

Figure 1 - Supplement 2. Phylogenetic tree based on maximum liklihood genomic distance among *E. coli* str. ECOR2 (*Ochman and Selander*, 1984), the strain used in the HIO colonization experiments, closely related *E. coli* isolates available on the PATRIC (*Wattam et al., 2017*) database, and pathogenic type strains from the genera *Esherichia*, *Shigella*, and *Salmonella*. A PATRIC genome reference number follows name of each taxa.

References

Ochman H, Selander RK. Standard reference strains of Escherichia coli from natural populations. J Bacteriol. 1984 Feb; 157(2):690–3.

Wattam AR, Davis JJ, Assaf R, Boisvert S, Brettin T, Bun C, Conrad N, Dietrich EM, Disz T, Gabbard JL, Gerdes S, Henry CS, Kenyon RW, Machi D, Mao C, Nordberg EK, Olsen GJ, Murphy-Olson DE, Olson R, Overbeek R, et al. Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. Nucleic Acids Res. 2017 Jan; 45(D1):D535–D542. doi: 10.1093/nar/gkw1017.