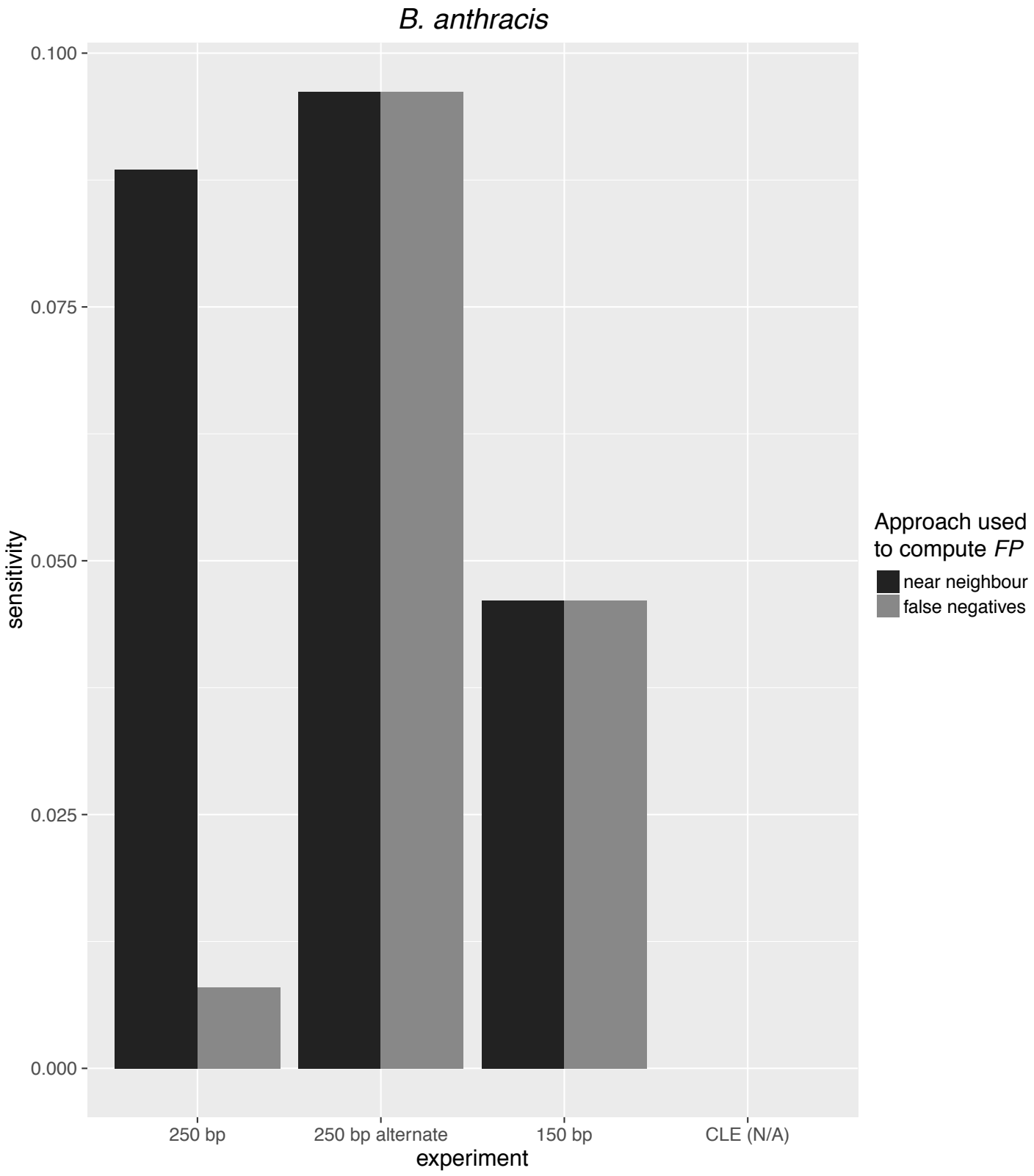
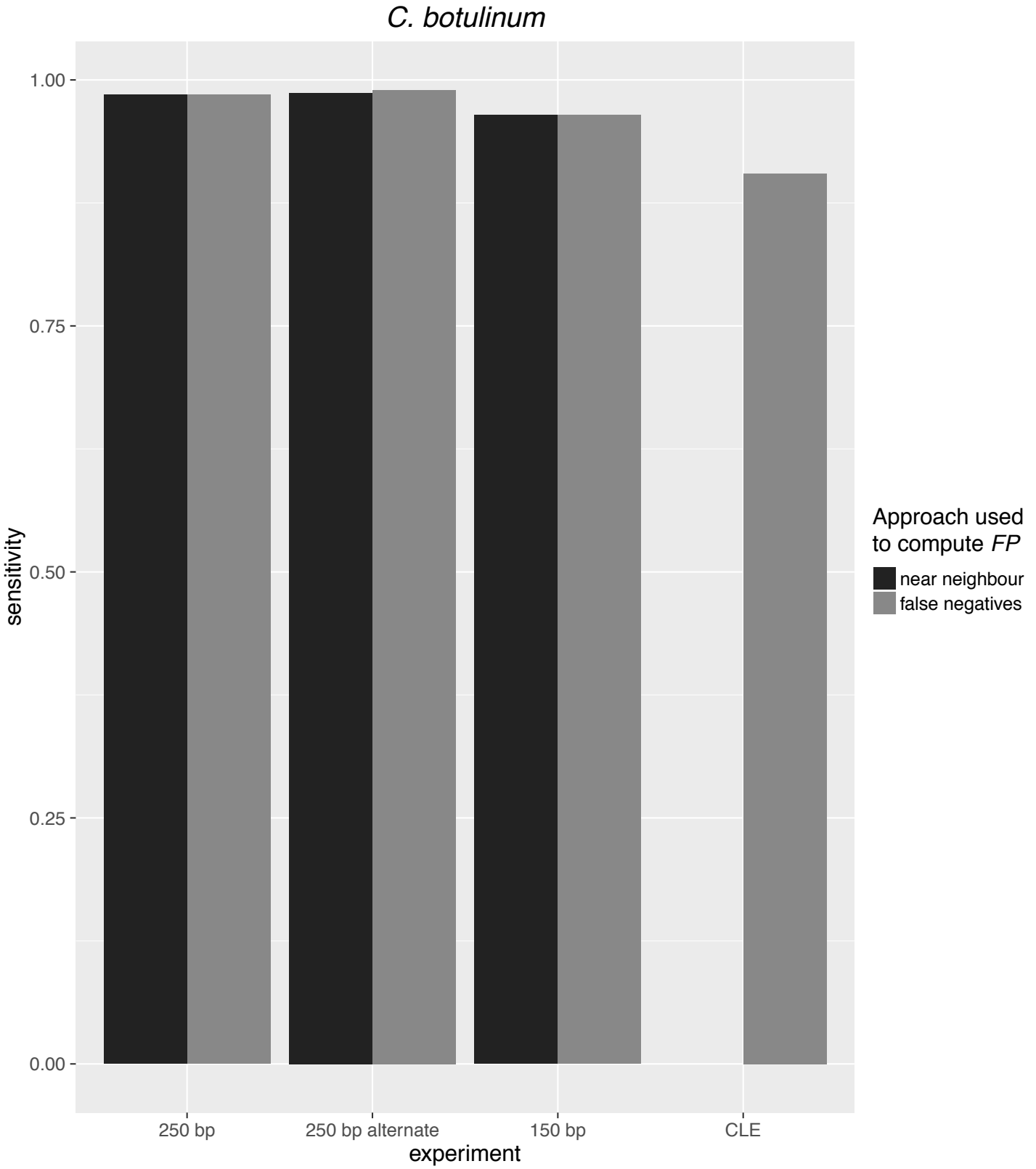
BLAST-based validation of metagenomic sequence assignments

Adam L. Bazinet, Brian D. Ondov, Daniel D. Sommer, and Shashikala Ratnayake

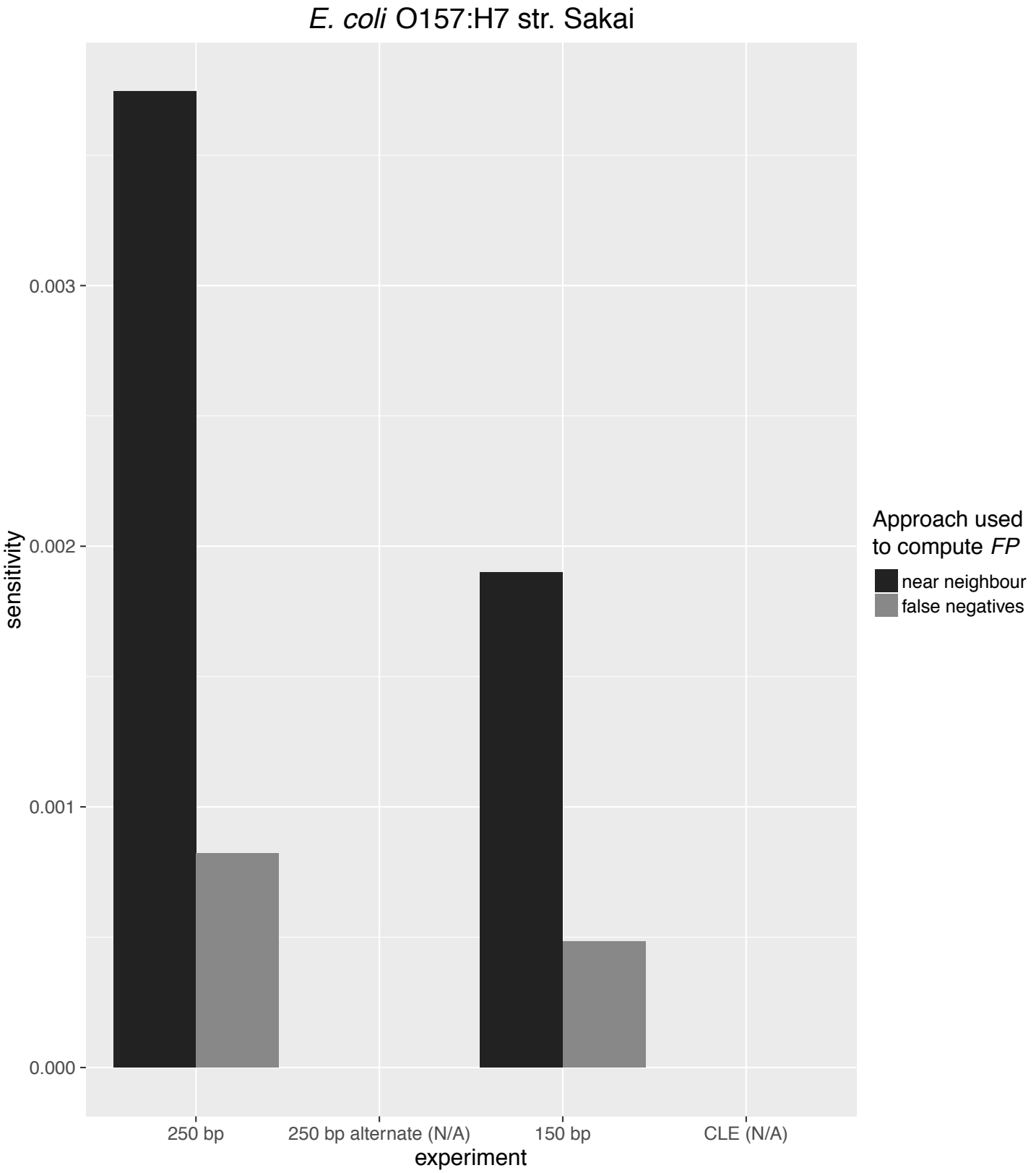
Supplementary Information



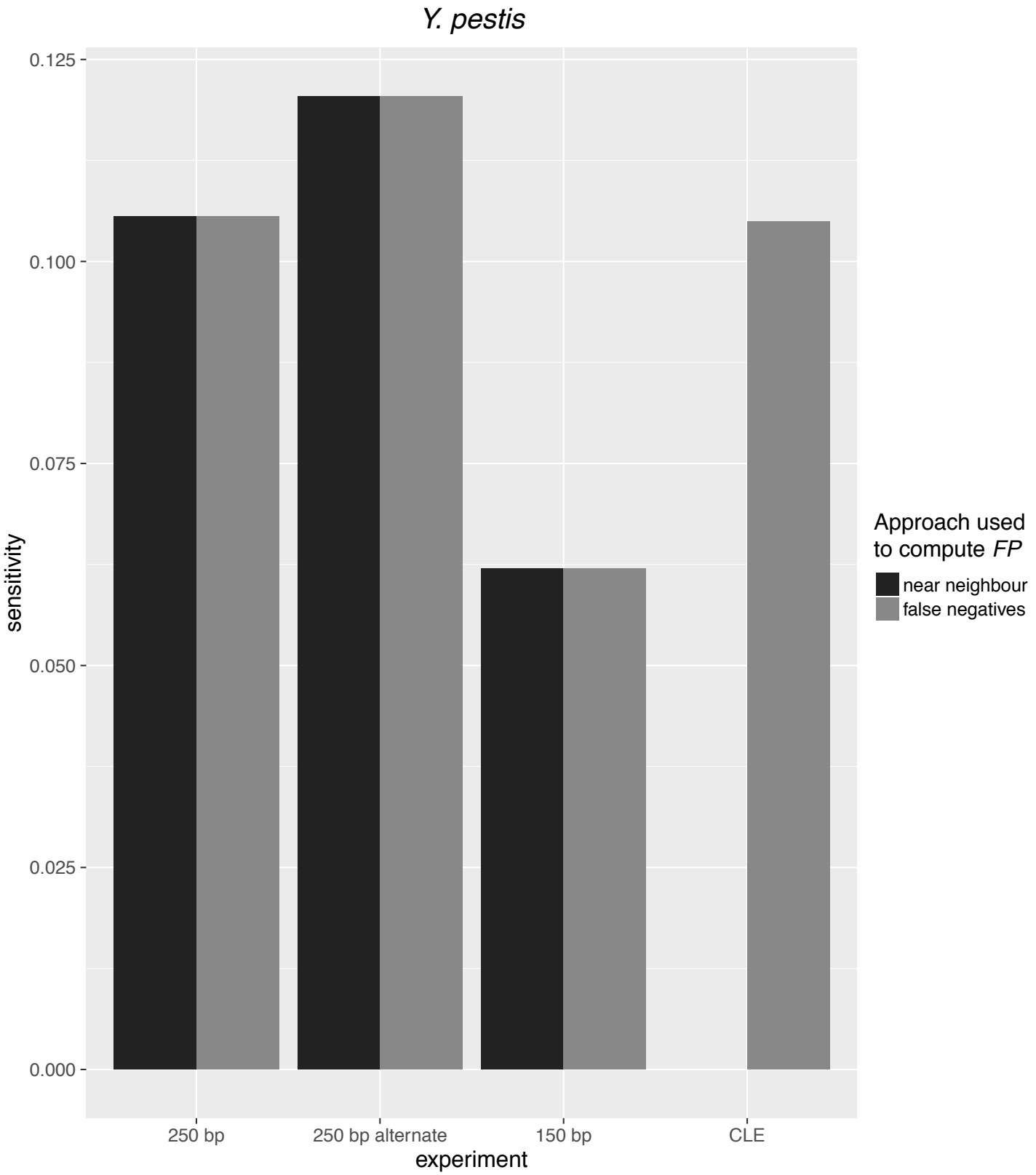
Supplementary Figure S1. Sensitivity for detection of *B. anthracis* is plotted across four experiments: 250-bp simulated reads, 250-bp simulated reads using an alternate representative genome, 150-bp simulated reads, and clade-level exclusion (CLE). The two approaches used to compute false positives, "near neighbour" and "false negatives", are also compared.



Supplementary Figure S2. Sensitivity for detection of *C. botulinum* is plotted across four experiments: 250-bp simulated reads, 250-bp simulated reads using an alternate representative genome, 150-bp simulated reads, and clade-level exclusion (CLE). The two approaches used to compute false positives, "near neighbour" and "false negatives", are also compared.



Supplementary Figure S3. Sensitivity for detection of *E. coli* O157:H7 str. Sakai is plotted across four experiments: 250-bp simulated reads, 250-bp simulated reads using an alternate representative genome, 150-bp simulated reads, and clade-level exclusion (CLE). The two approaches used to compute false positives, "near neighbour" and "false negatives", are also compared.



Supplementary Figure S4. Sensitivity for detection of *Y. pestis* is plotted across four experiments: 250-bp simulated reads, 250-bp simulated reads using an alternate representative genome, 150-bp simulated reads, and clade-level exclusion (CLE). The two approaches used to compute false positives, "near neighbour" and "false negatives", are also compared.