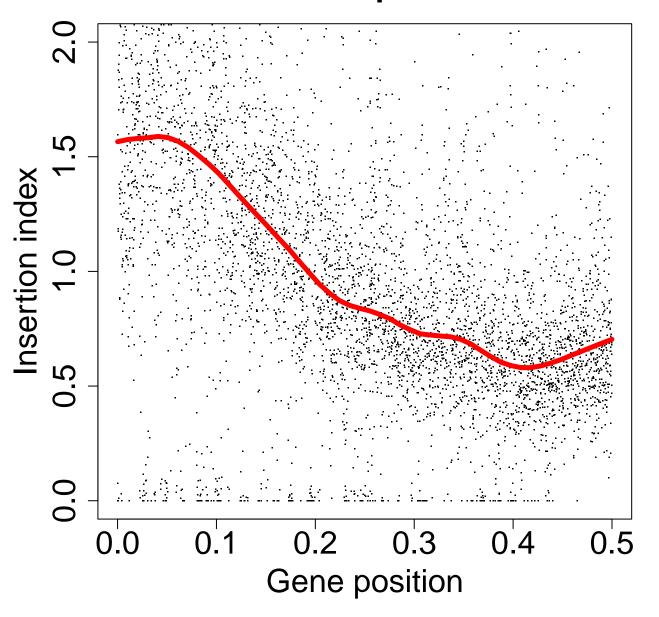
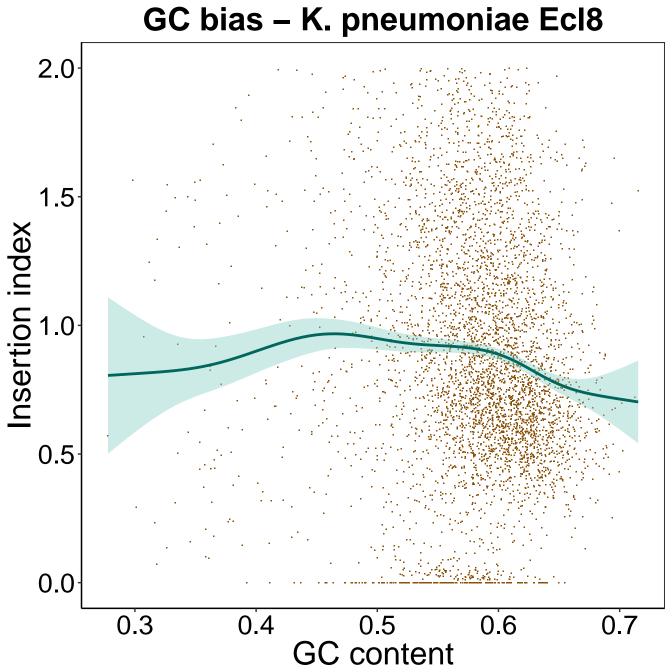
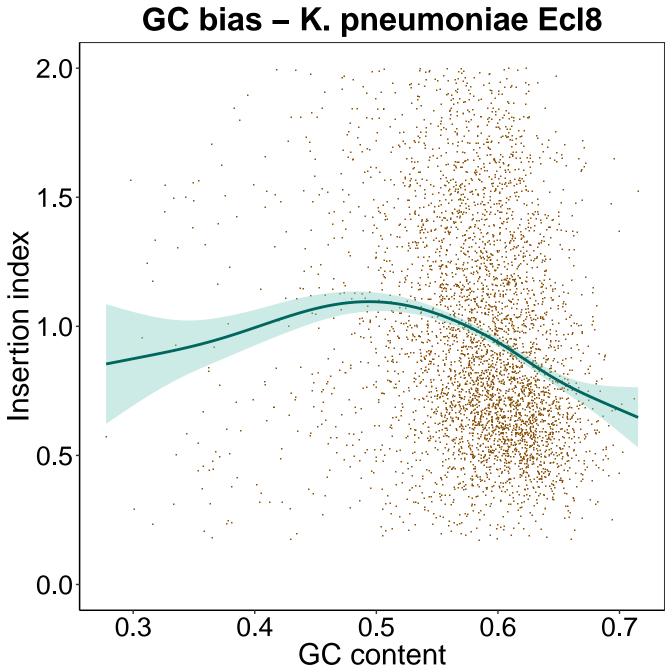


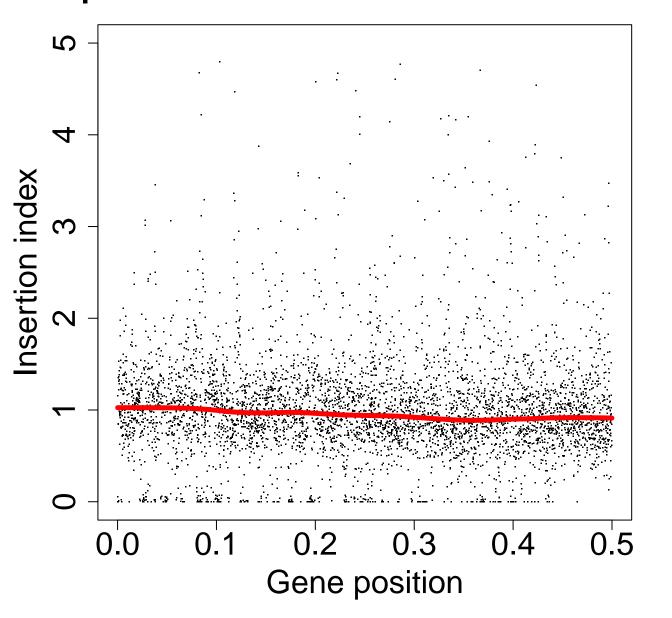
Distance bias - K. pneumoniae Ecl8



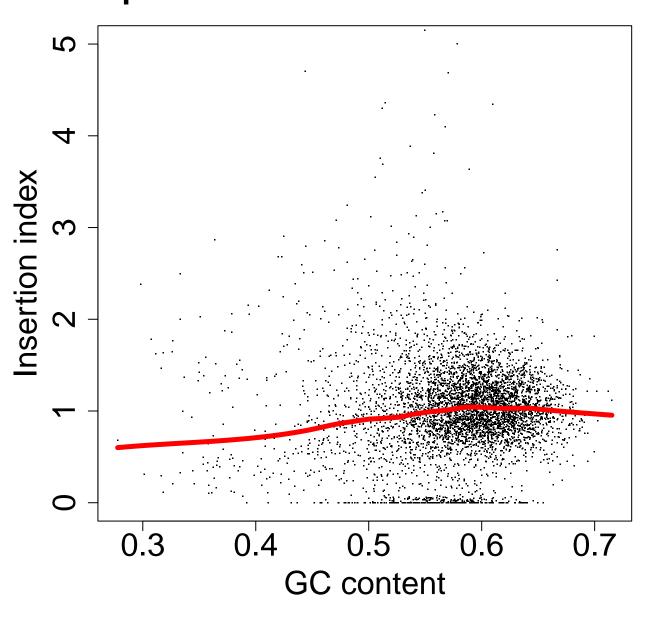


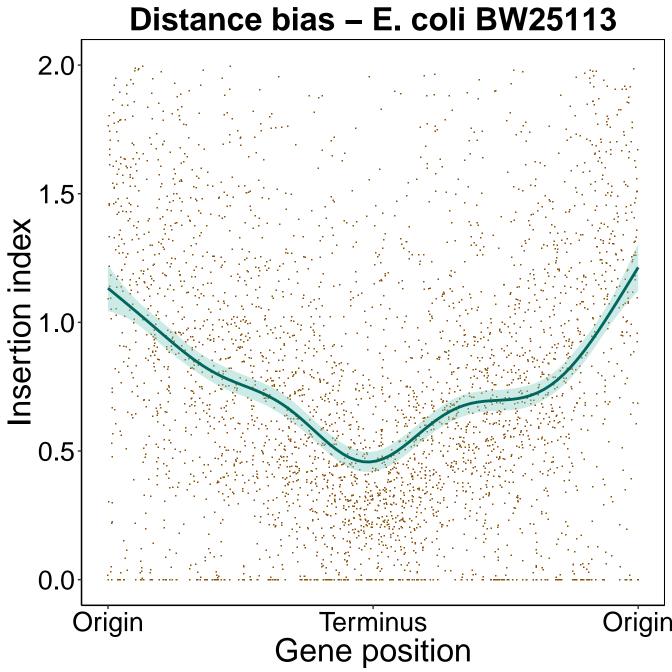


K. pneumoniae Ecl8 - normalised distanc

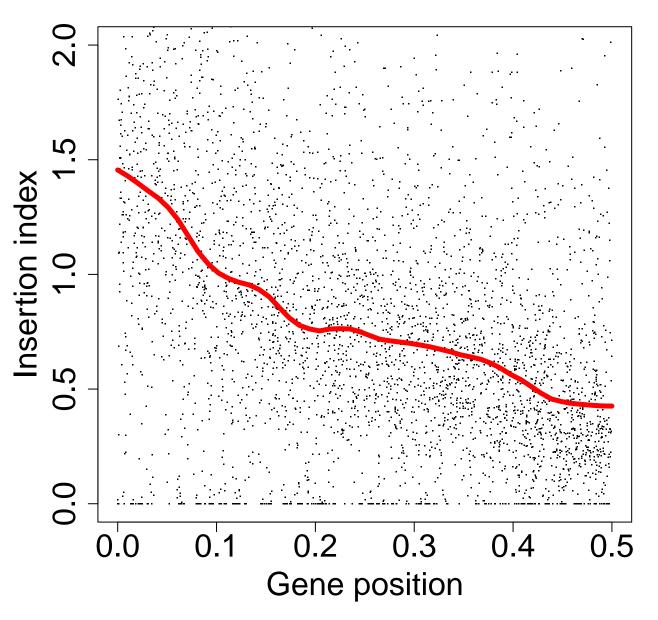


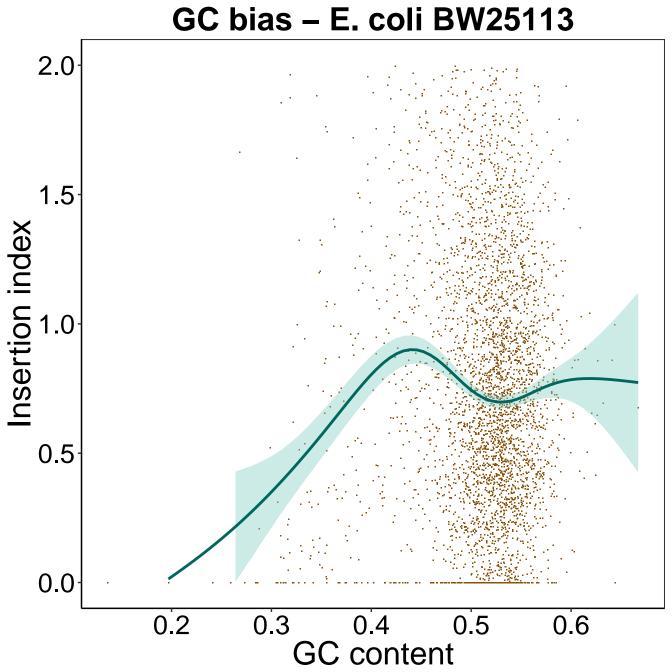
K. pneumoniae Ecl8 - normalised GC

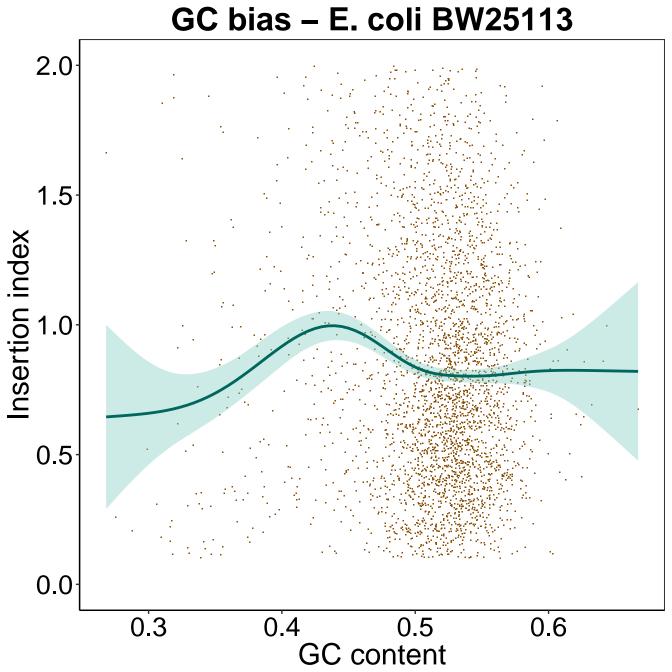




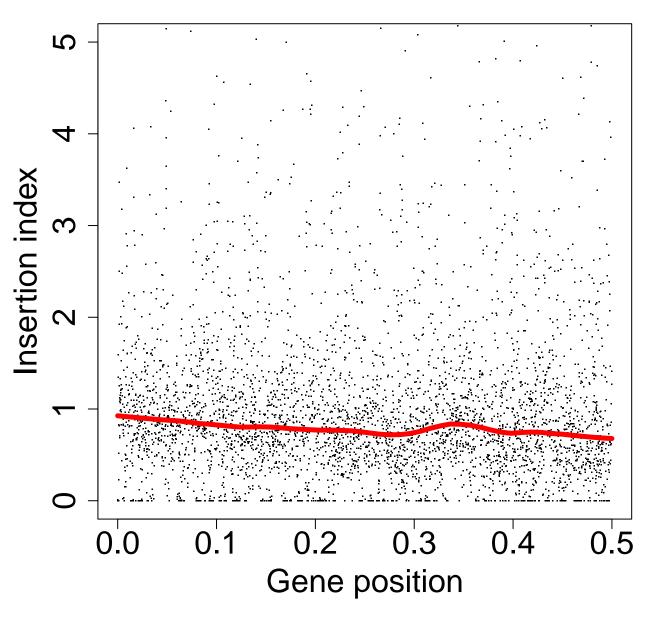
Distance bias - E. coli BW25113



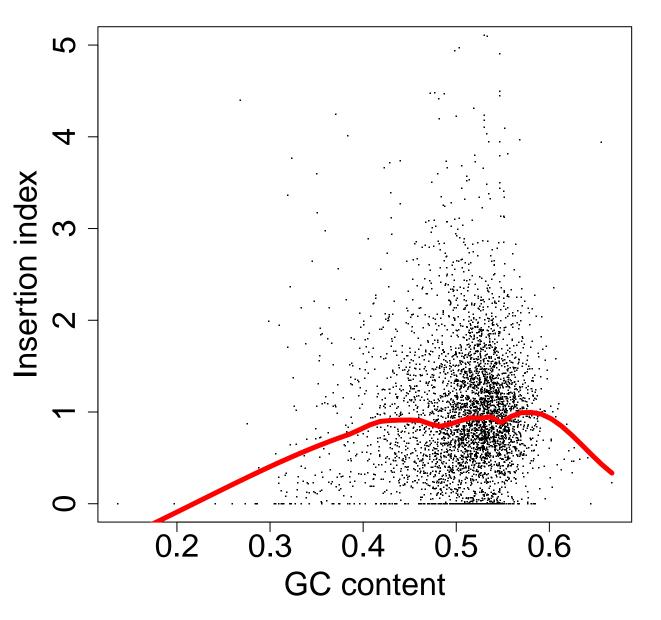


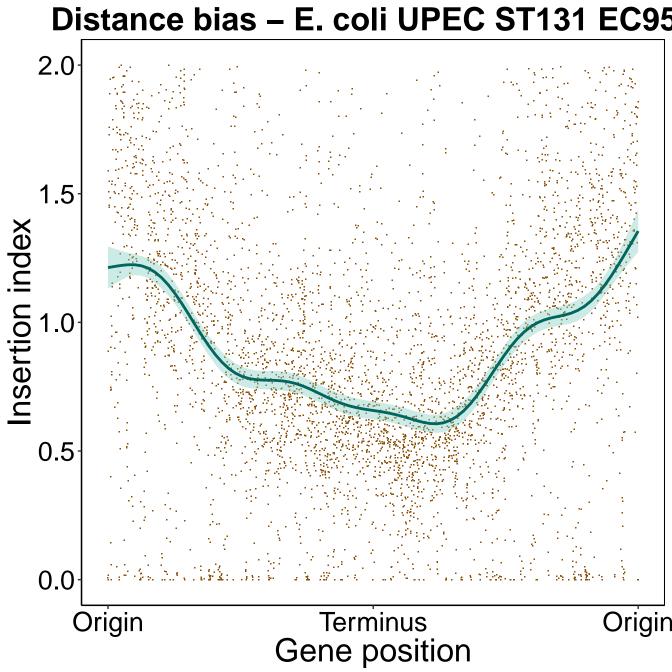


E. coli BW25113 - normalised distance

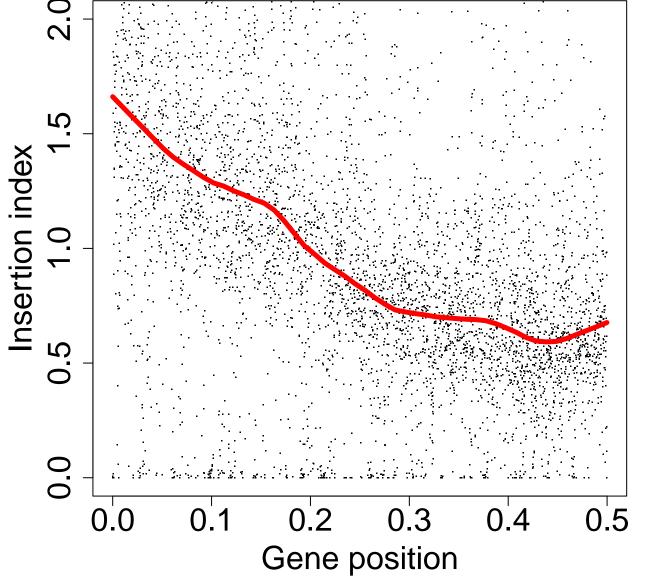


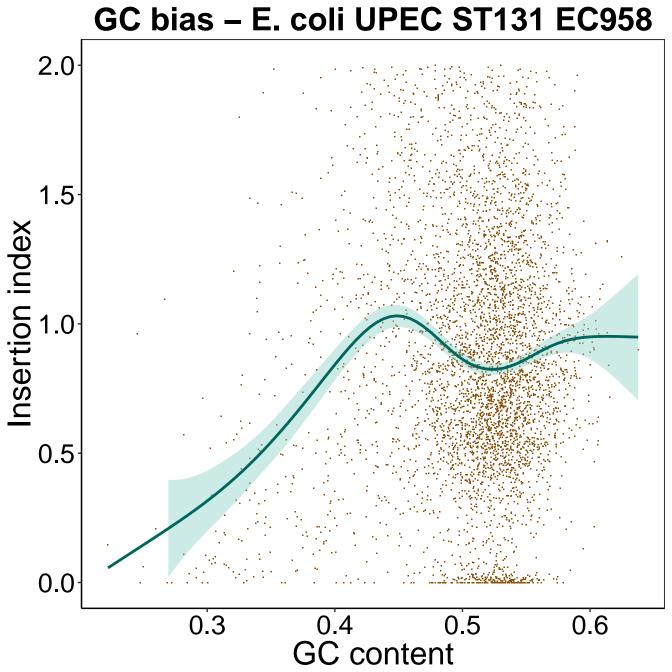
E. coli BW25113 - normalised GC

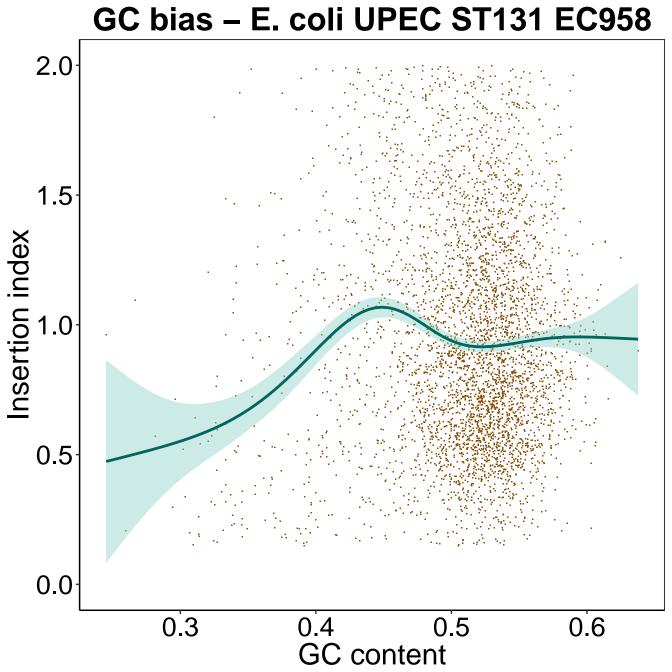




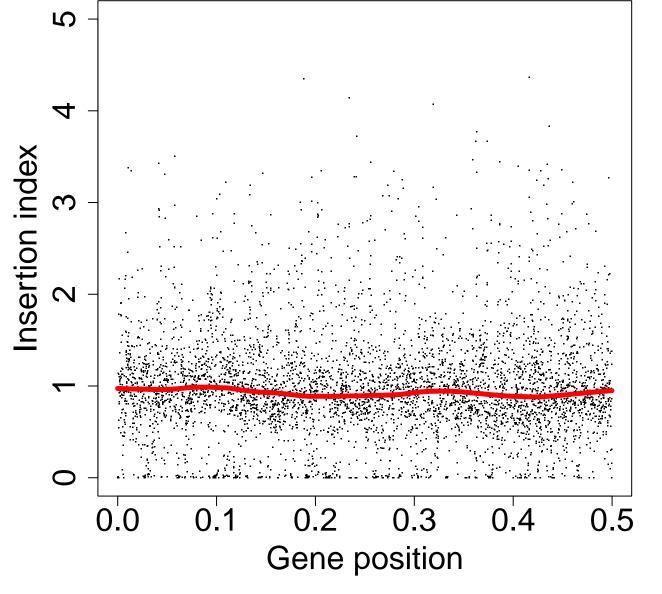
Distance bias – E. coli UPEC ST131 EC95



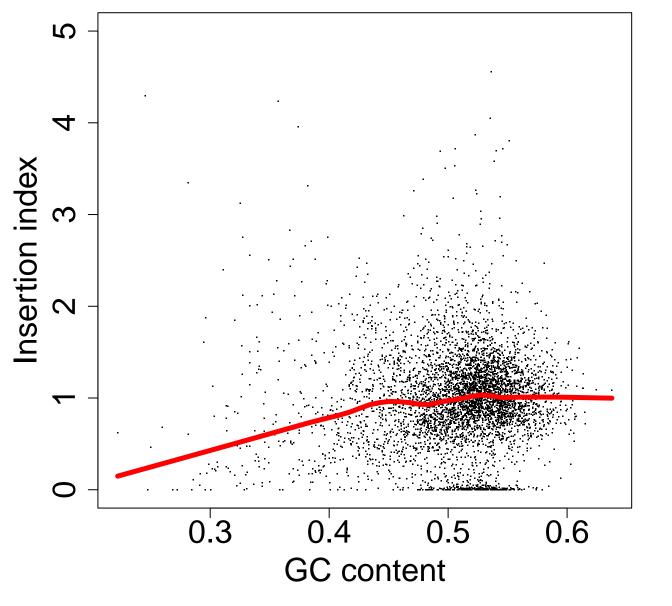


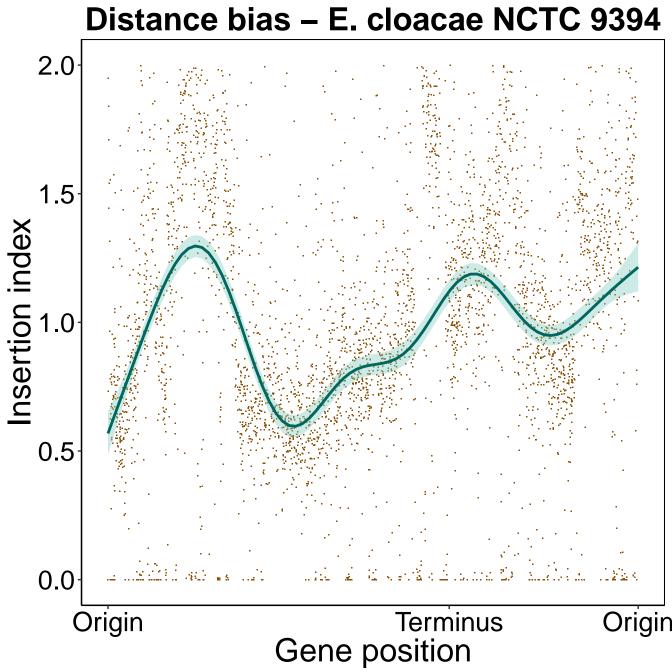


E. coli UPEC ST131 EC958 – normalised dista

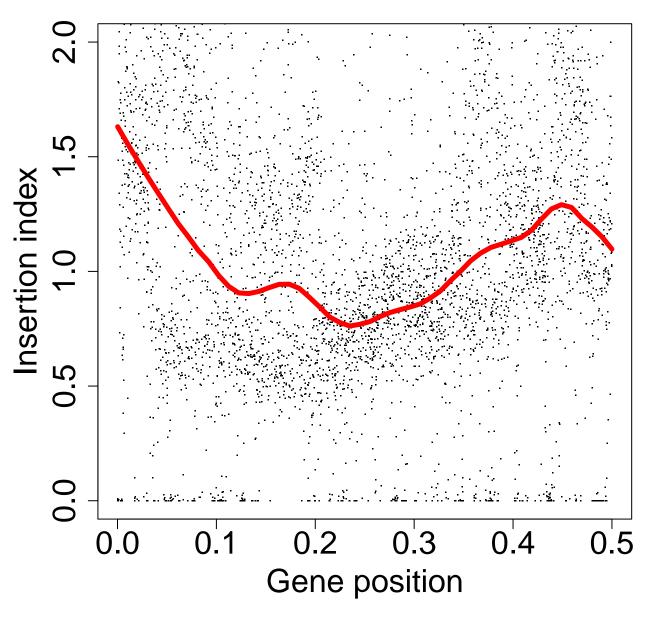


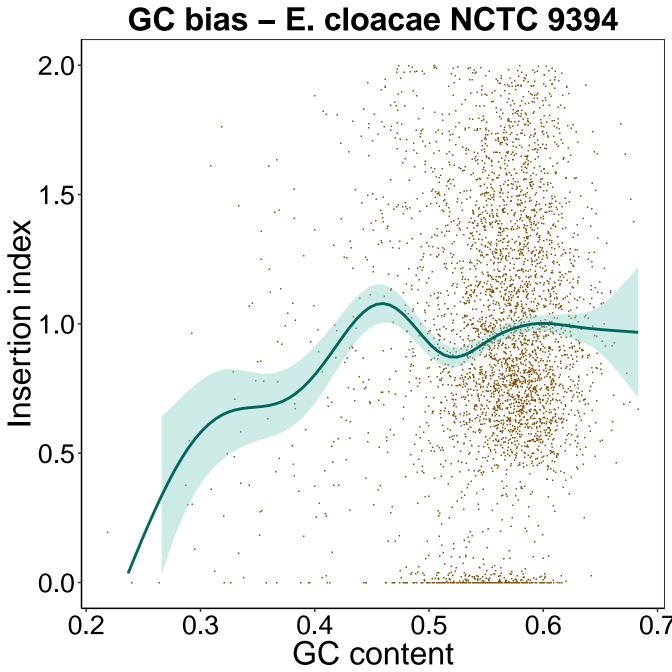
E. coli UPEC ST131 EC958 – normalised G

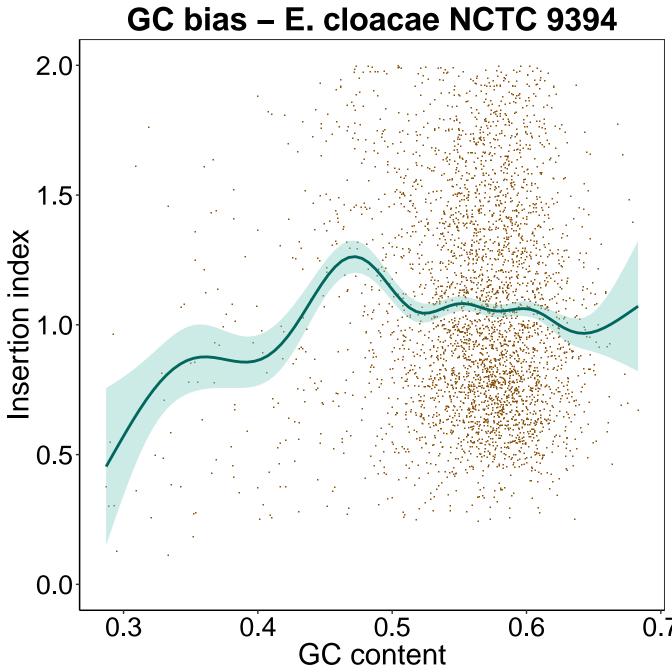




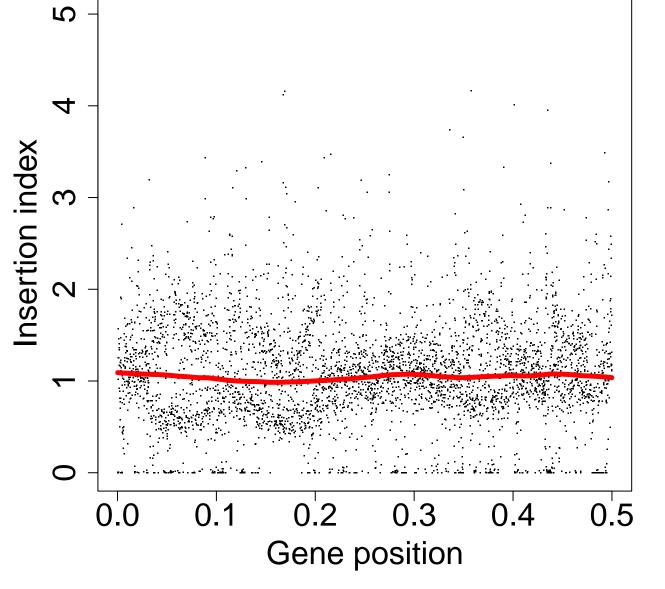
Distance bias - E. cloacae NCTC 9394



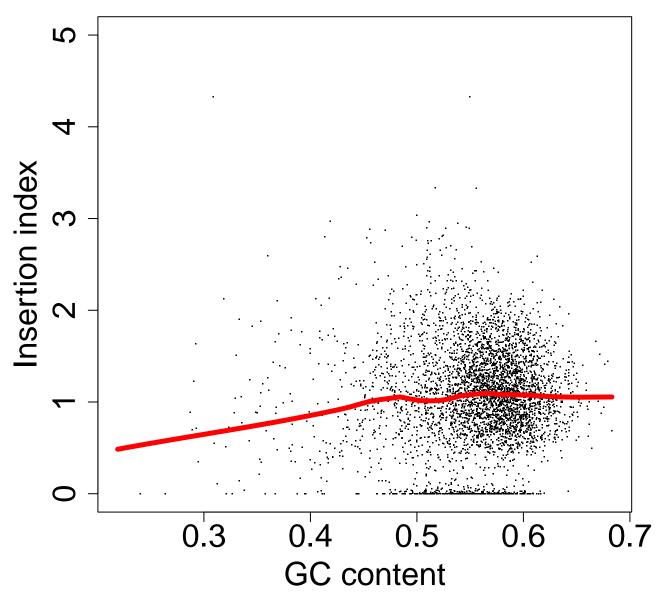




E. cloacae NCTC 9394 – normalised distant

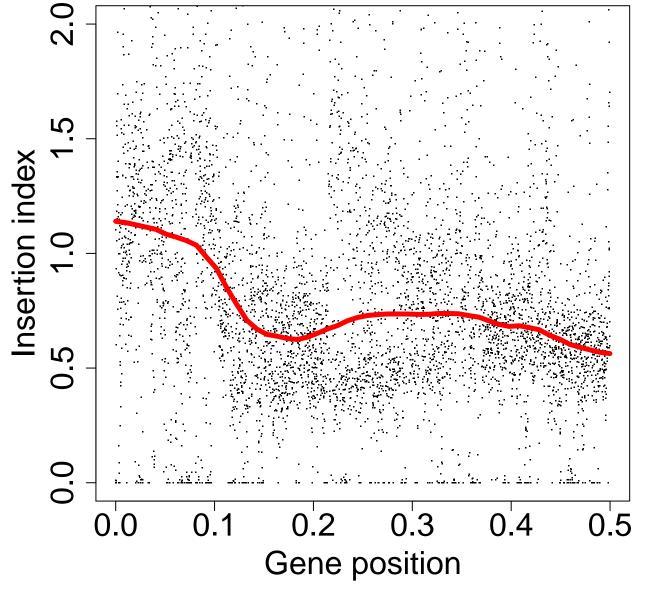


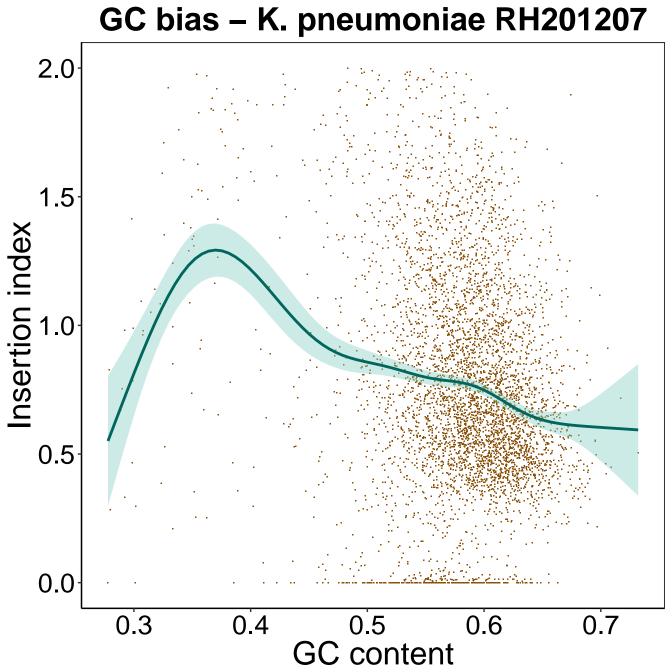
E. cloacae NCTC 9394 – normalised GC



Distance bias - K. pneumoniae RH20120 2.0 1.5 Insertion index 0.5 Origin **Terminus** Origin Gene position

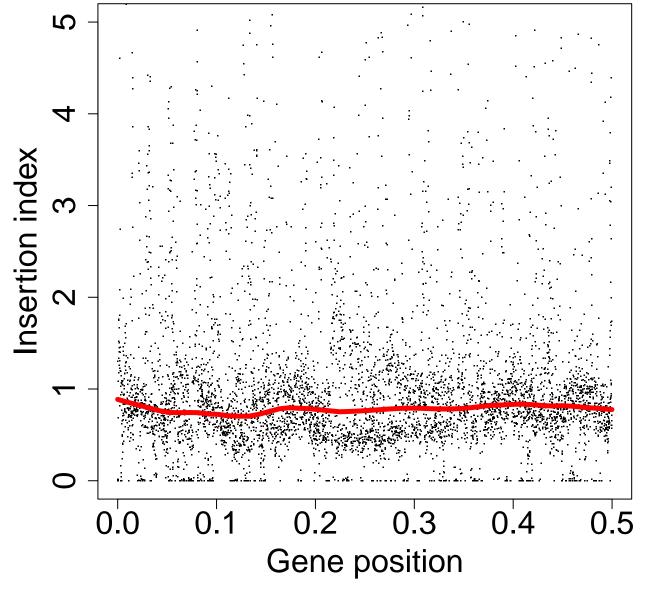
Distance bias – K. pneumoniae RH201207



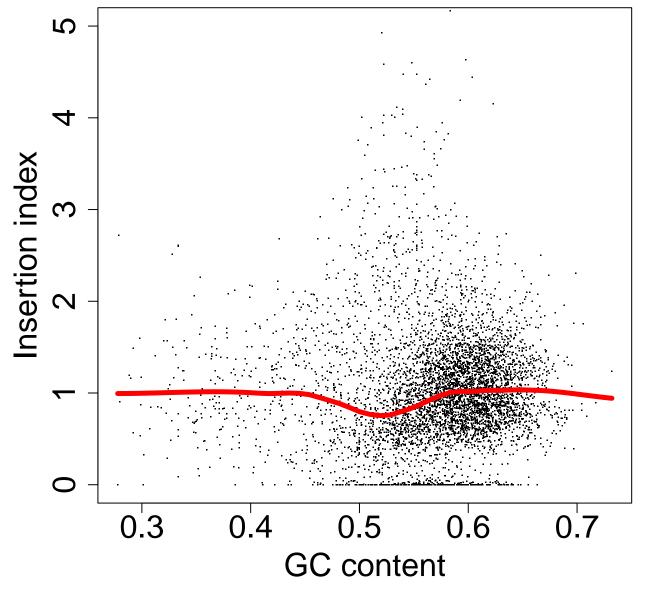


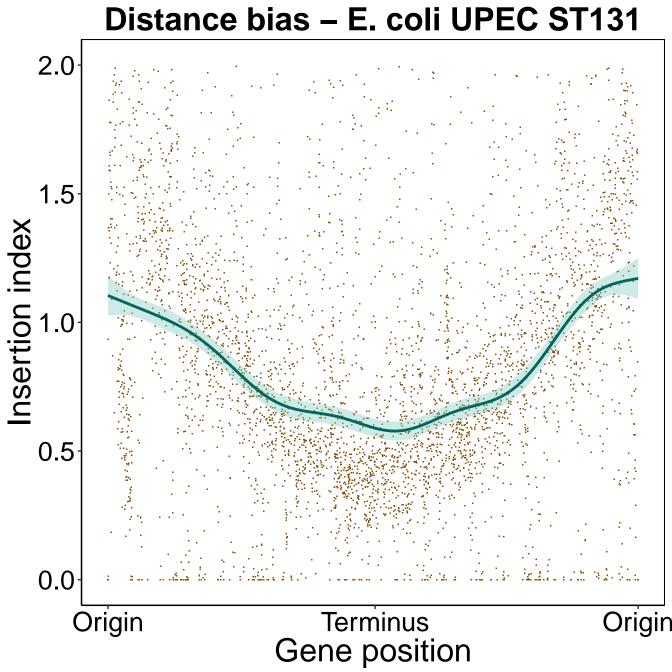
GC bias - K. pneumoniae RH201207 2.0 1.5 Insertion index 1.00 0.5 0.0 0.4 0.5 GC content 0.6 0.3 0.7

K. pneumoniae RH201207 – normalised dista

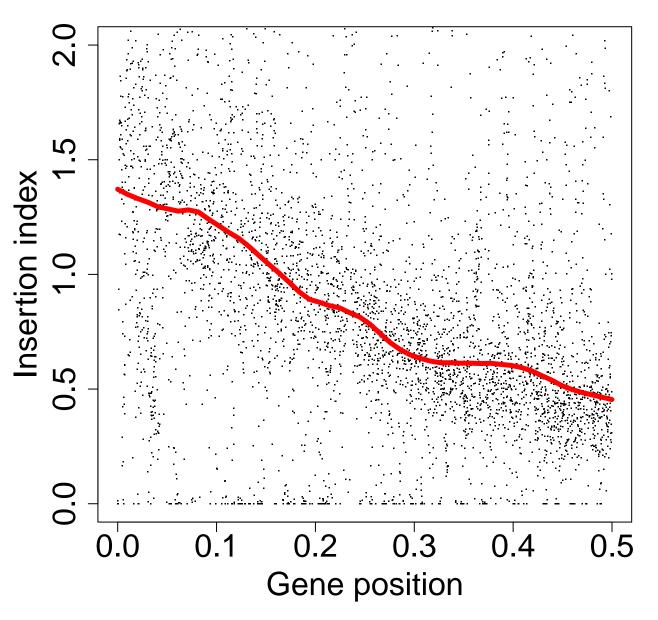


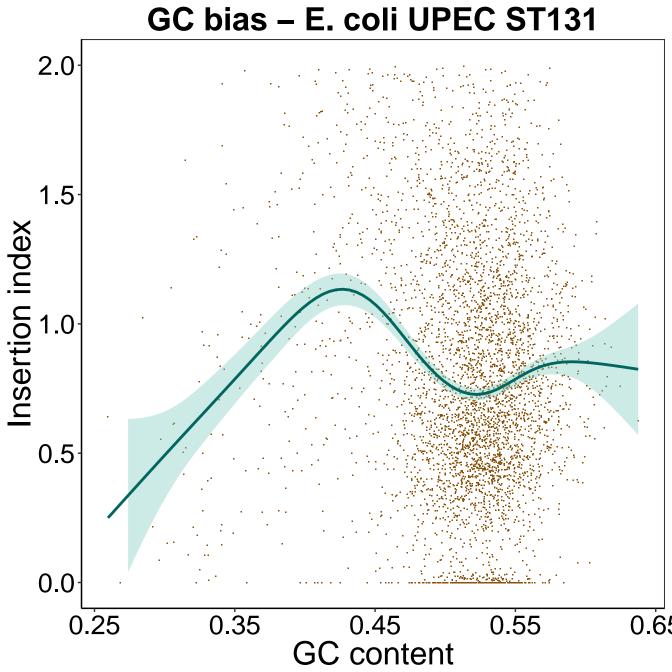
K. pneumoniae RH201207 – normalised G

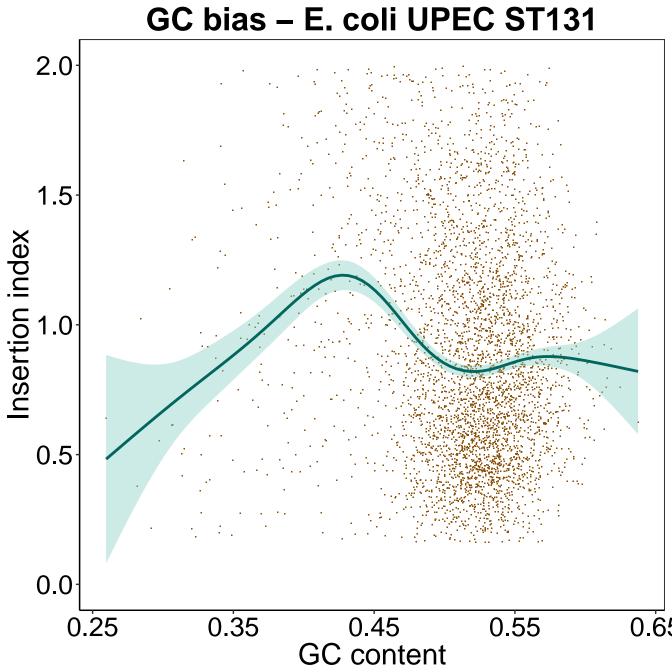




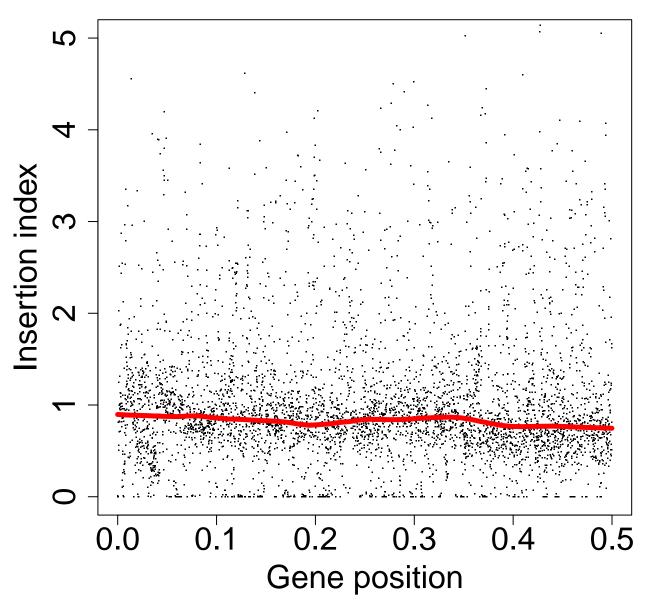
Distance bias - E. coli UPEC ST131



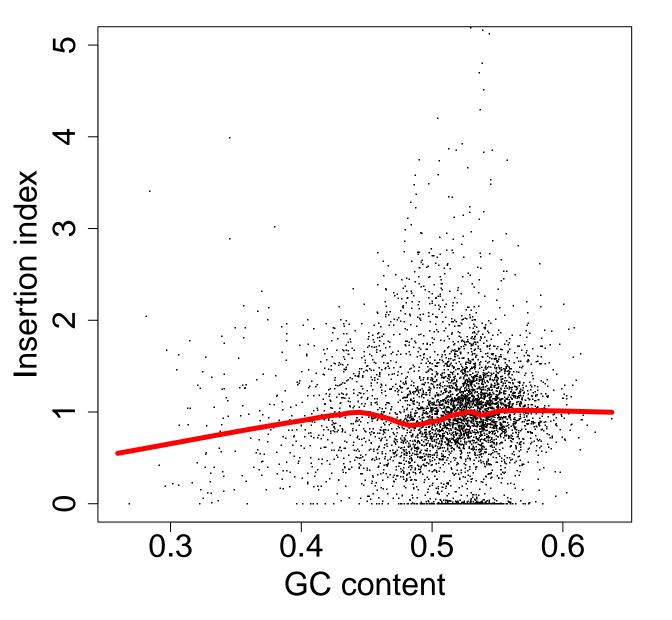


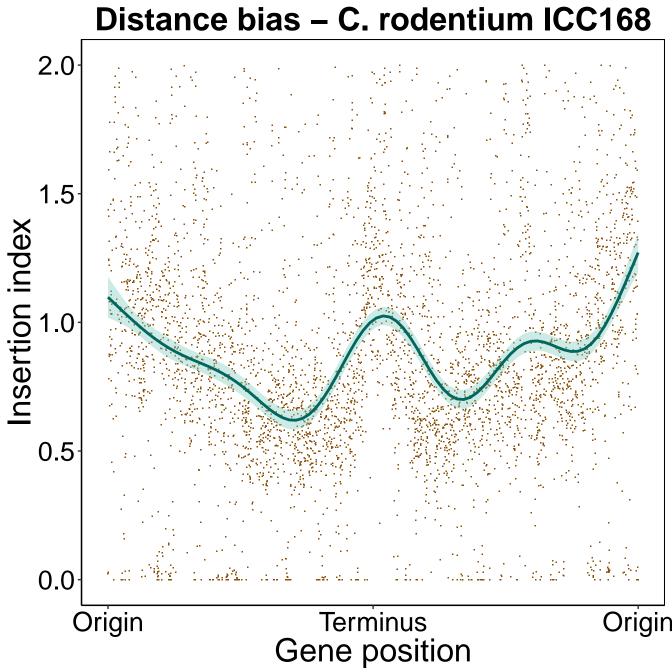


E. coli UPEC ST131 – normalised distance

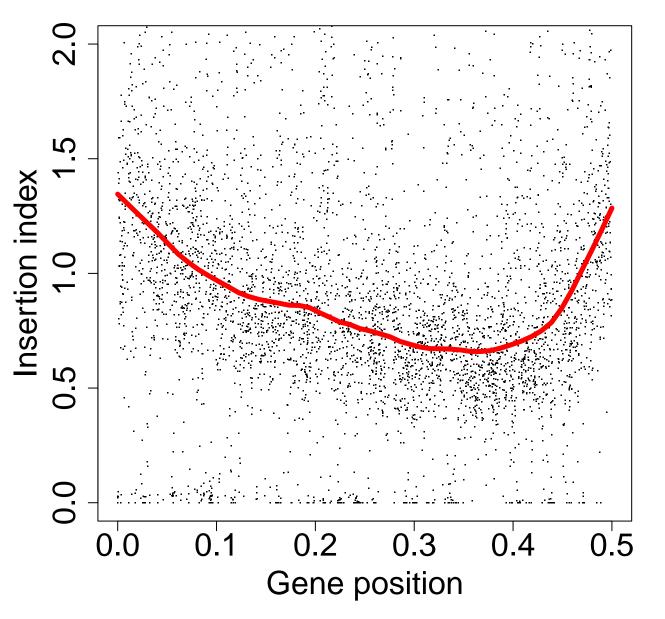


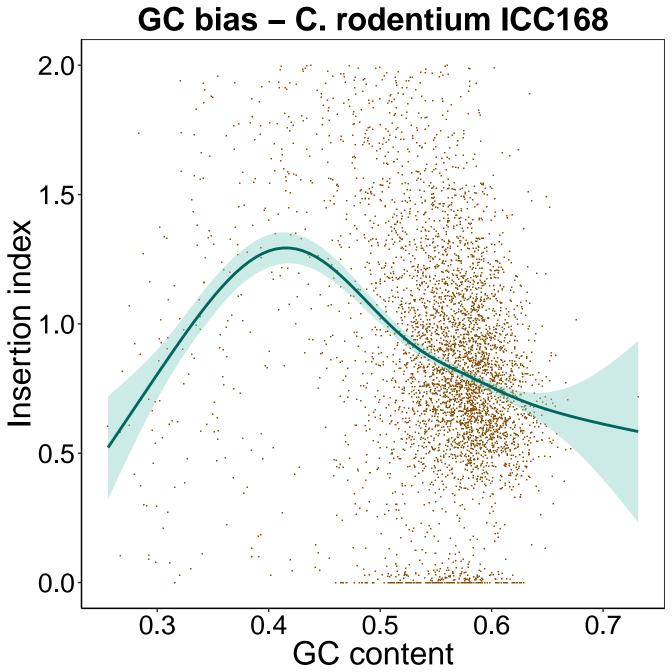
E. coli UPEC ST131 - normalised GC

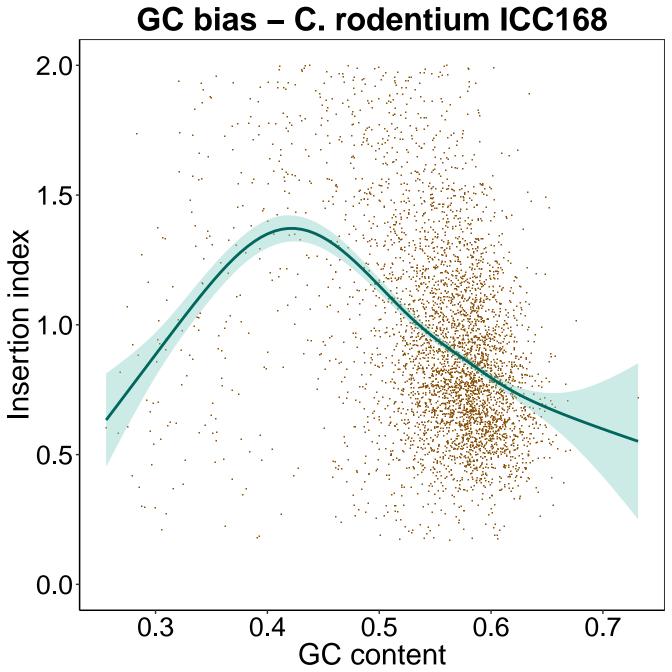




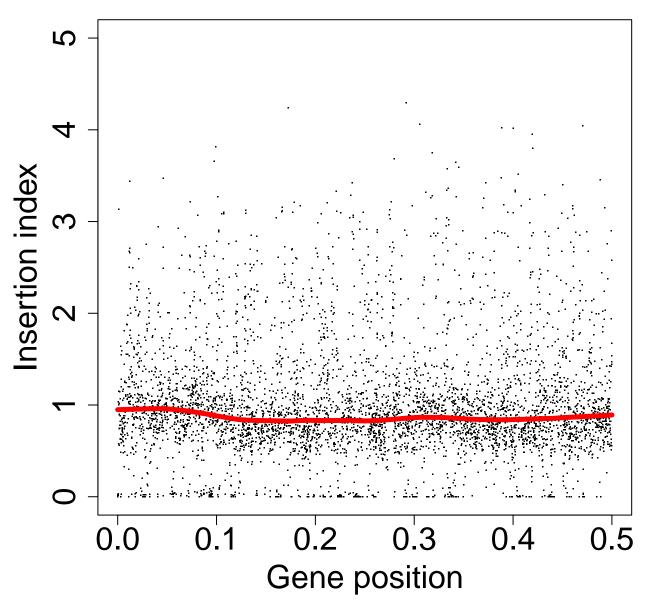
Distance bias - C. rodentium ICC168



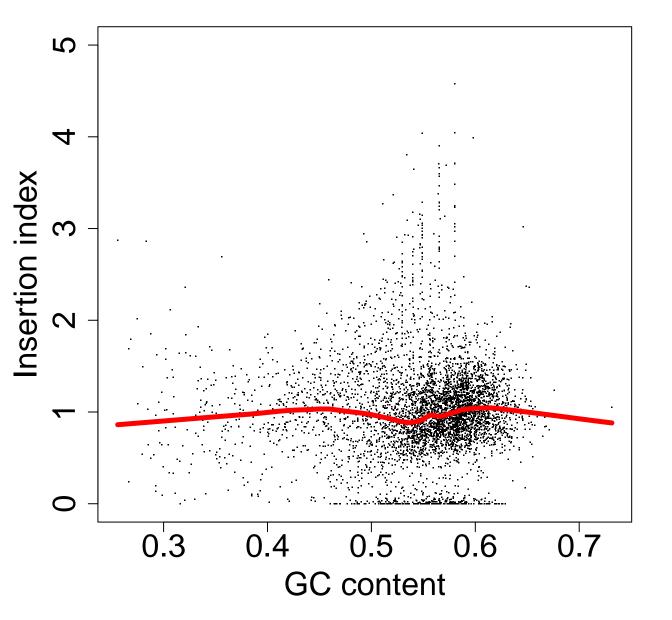


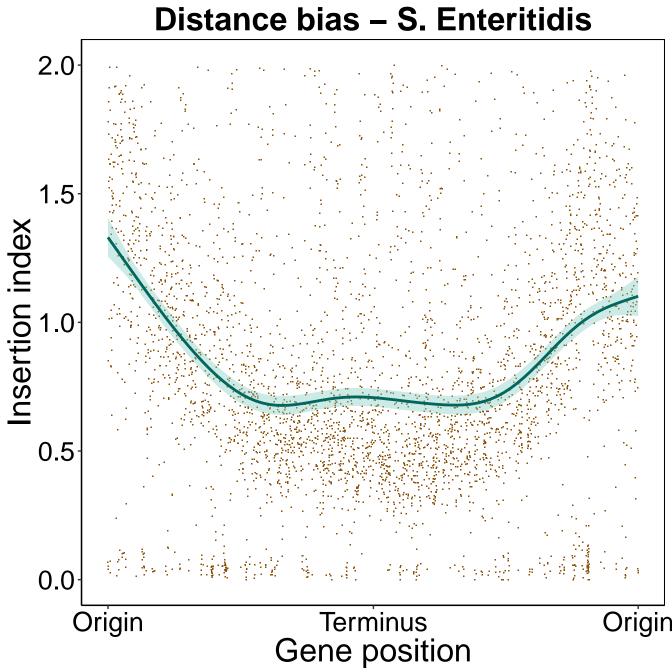


C. rodentium ICC168 - normalised distance

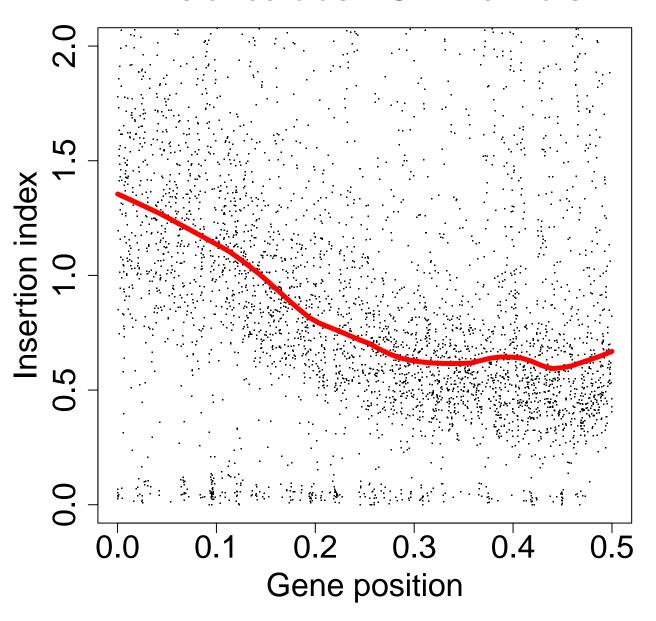


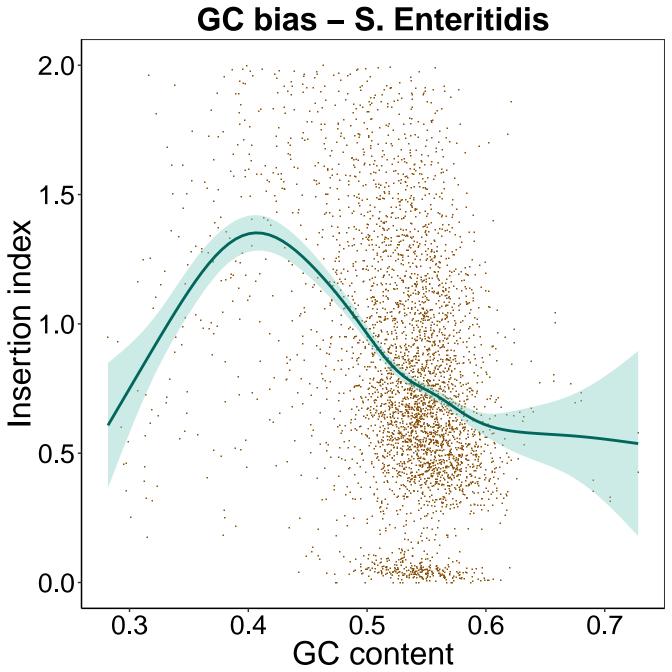
C. rodentium ICC168 - normalised GC

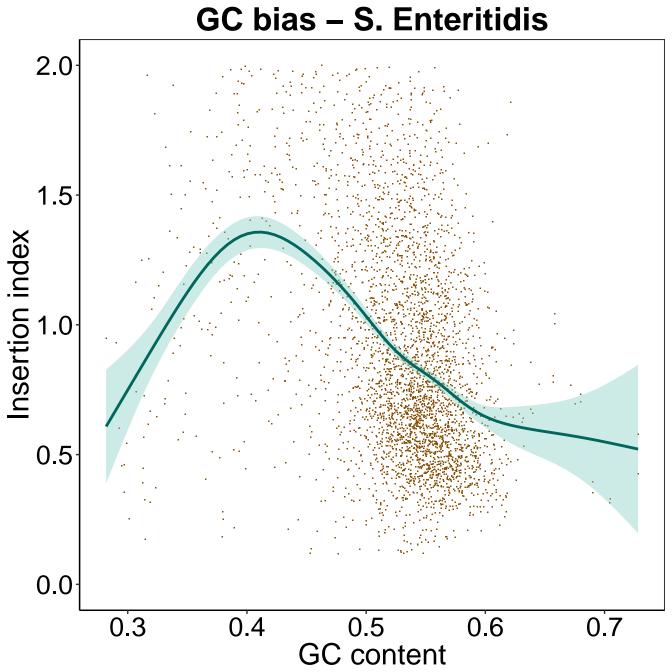




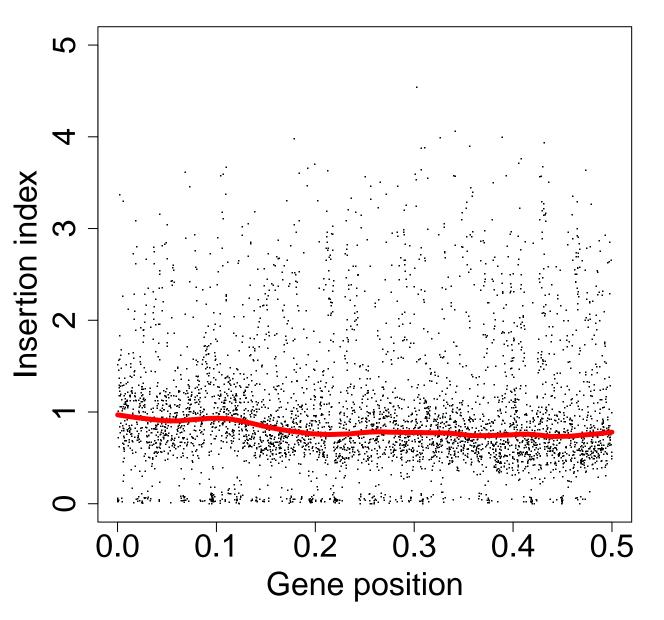
Distance bias - S. Enteritidis



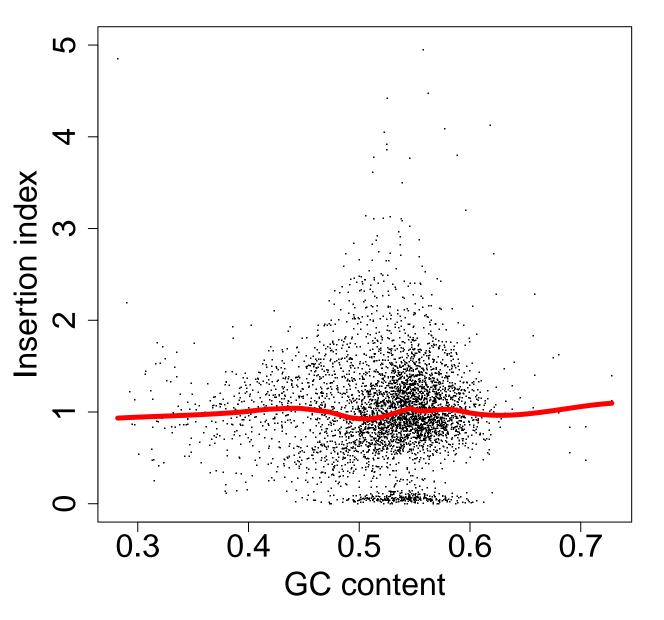




S. Enteritidis - normalised distance

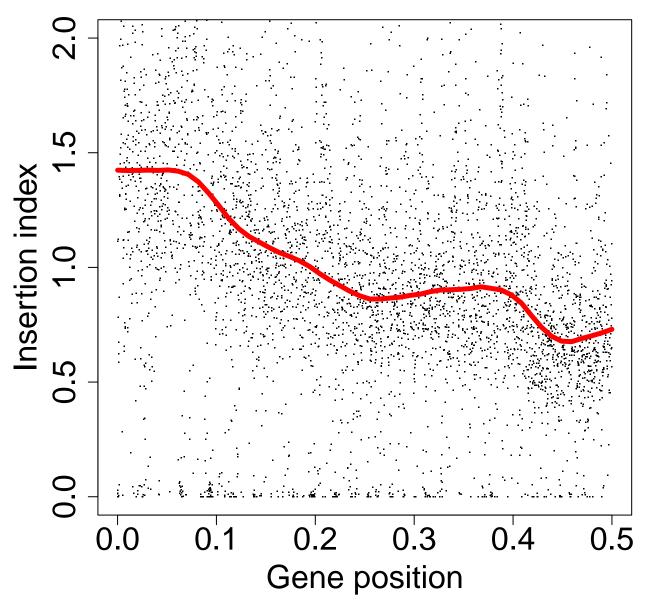


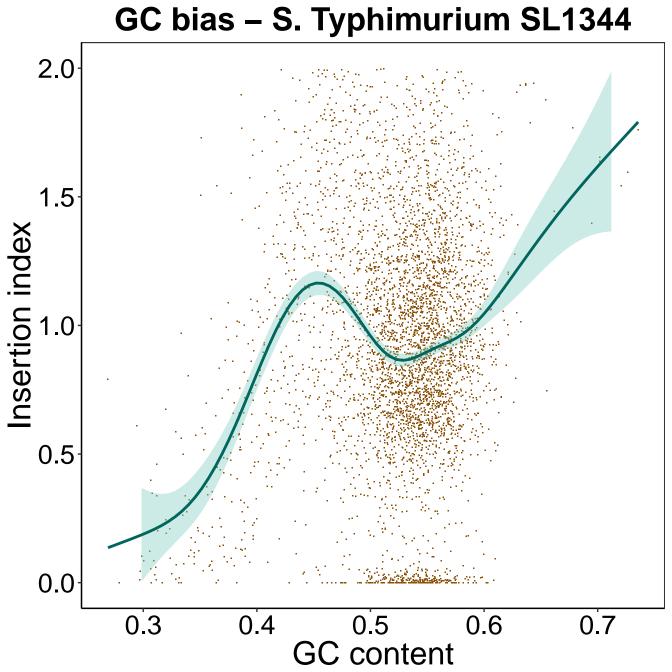
S. Enteritidis - normalised GC



Distance bias - S. Typhimurium SL1344 2.0 1.5 Insertion index 0.5 Origin **Terminus** Origin Gene position

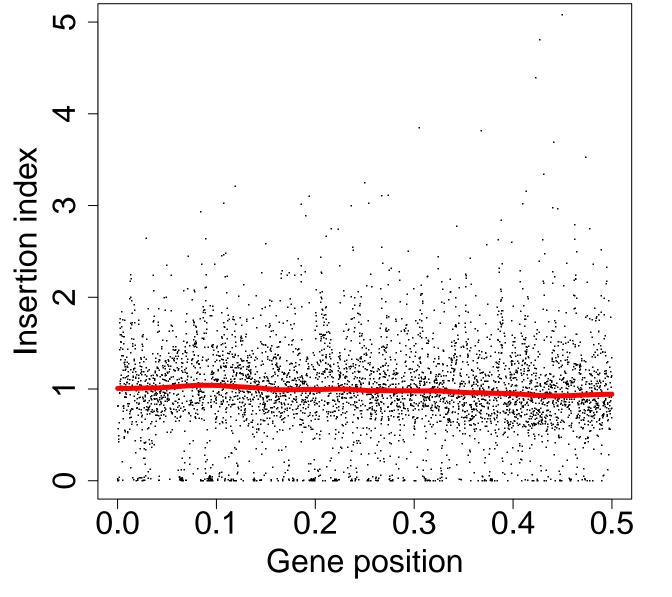
Distance bias – S. Typhimurium SL1344



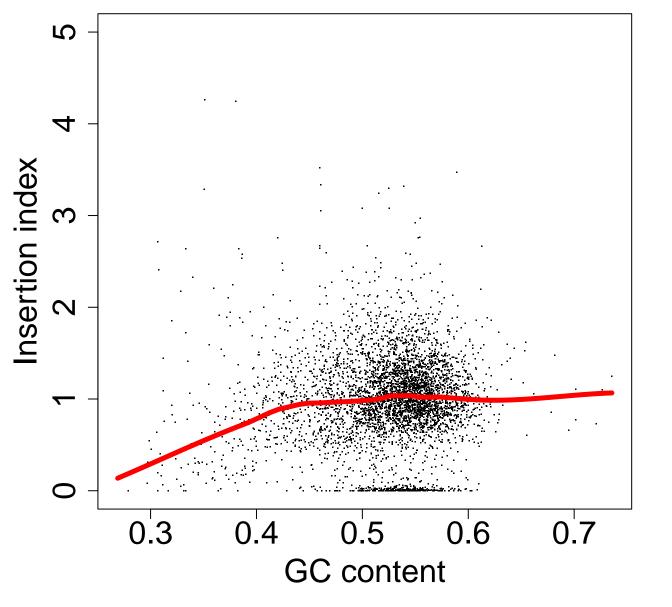


GC bias - S. Typhimurium SL1344 2.0 1.5 Insertion index 1.00 0.5 0.0 0.4 0.6 0.7 0.3 0.5 GC content

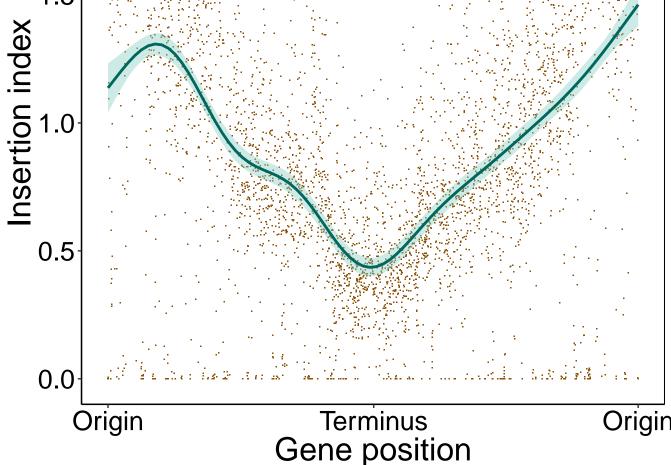
S. Typhimurium SL1344 – normalised distar



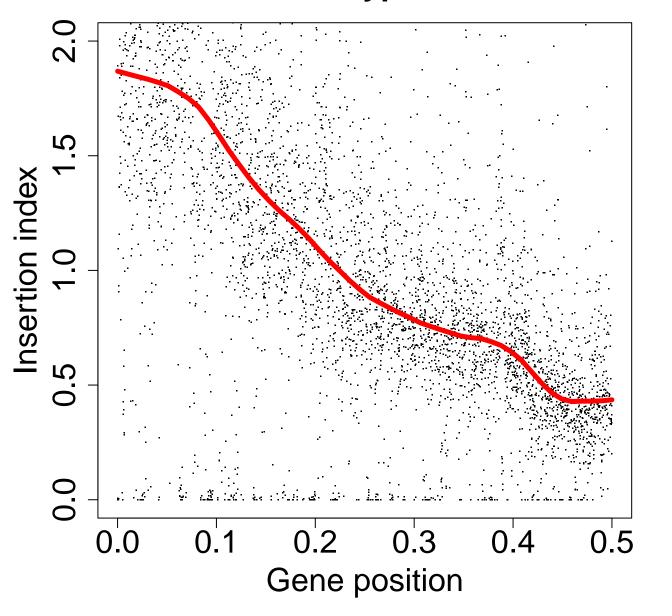
S. Typhimurium SL1344 – normalised GC



Distance bias – S. Typhimurium SL3261



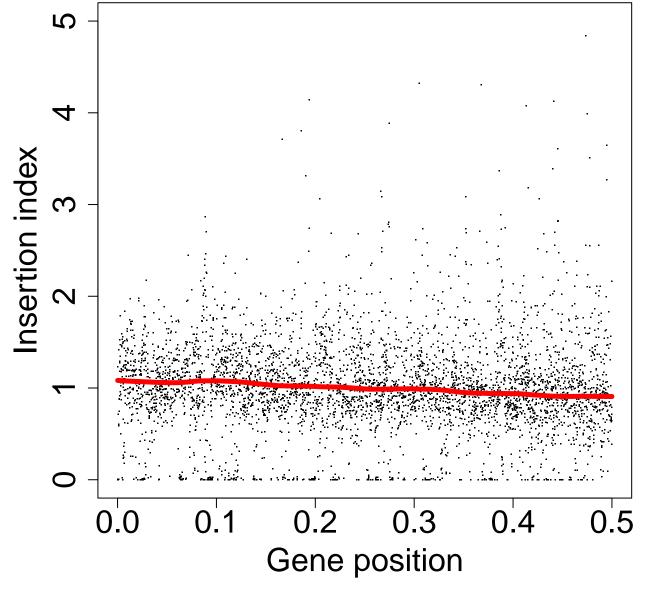
Distance bias – S. Typhimurium SL3261



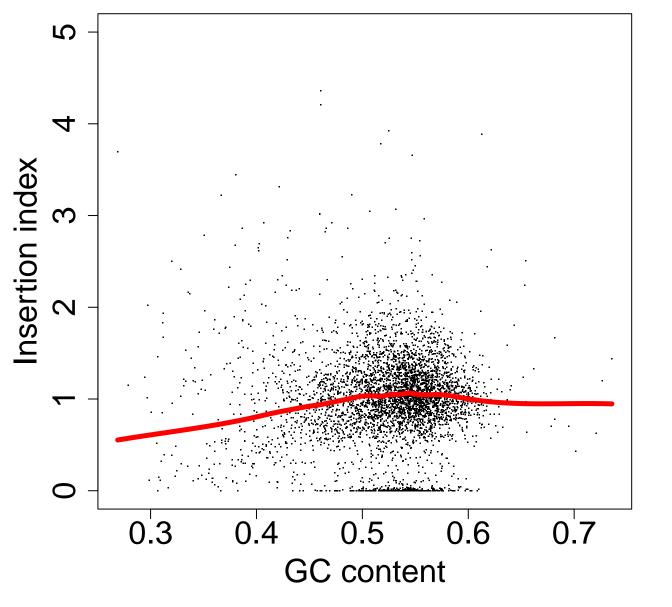
GC bias - S. Typhimurium SL3261 2.0 1.5 Insertion index 0.5 0.0 0.6 0.3 0.4 0.5 0.7 GC content

GC bias - S. Typhimurium SL3261 2.0 1.5 Insertion index 1.00 0.5 0.0 0.5 0.4 0.6 0.7 0.3 GC content

S. Typhimurium SL3261 – normalised distar



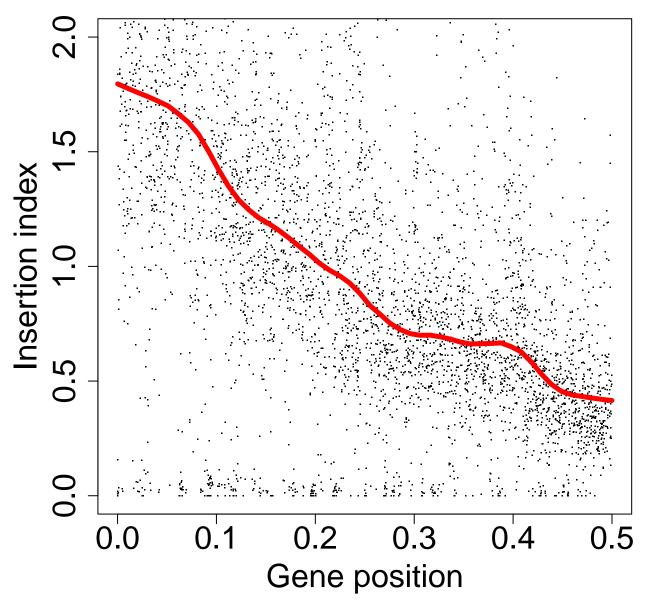
S. Typhimurium SL3261 – normalised GC



Distance bias - S. Typhimurium D23580 2.0 1.5 Insertion index 0.5 0.0 Origin **Terminus** Origin

Gene position

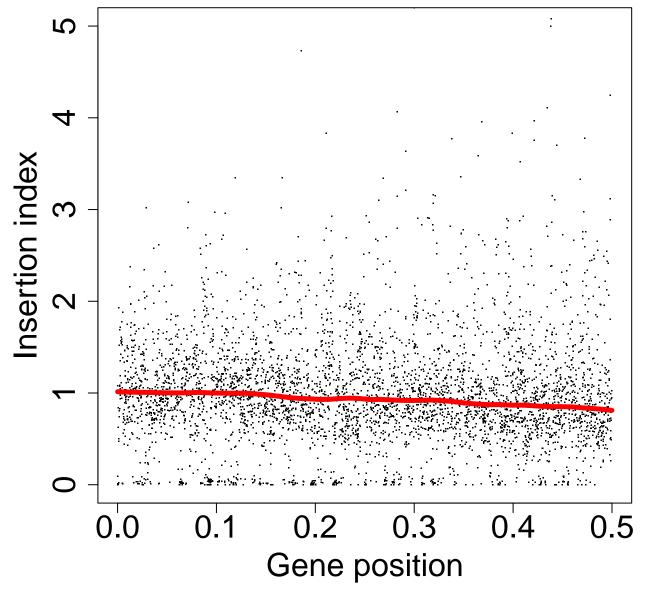
Distance bias – S. Typhimurium D23580



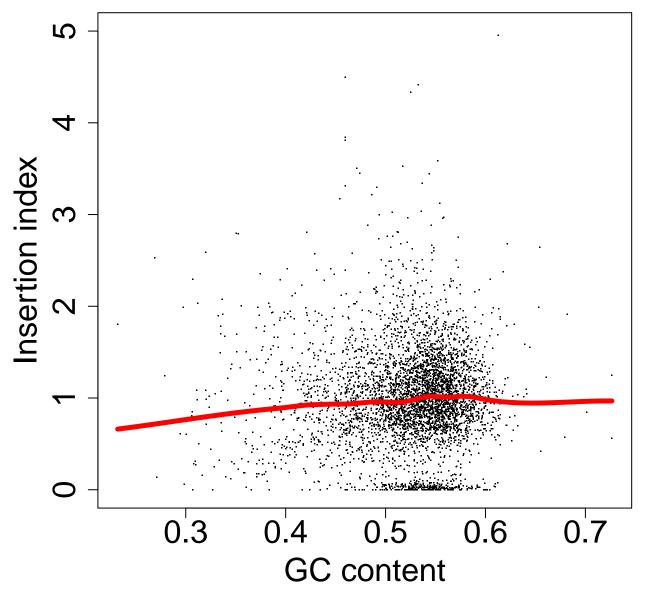
GC bias - S. Typhimurium D23580 2.0 1.5 Insertion index 0.5 0.0 0.3 0.4 0.5 0.6 0.7 GC content

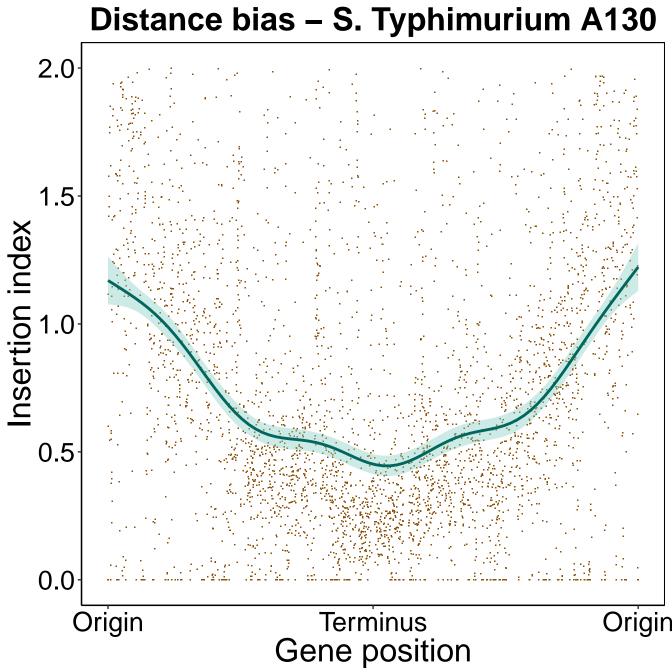
GC bias - S. Typhimurium D23580 2.0 1.5 Insertion index 1.00 0.5 0.0 0.3 0.4 0.5 0.6 0.7 GC content

S. Typhimurium D23580 – normalised distar

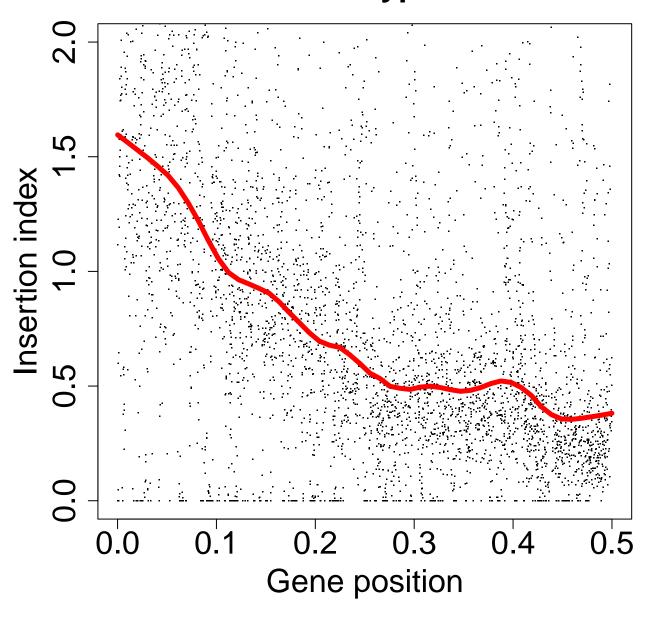


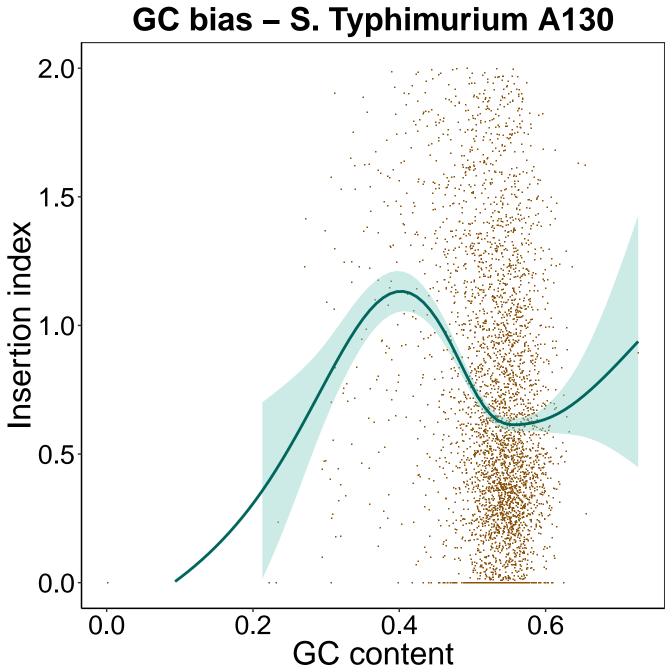
S. Typhimurium D23580 – normalised GC

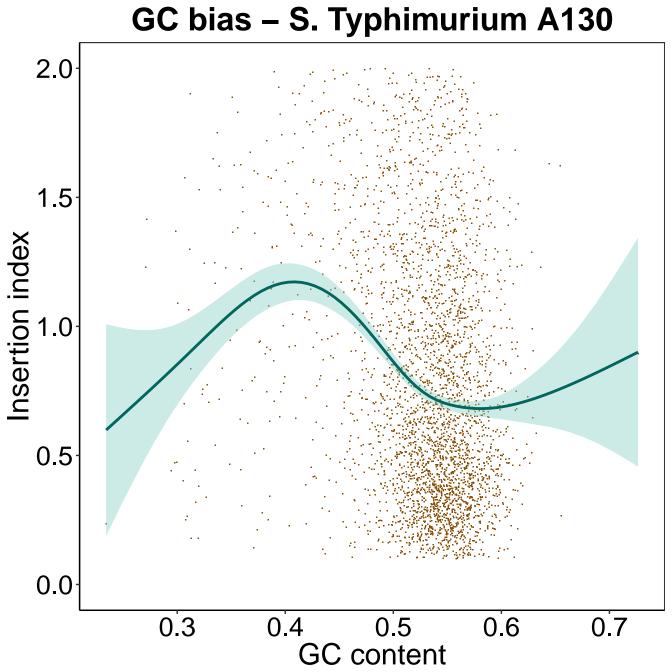




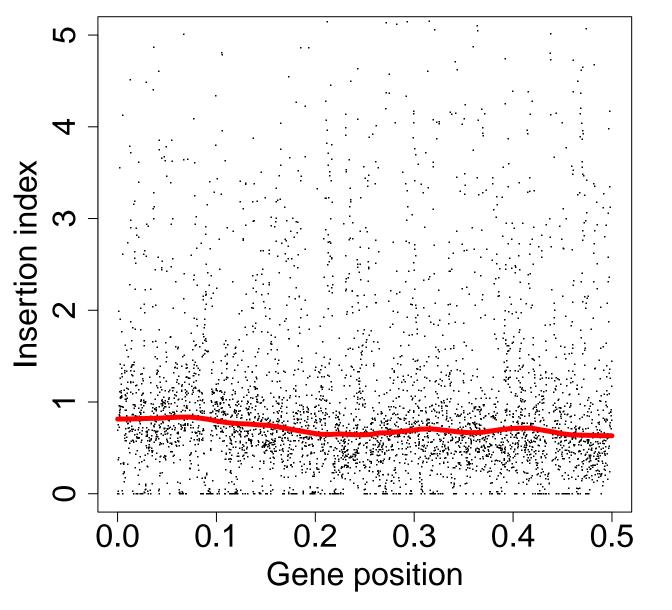
Distance bias - S. Typhimurium A130



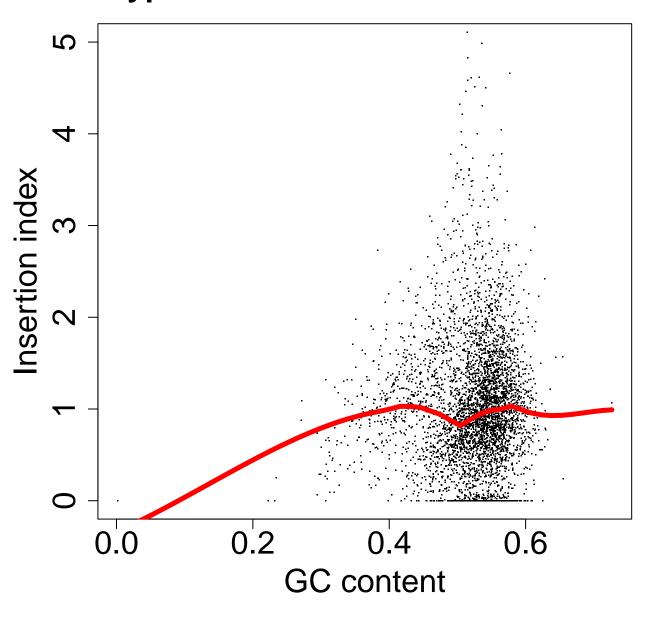


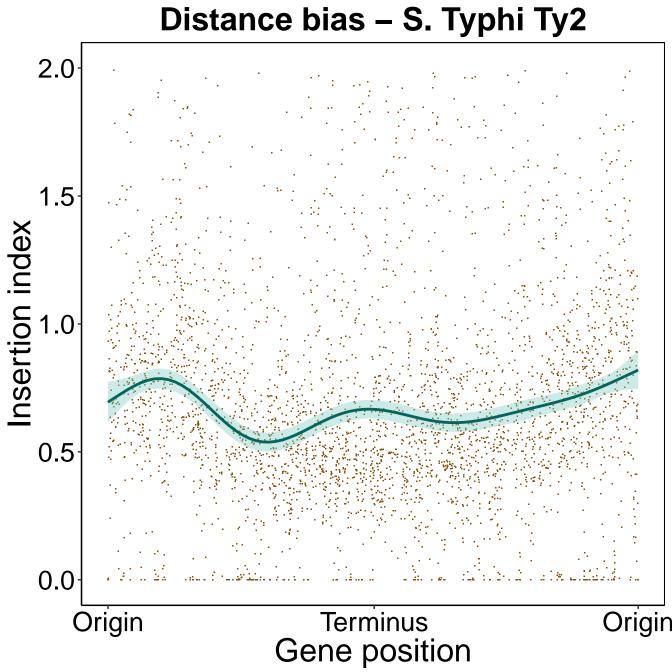


S. Typhimurium A130 – normalised distance

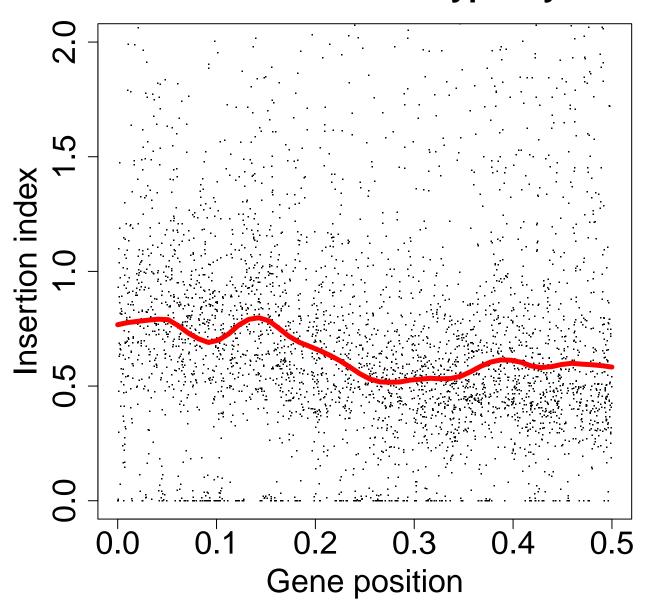


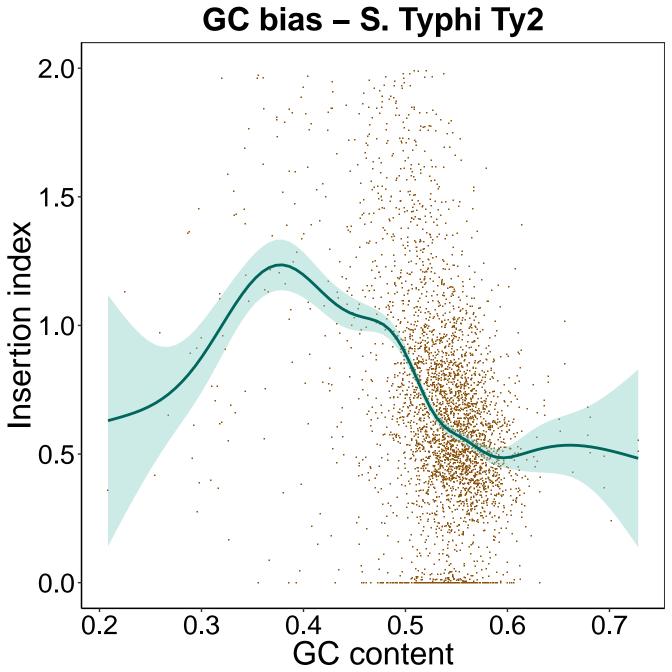
S. Typhimurium A130 – normalised GC

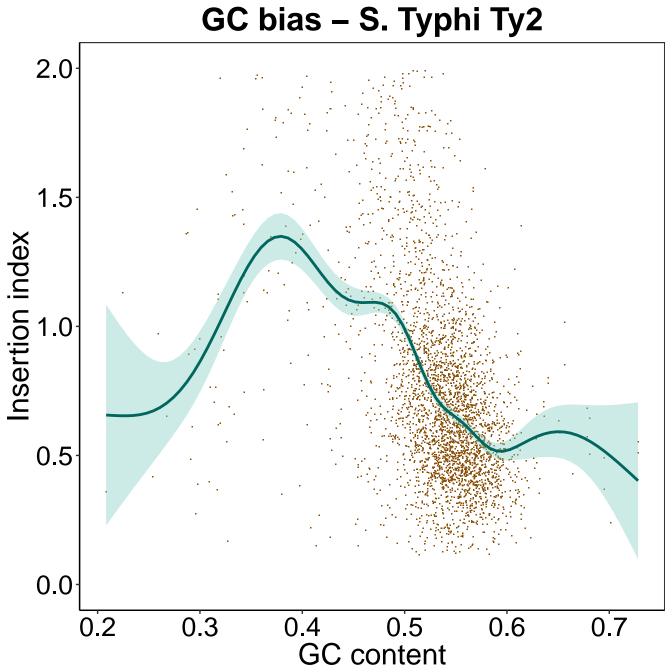




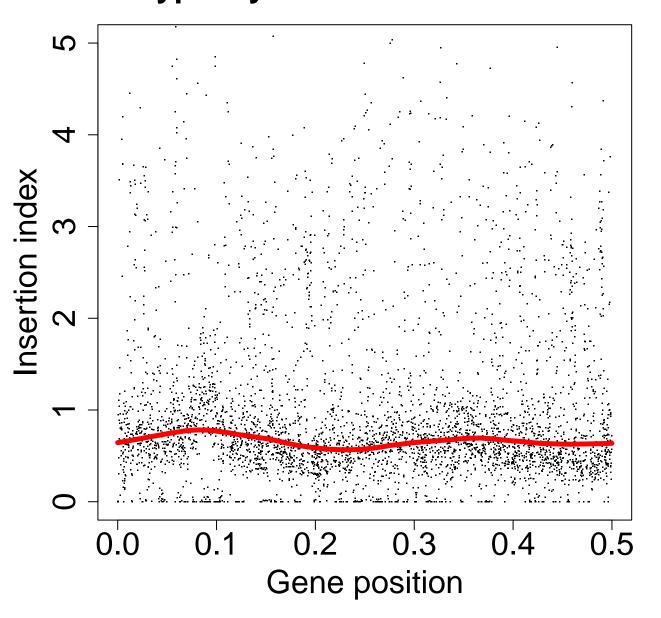
Distance bias - S. Typhi Ty2



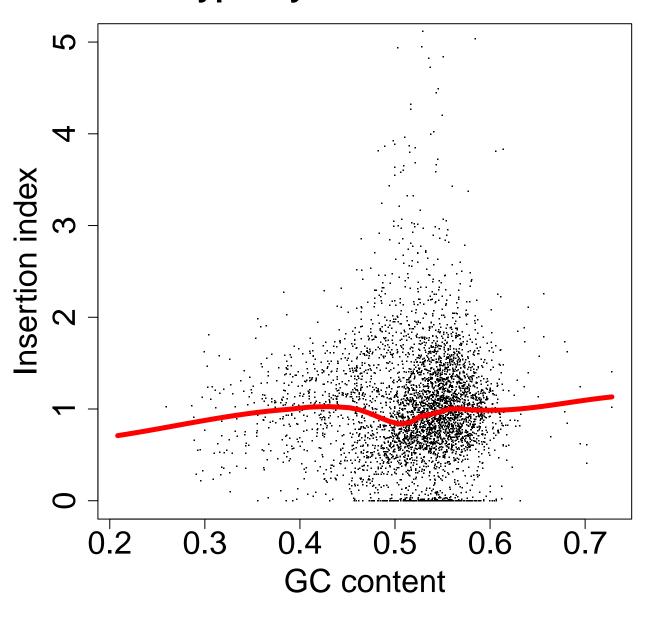




S. Typhi Ty2 - normalised distance



S. Typhi Ty2 – normalised GC



GC bias

