Figure 1: $ii = \dfrac{\frac{insertions(gene)}{length(gene)}}{\frac{insertions(genome)}{length(genome)}}$

Method: gammamixEM

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

plot manipulations: Added 0.001 to all numbers, used Lars' shape and rate parameters

Number of essential genes:

Klebsiella pneumoniae Ecl8: 333

Escherichia coli ETEC CS17: 563

Enterobacter: 336

Klebsiella pneumoniae RH201207: 329

Escherichia coli ETEC H10407: 410

Escherichia coli UPEC: 314

Citrobacter: 319

Salmonella enteritidis: 202

Salmonella typhimurium SL1344: 423

Salmonella typhimurium D23580: 309

Salmonella typhimurium A130: 226
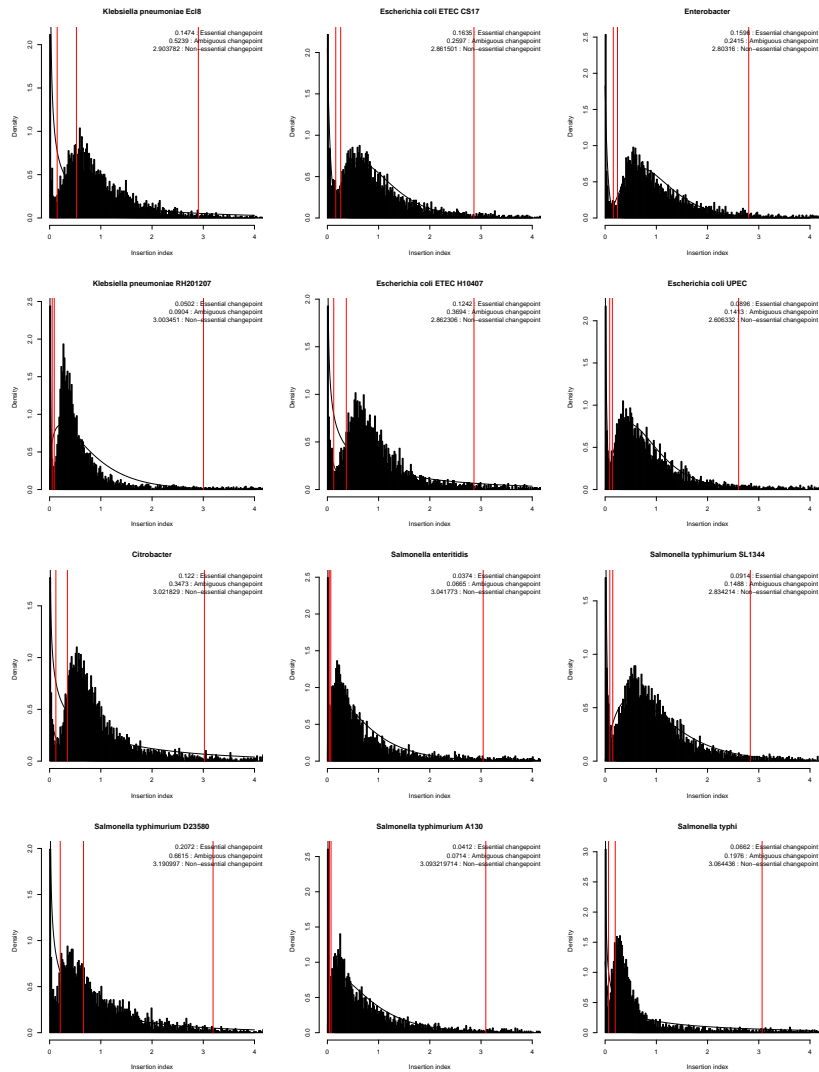
Salmonella typhi: 266

1

Figure 2: $ii = \dfrac{\frac{reads(gene)}{length(gene)}}{\frac{reads(genome)}{length(genome)}}$

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: 407

Escherichia coli ETEC CS17: 549

Enterobacter: 348

Klebsiella pneumoniae RH201207: 366

Escherichia coli ETEC H10407: 403

Escherichia coli UPEC: 369

Citrobacter: 343

Salmonella enteritidis: 269

Salmonella typhimurium SL1344: 353

Salmonella typhimurium D23580: 580

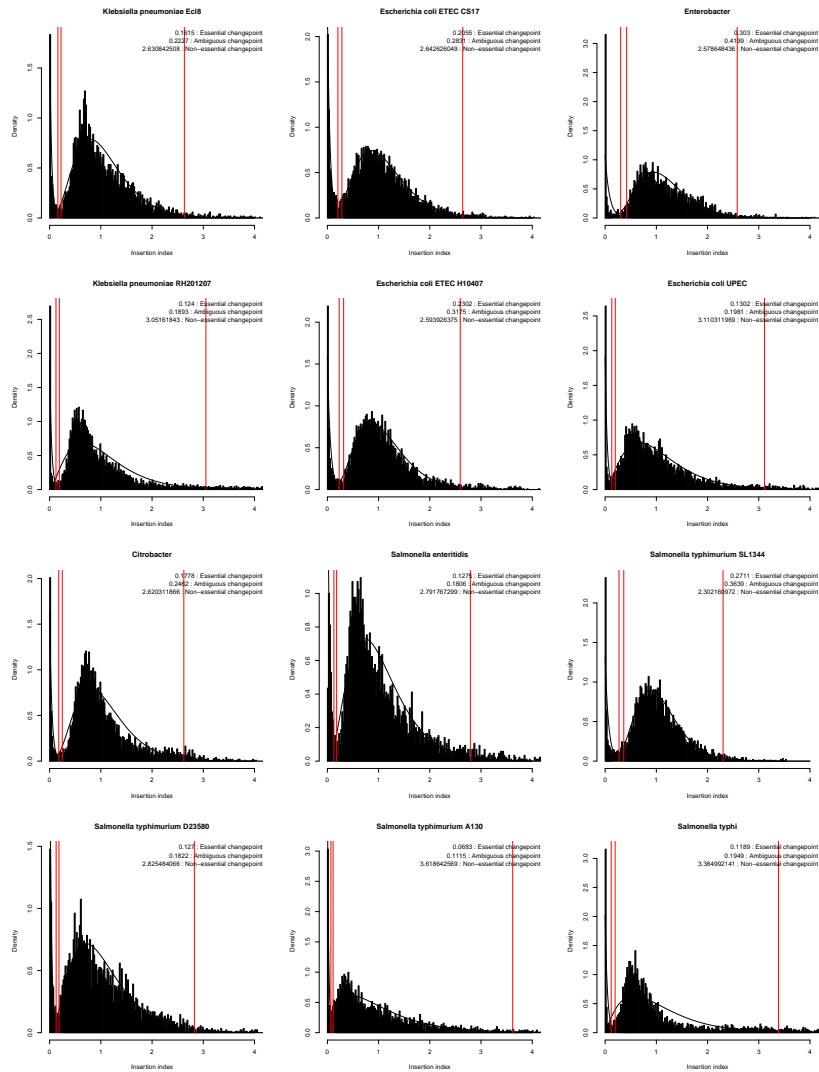Salmonella typhimurium A130: 315

Salmonella typhi: 386

2

Figure 3: $ii = \dfrac{\frac{insertions(gene)}{length(gene)}}{\frac{insertions(genome)}{length(genome)}}$

Method: Lars' method

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

plot manipulations: Lars' manipulations

Number of essential genes:

Klebsiella pneumoniae Ecl8: 299

Escherichia coli ETEC CS17: 493

Enterobacter: 323

Klebsiella pneumoniae RH201207: 346

Escherichia coli ETEC H10407: 417

Escherichia coli UPEC: 323

Citrobacter: 311

Salmonella enteritidis: 248

Salmonella typhimurium SL1344: 405

Salmonella typhimurium D23580: 283
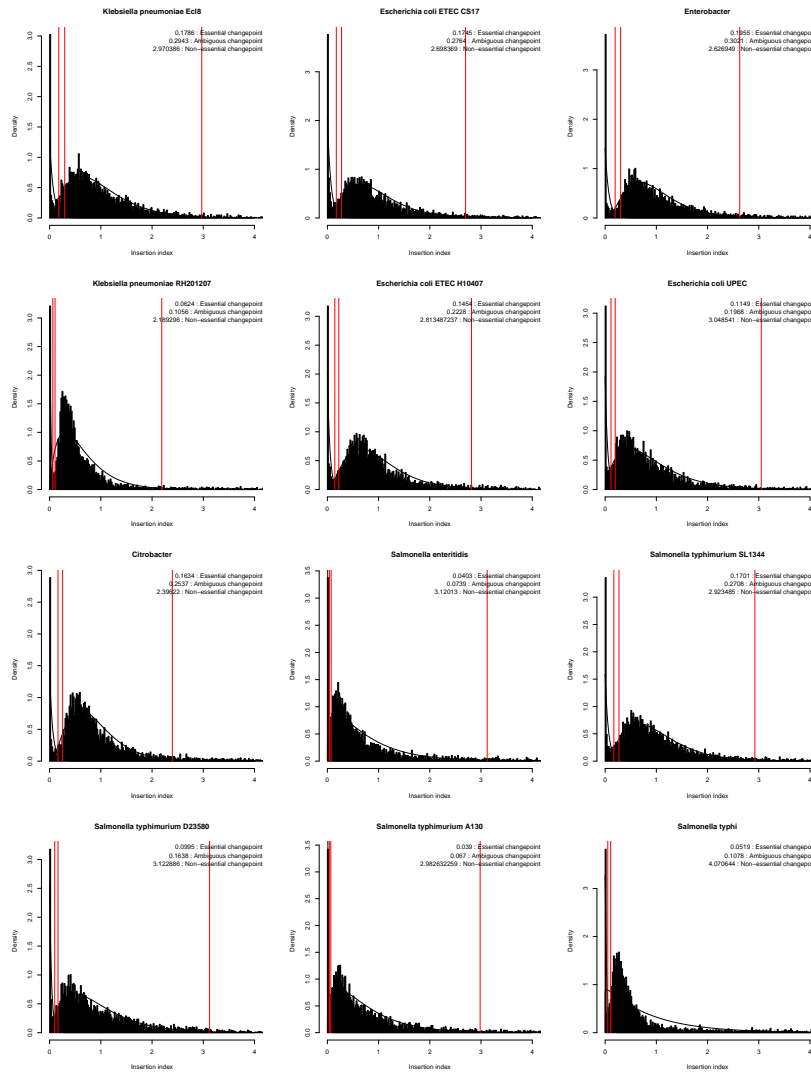
Salmonella typhimurium A130: 292

Salmonella typhi: 331

3

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

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

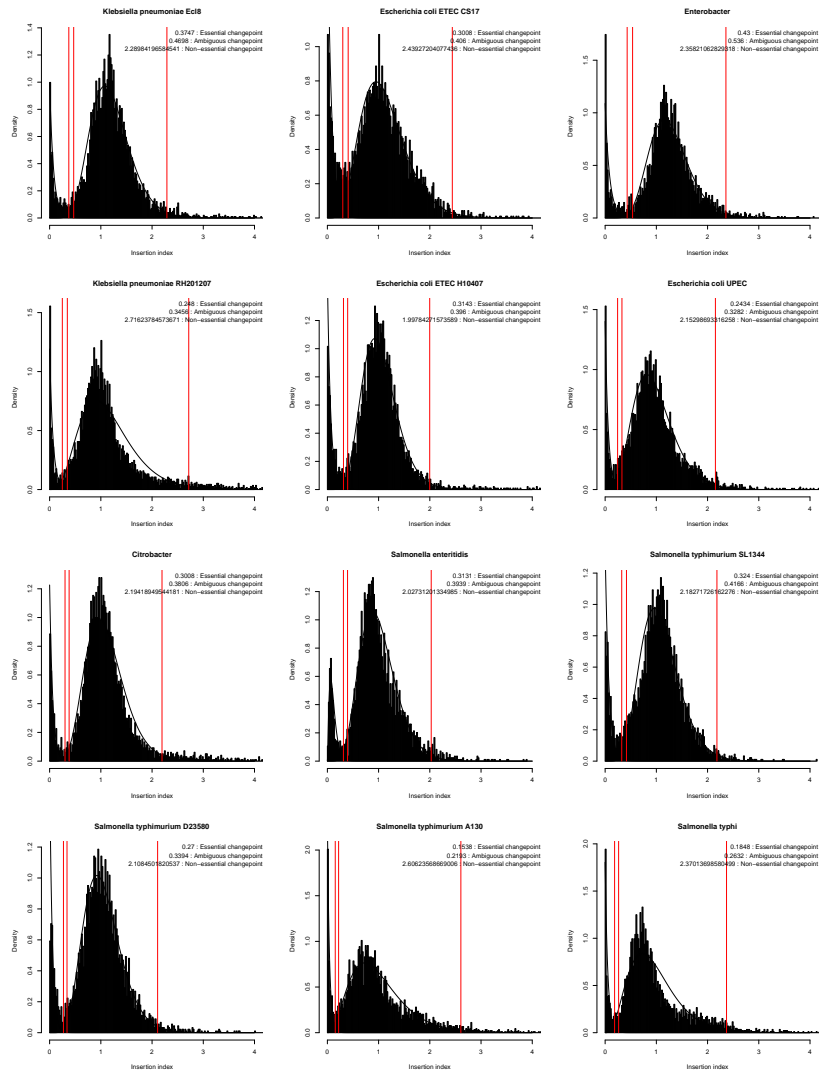Salmonella typhimurium A130: 357

Salmonella typhi: 361

4

Figure 5: $ii = \dfrac{\frac{insertion(gene)}{length(gene)}}{\frac{insertionss(genome)}{length(genome)}}$

Method: Lars' method

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

plot manipulations: Lars' manipulations + normalised ii for GC bias and gene location

Number of essential genes:

Klebsiella pneumoniae Ecl8: 399

Escherichia coli ETEC CS17: 648

Enterobacter: 389

Klebsiella pneumoniae RH201207: 433

Escherichia coli ETEC H10407: 480

Escherichia coli UPEC: 411

Citrobacter: 358

Salmonella enteritidis: 354

Salmonella typhimurium SL1344: 453

Salmonella typhimurium D23580: 384

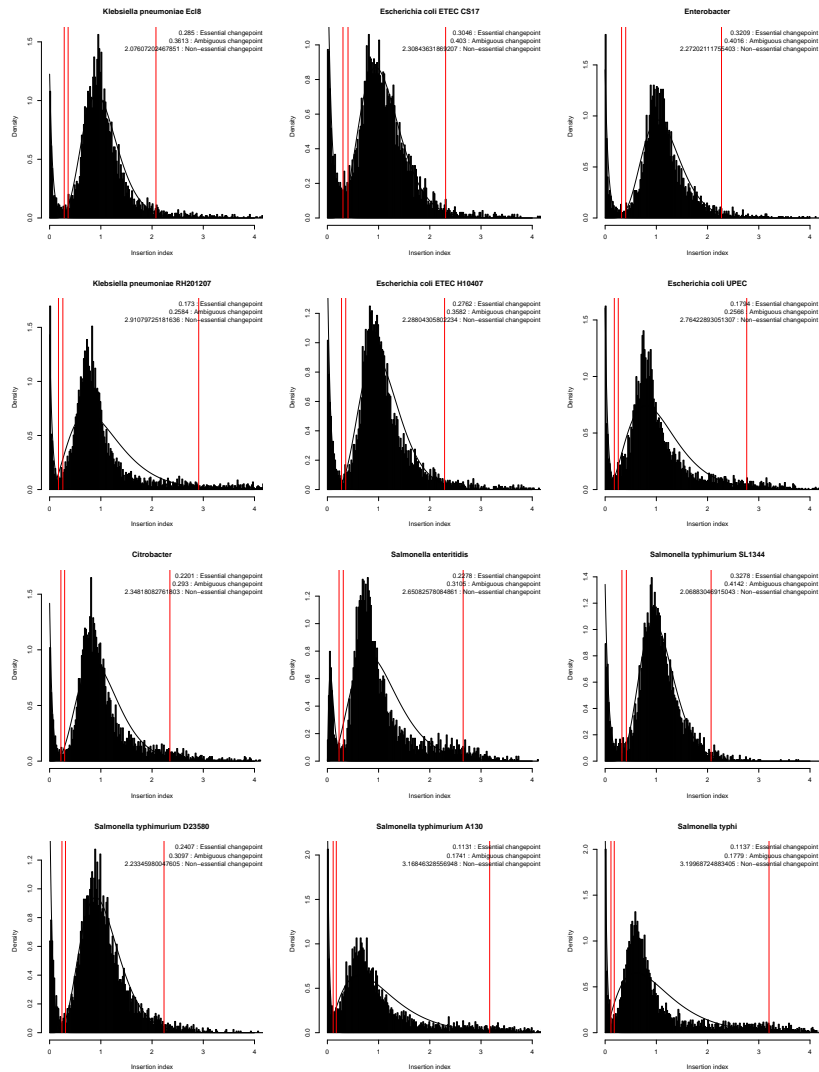Salmonella typhimurium A130: 385

Salmonella typhi: 380

Figure 6: $ii = \dfrac{\frac{insertion(gene)}{length(gene)}}{\frac{insertionss(genome)}{length(genome)}}$

Method: Lars' method

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

plot manipulations: Lars' manipulations + normalised ii for gene location

Number of essential genes:

Klebsiella pneumoniae Ecl8: 351

Escherichia coli ETEC CS17: 555

Enterobacter: 347

Klebsiella pneumoniae RH201207: 400

Escherichia coli ETEC H10407: 432

Escherichia coli UPEC: 353

Citrobacter: 325

Salmonella enteritidis: 317

Salmonella typhimurium SL1344: 427

Salmonella typhimurium D23580: 358

Salmonella typhimurium A130: 354

Salmonella typhi: 334

6