

Figure 1: $ii = \frac{\frac{insertioncites(gene)}{length(gene)}}{\frac{length(genome)}{length(genome)}}$ Method: gammamixEM

trimming: 5 prime site: 5%, 3 prime site: 10% plot manipulations: Added 0.001 to all numbers

Number of essential genes: Klebsiella pneumoniae Ecl8: 287 Escherichia coli ETEC CS17: 622

Enterobacter: 344

Klebsiella pneumoniae RH201207: 5579 Escherichia coli ETEC H10407: 460

Escherichia coli UPEC: 365

Citrobacter: 339

Salmonella enteritidis: 380

Salmonella typhimurium SL1344: 428 Salmonella typhimurium D23580: 366 Salmonella typhimurium A130: 413 Salmonella typhi: 568

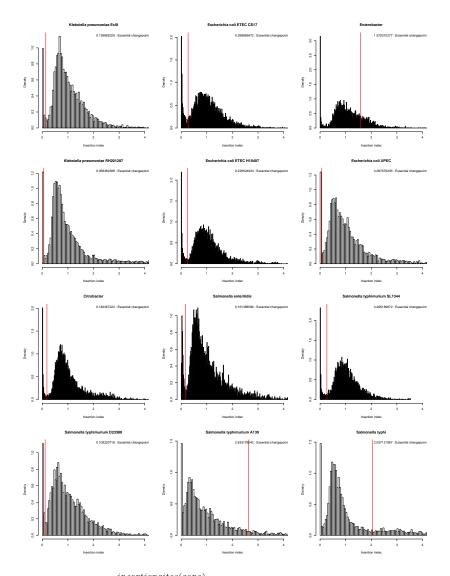


Figure 2: $ii = \frac{\frac{insertioncites(gene)}{length(gene)}}{\frac{length(genome)}{length(genome)}}$ Method: gammamixEM

trimming: 5 prime site: 5%, 3 prime site: 10%

plot manipulations: Removed the tail after visiting the first bin with fre-

quency less than 10, added 0.001 to all numbers

Number of essential genes: Klebsiella pneumoniae Ecl8: 310 Escherichia coli ETEC CS17: 569

Enterobacter: 2961

Klebsiella pneumoniae RH201207: 350 Escherichia coli ETEC H10407: 433

Escherichia coli UPEC: 307

Citrobacter: 330

Salmonella enteritidis: 303

Salmonella typhimurium SL1344: 411 Salmonella typhimurium D23580: 316 Salmonella typhimurium A130: 4094 2

Salmonella typhi: 3697

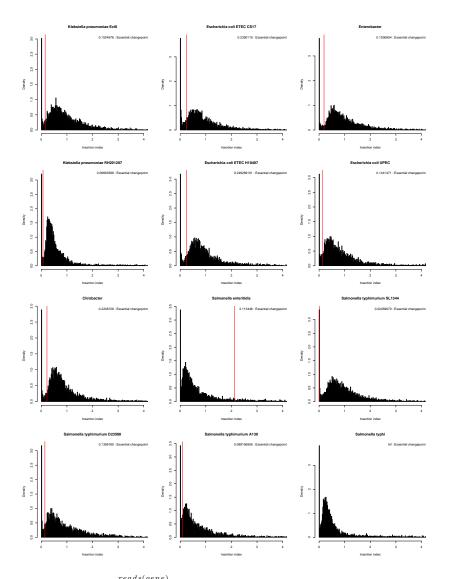


Figure 3: $ii = \frac{\frac{reads(gene)}{length(gene)}}{\frac{reads(genome)}{length(genome)}}$ Method: gammamixEM

trimming: 5 prime site: 5%, 3 prime site: 10% **plot manipulations:** Added 0.001 to all numbers

Number of essential genes: Klebsiella pneumoniae Ecl8: 159 Escherichia coli ETEC CS17: 87

Enterobacter: 175

Klebsiella pneumoniae RH201207: 252 Escherichia coli ETEC H10407: 569

Escherichia coli UPEC: 194

Citrobacter: 145

Salmonella enteritidis: 1297

Salmonella typhimurium SL1344: 103 Salmonella typhimurium D23580: 65 Salmonella typhimurium A130: 522 Salmonella typhi: 4321

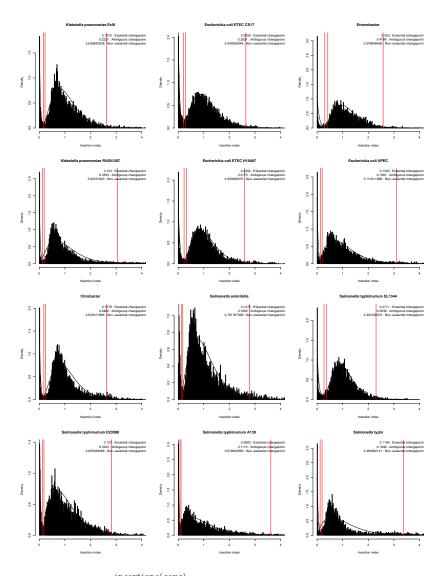


Figure 4: $ii = \frac{\frac{insertions(gene)}{length(gene)}}{\frac{insertions(genome)}{length(genome)}}$

Method: Lars' method

trimming: 5 prime site: 5%, 3 prime site: 10%

plot manipulations: Lars' manipulations Number of essential genes:

Klebsiella pneumoniae Ecl8: 322 Escherichia coli ETEC CS17: 528

Enterobacter: 351

Klebsiella pneumoniae RH201207: 387 Escherichia coli ETEC H10407: 429

Escherichia coli UPEC: 354

Citrobacter: 330

Salmonella enteritidis: 285

Salmonella typhimurium SL1344: 416 Salmonella typhimurium D23580: 333 Salmonella typhimurium A130: 357

Salmonella typhi: 361

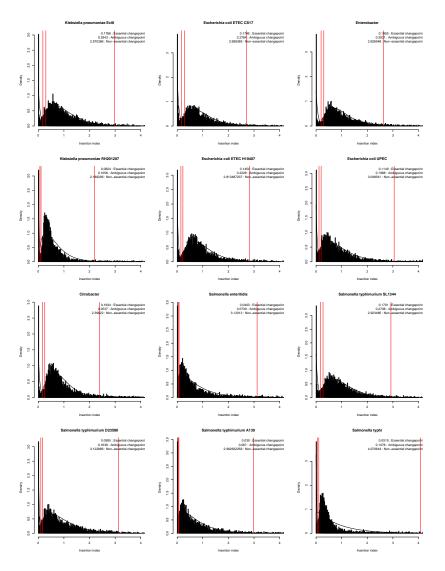


Figure 5: $ii = \frac{\frac{reads(gene)}{length(gene)}}{\frac{reads(genome)}{length(genome)}}$

Method: Lars' method

trimming: 5 prime site: 5%, 3 prime site: 10%

plot manipulations: Lars' manipulations Number of essential genes:

Klebsiella pneumoniae Ecl8: 322 Escherichia coli ETEC CS17: 528

Enterobacter: 351

Klebsiella pneumoniae RH201207: 387 Escherichia coli ETEC H10407: 429

Escherichia coli UPEC: 354

Citrobacter: 330

Salmonella enteritidis: 285

Salmonella typhimurium SL1344: 416 Salmonella typhimurium D23580: 333 Salmonella typhimurium A130: 357

Salmonella typhi: 361