

Supplementary Table 1: Parameter values used for the *E. coli* study.

Method	Parameter Settings
PathoScope 2.0	PathoLib: -taxonIds 562 --subTax PathoMap: -targetAlignParams "--very-sensitive-local -k 500 --score-min L,205,0.0" PathoID: default settings PathoReport: --contig
PathoScope 1.0	default settings
ReadScan	index: -k 13 -s 6 smalt: -d -1 -y 0.94 -n 2 -f samsoft
RINS	bowtie_mismatch = 3 paired_fragment_length = 350 min_contig_length = 300 trinity_threads = 10 blastn_evalue_thrd = 0.05 similarity_thrd = 0.8 iteration = 2 raw_read_length = 150 chop_read_length = 25 minIdentity = 80 compress_ratio_thrd = 0.5