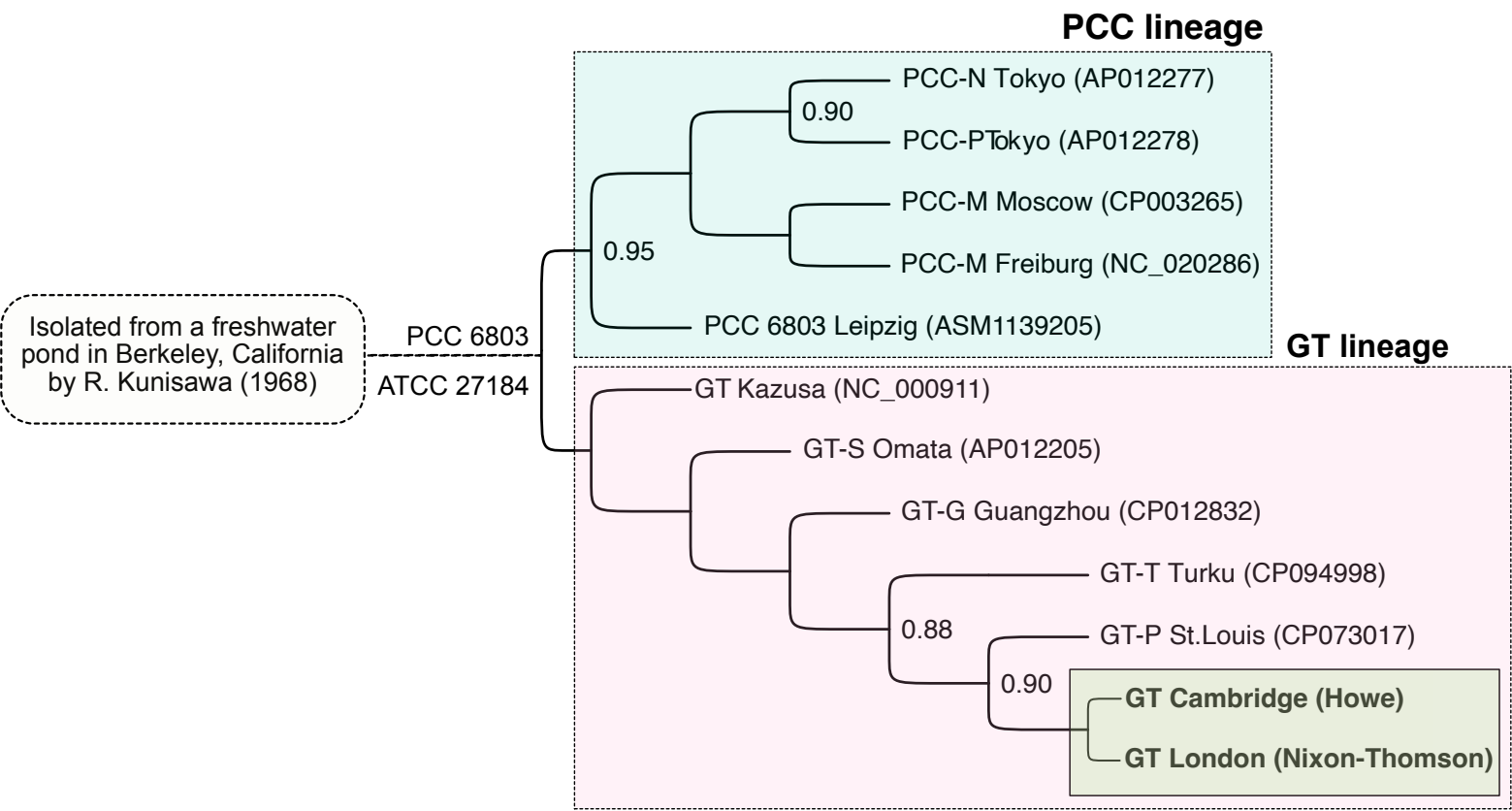
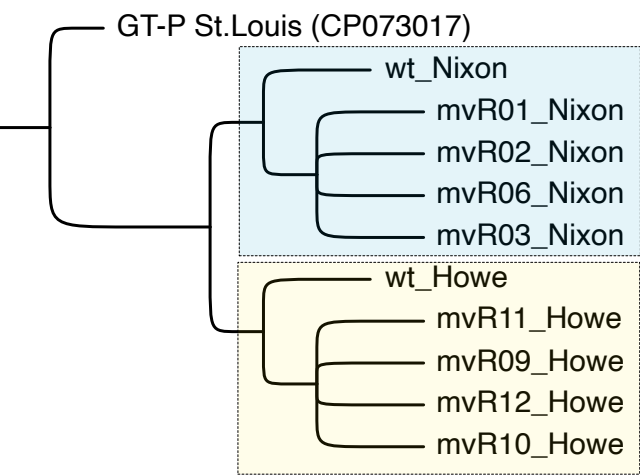


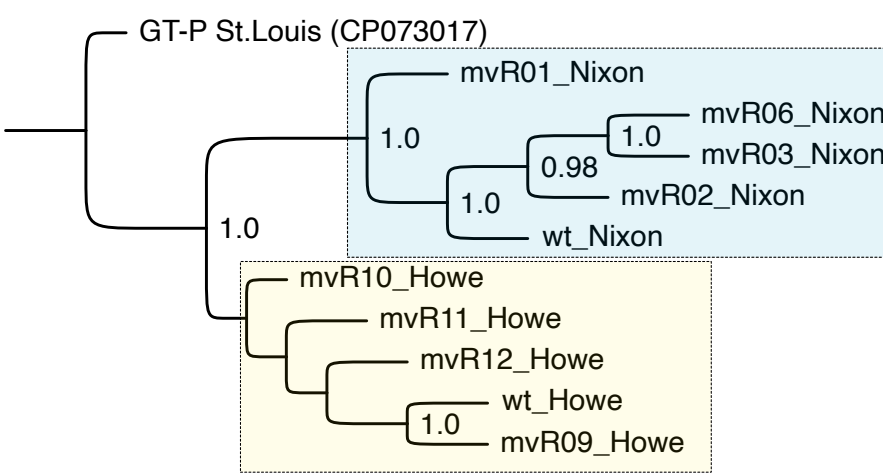
A) Maximum parsimony tree inferred from alignment of whole genome sequences (midpoint rooted)



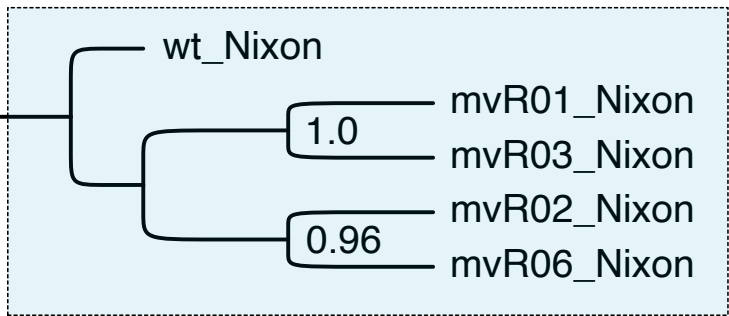
B) "Fake" tree showing the evolutionary history of the strains generated by adaptive laboratory evolution



C) Maximum parsimony tree inferred from alignment of whole genome sequences (GT-P St.Louis as outgroup)



D) Maximum parsimony tree inferred from whole genome sequences of *Synechocystis* "Nixon" substrains (wt_Nixon as outgroup)



E) Maximum parsimony tree inferred from whole genome sequences of *Synechocystis* "Howe" substrains (wt_Howe as outgroup)

