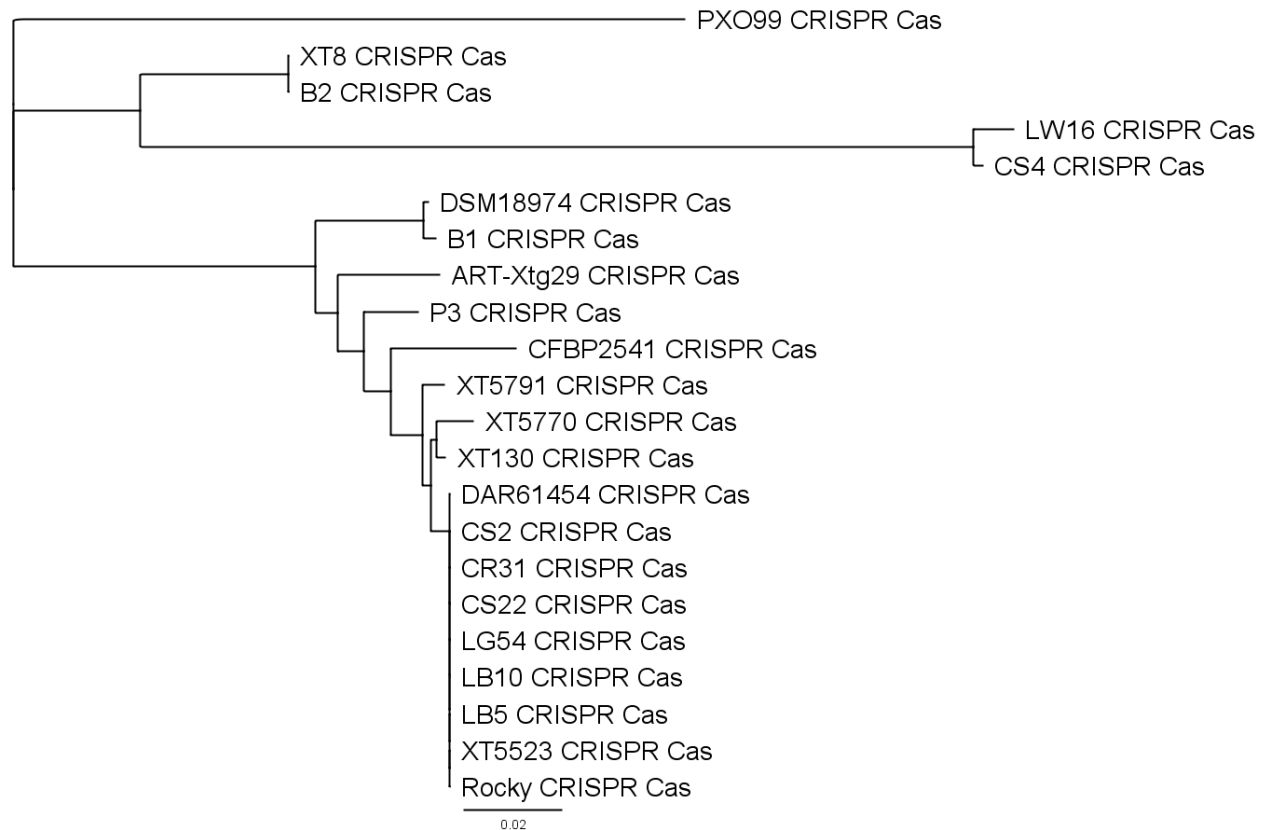


Figure S4. Phylogenetic tree based on CRISPR *Cas* loci of *X. translucens* strains. The sequence of CRISPR *Cas* genes is annotated in RAST website <http://rast.nmpdr.org>. The phylogenetic tree was generated using Geneious software Version 6 with the Tamura-Nei genetic distance model and the Neighbor-joining method, with PXO99 CRISPR *Cas* genes as outgroup. The scale bar indicates number of nucleotide substitutions per site.