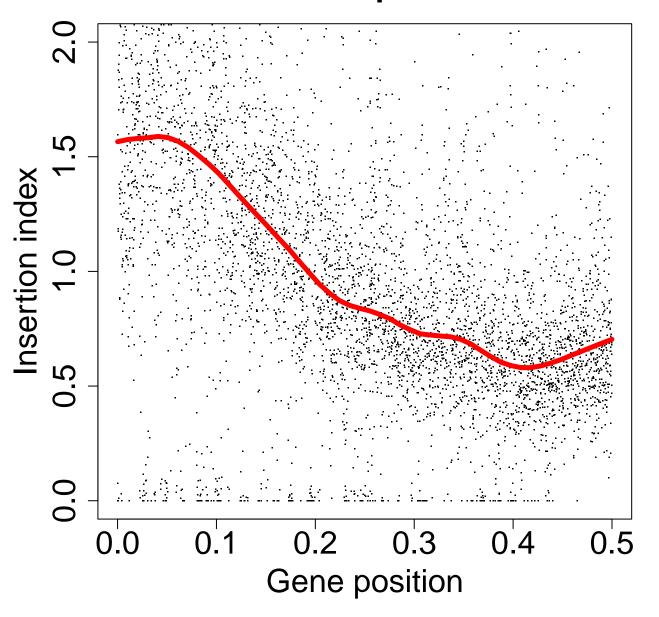
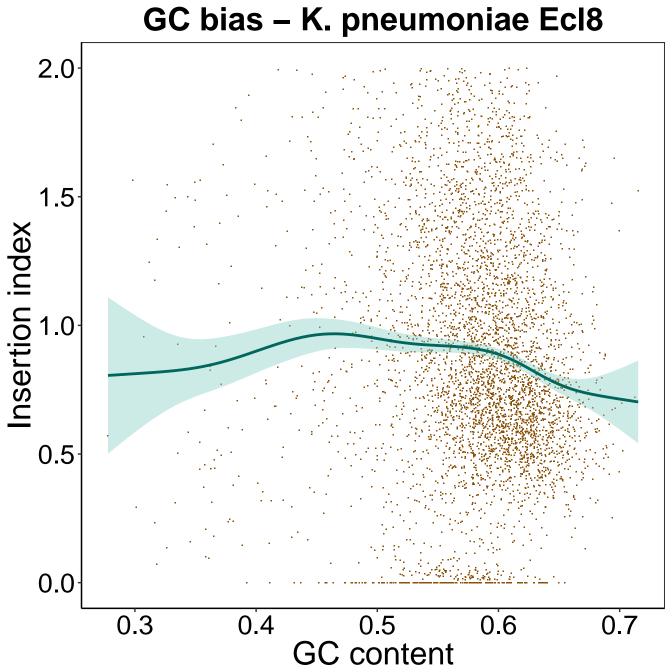
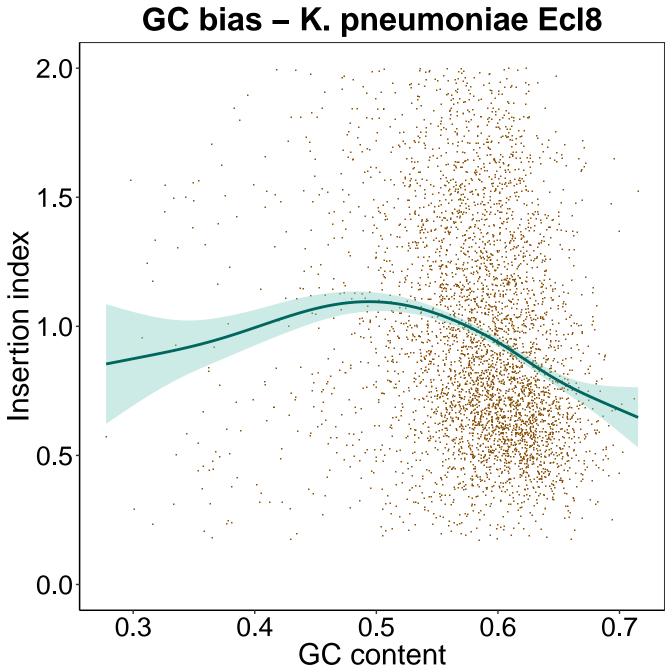


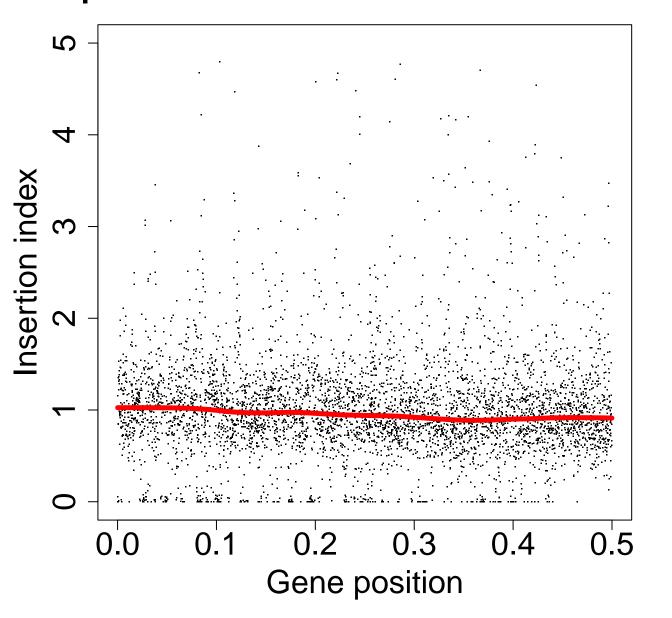
### Distance bias - K. pneumoniae Ecl8



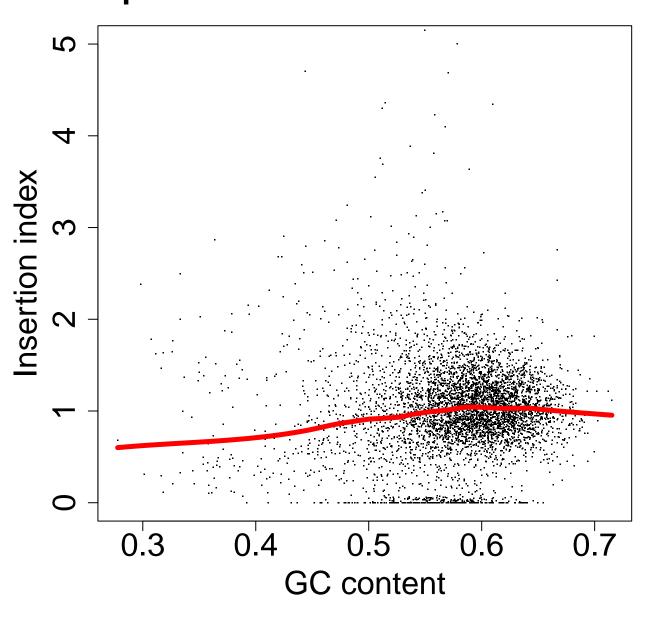


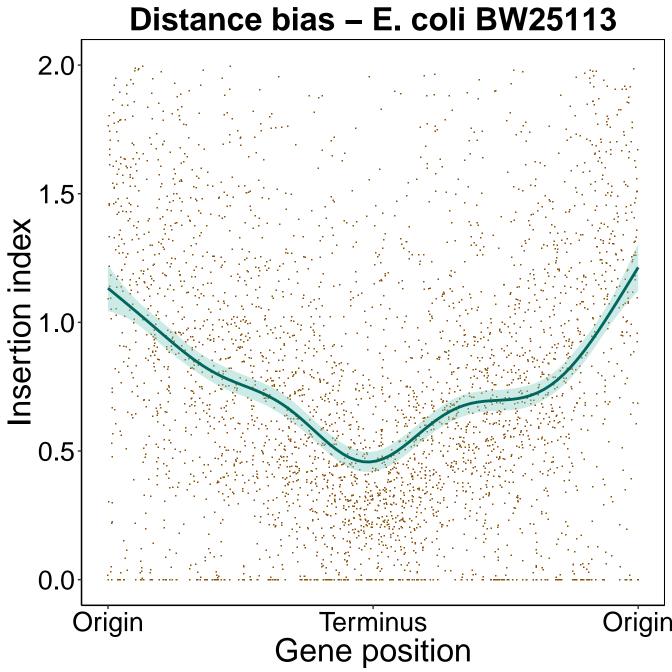


### K. pneumoniae Ecl8 - normalised distanc

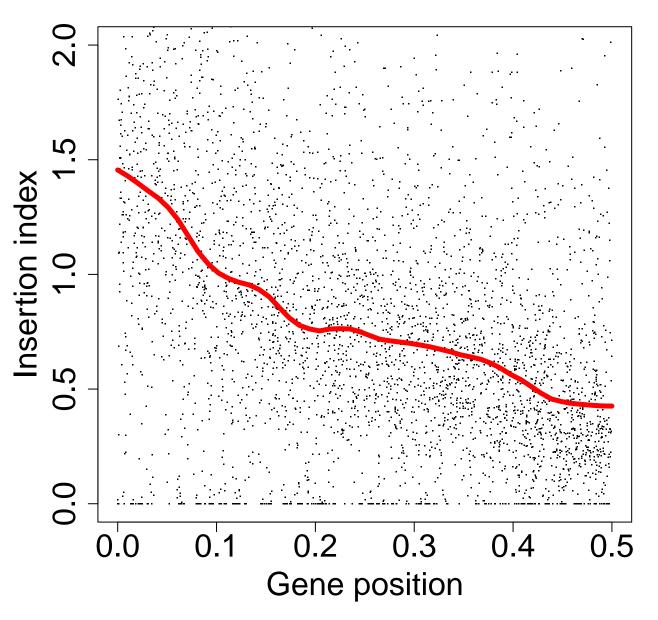


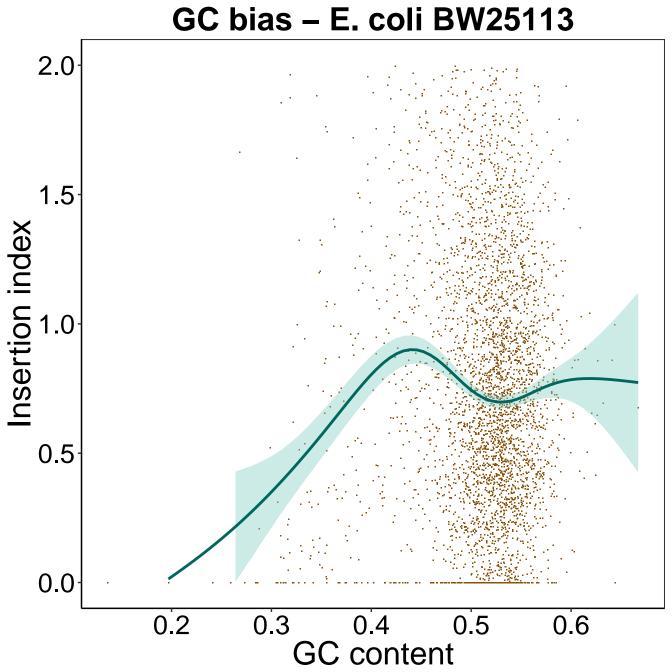
### K. pneumoniae Ecl8 - normalised GC

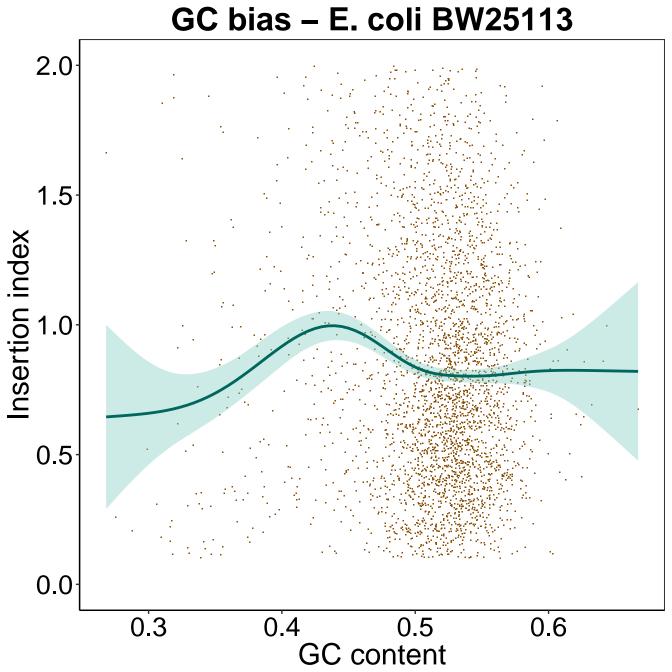




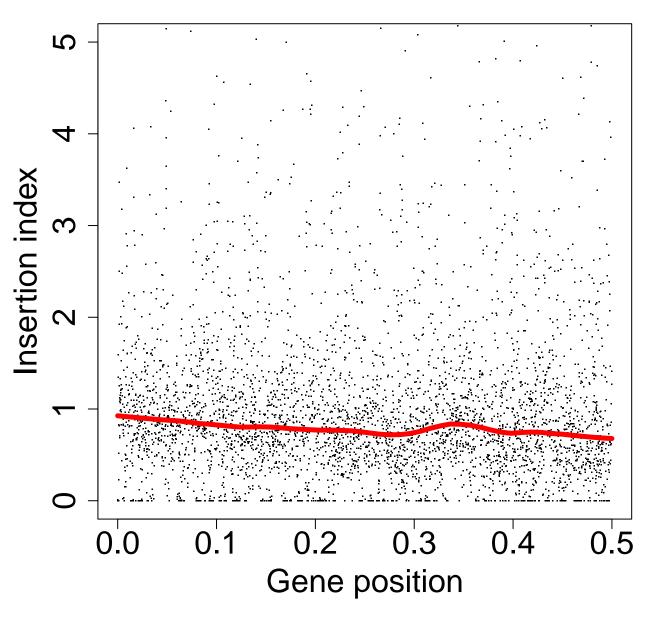
### Distance bias - E. coli BW25113



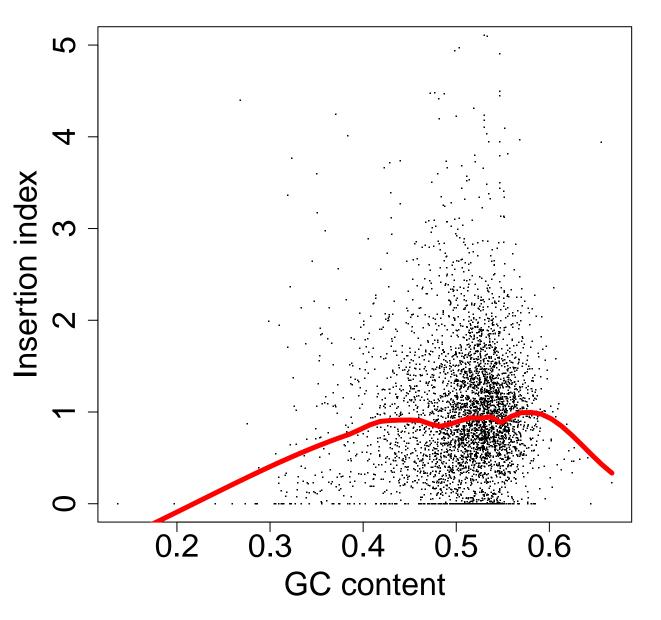


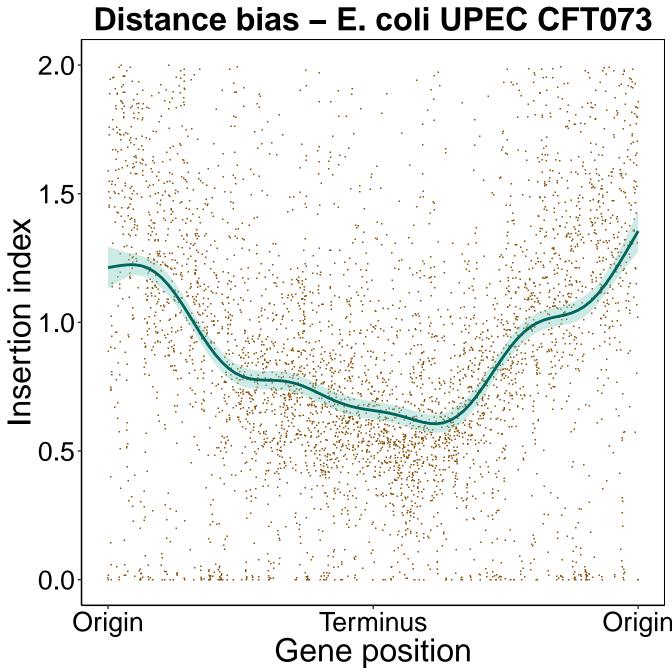


### E. coli BW25113 - normalised distance

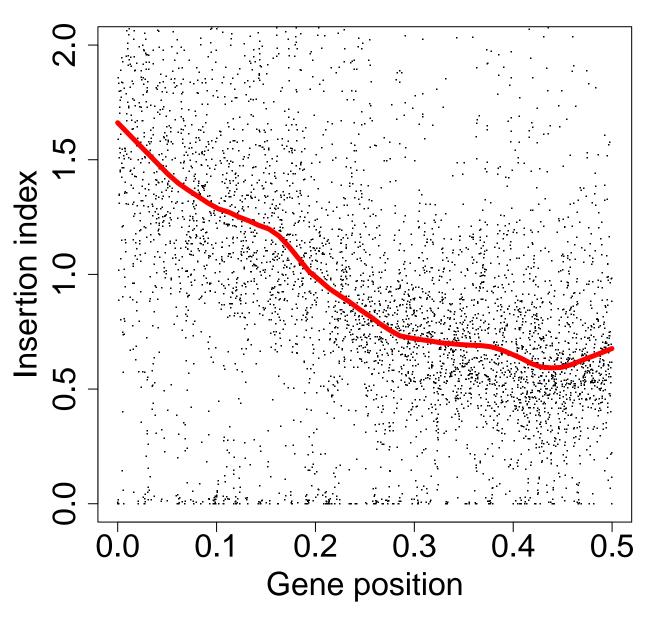


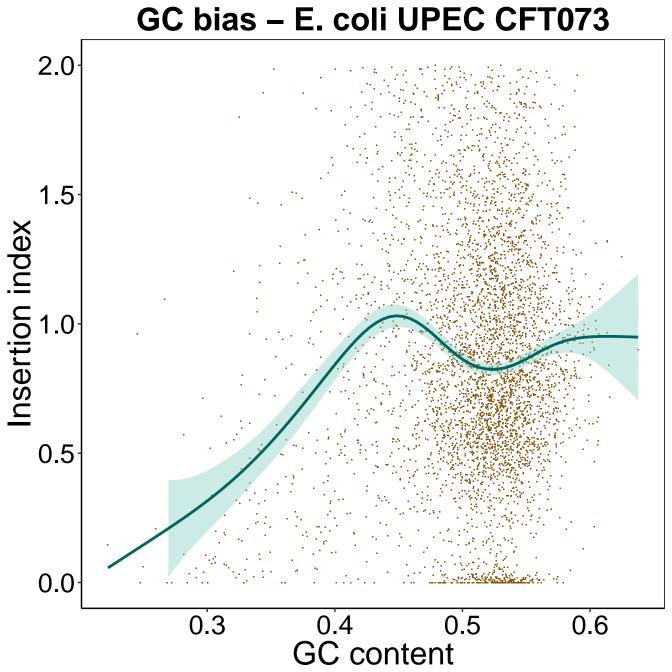
### E. coli BW25113 - normalised GC

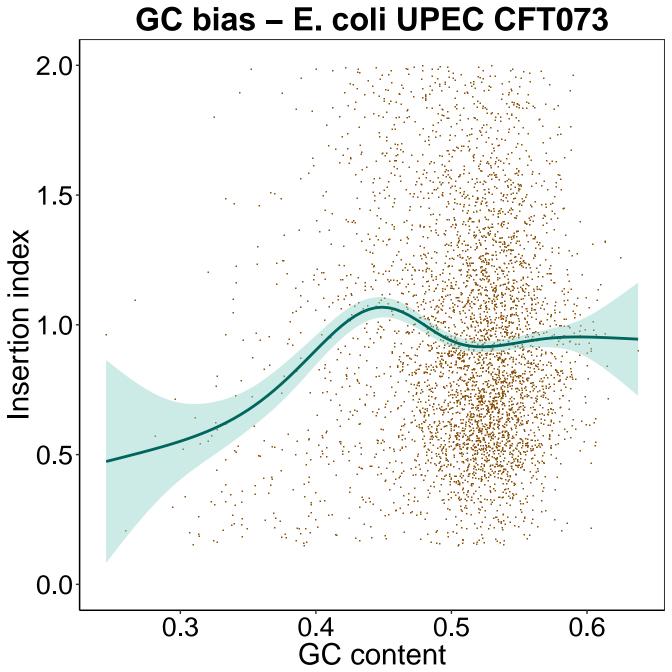




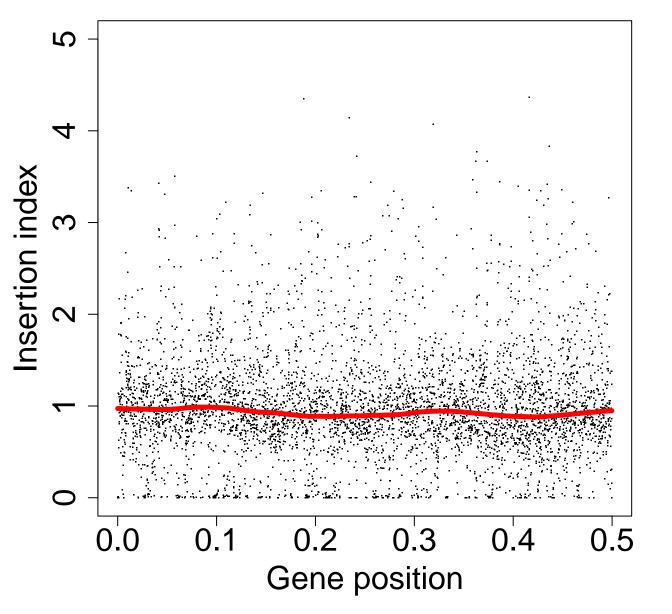
### Distance bias - E. coli UPEC CFT073



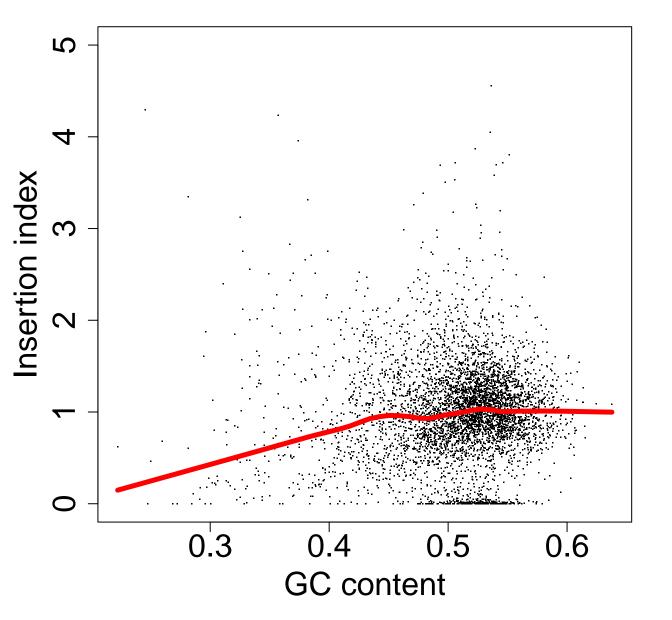


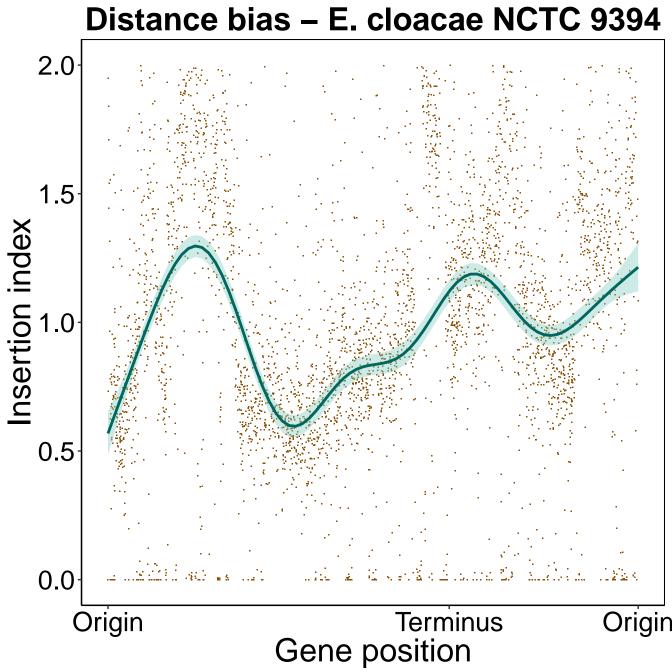


### E. coli UPEC CFT073 – normalised distanc

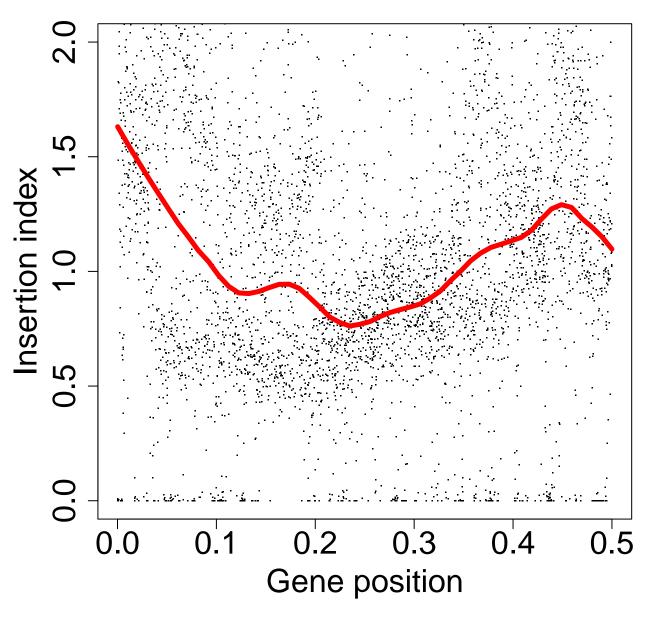


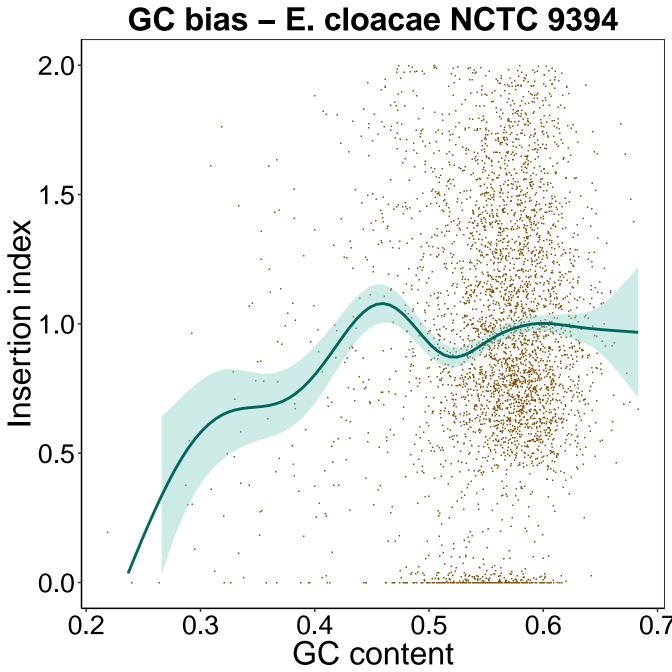
### E. coli UPEC CFT073 – normalised GC

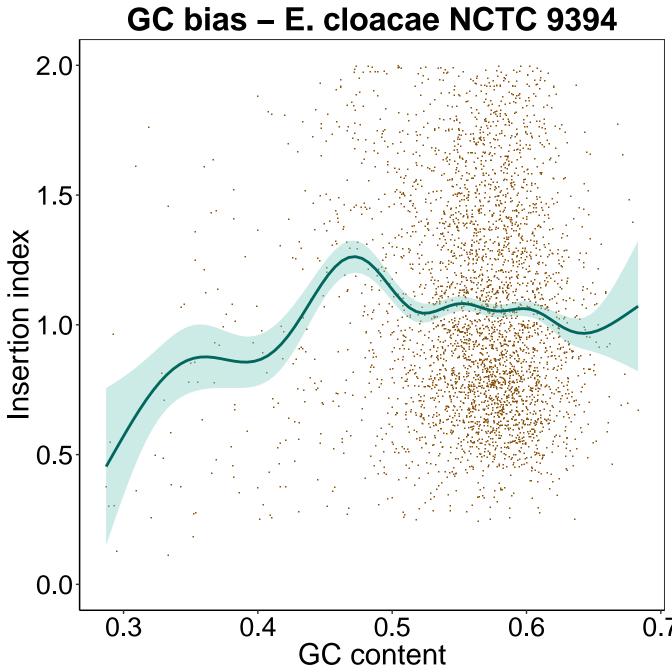




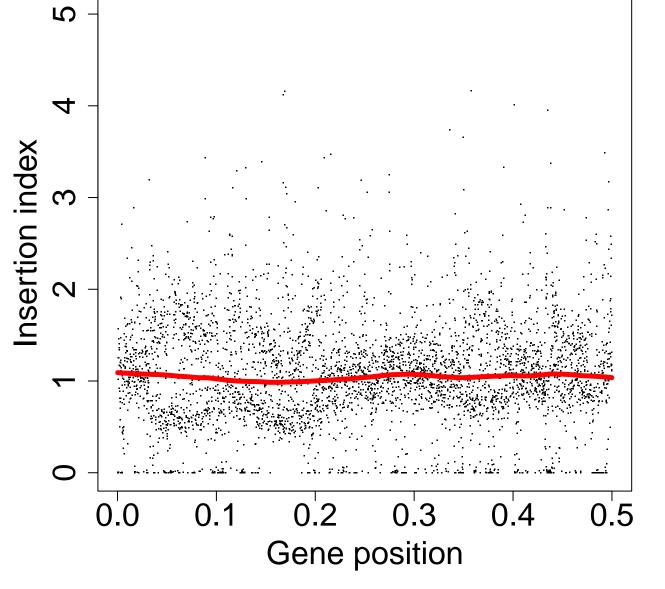
### Distance bias - E. cloacae NCTC 9394



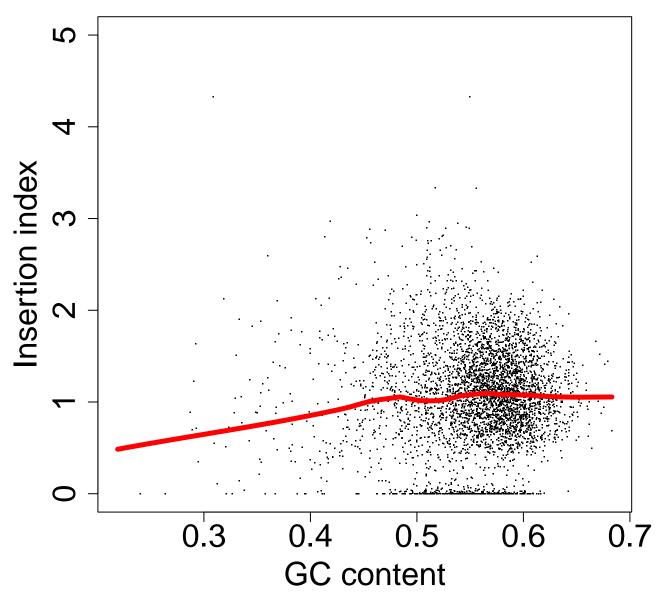




## E. cloacae NCTC 9394 – normalised distant

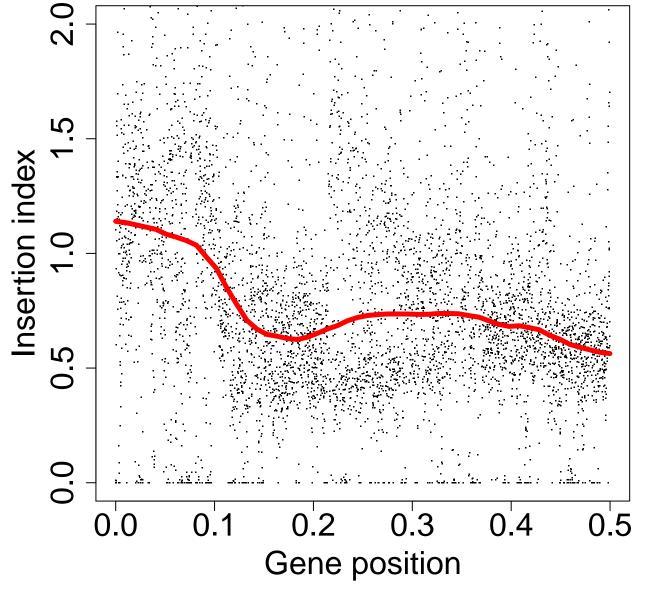


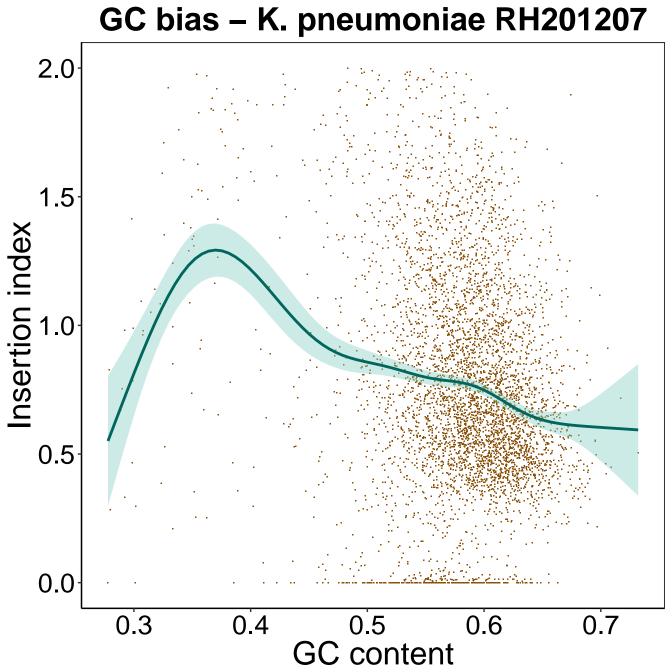
### E. cloacae NCTC 9394 – normalised GC



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

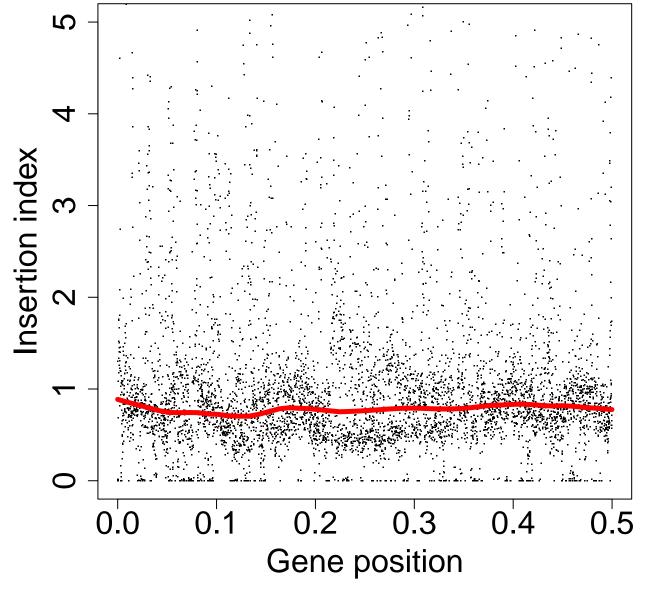
## Distance bias – K. pneumoniae RH201207



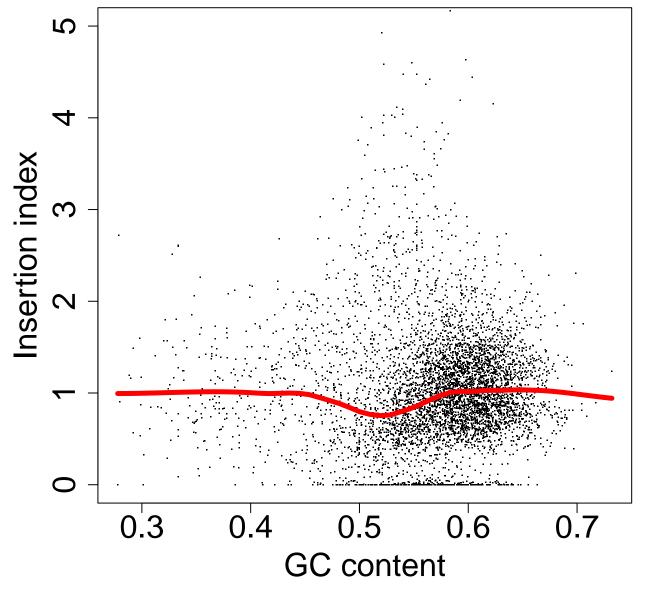


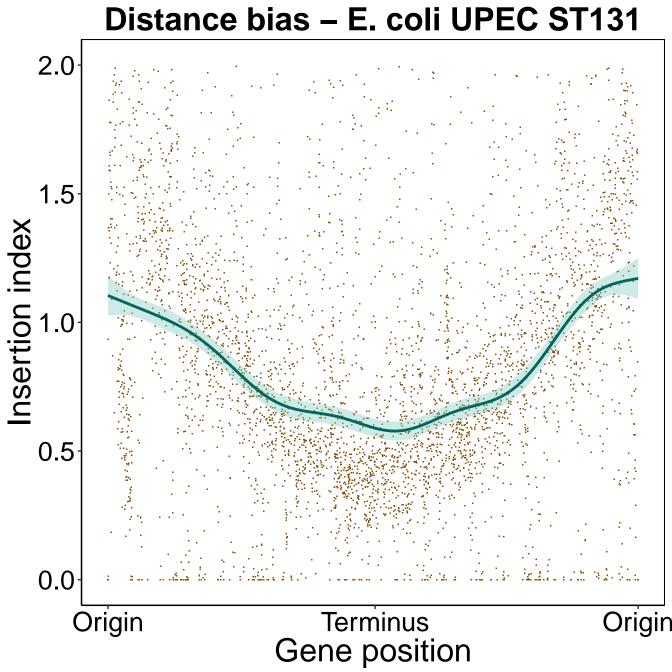
GC bias - K. pneumoniae RH201207 2.0 1.5 Insertion index 1.00 0.5 0.0 0.4 0.5 GC content 0.6 0.3 0.7

## K. pneumoniae RH201207 – normalised dista

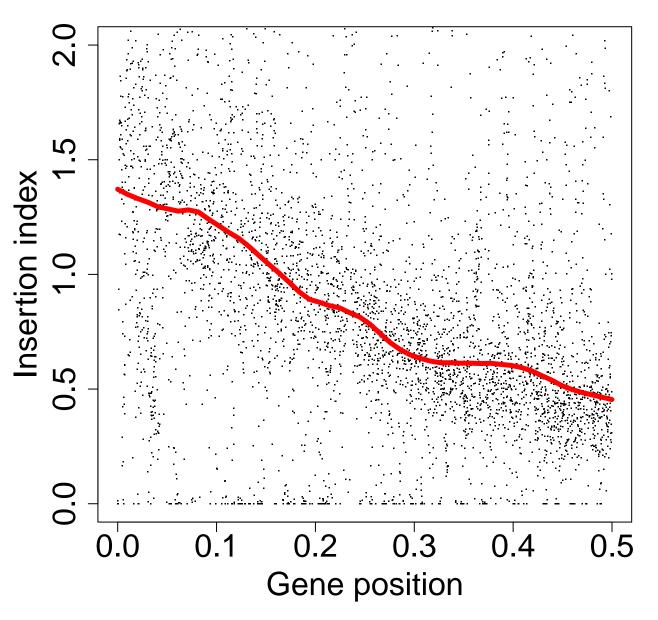


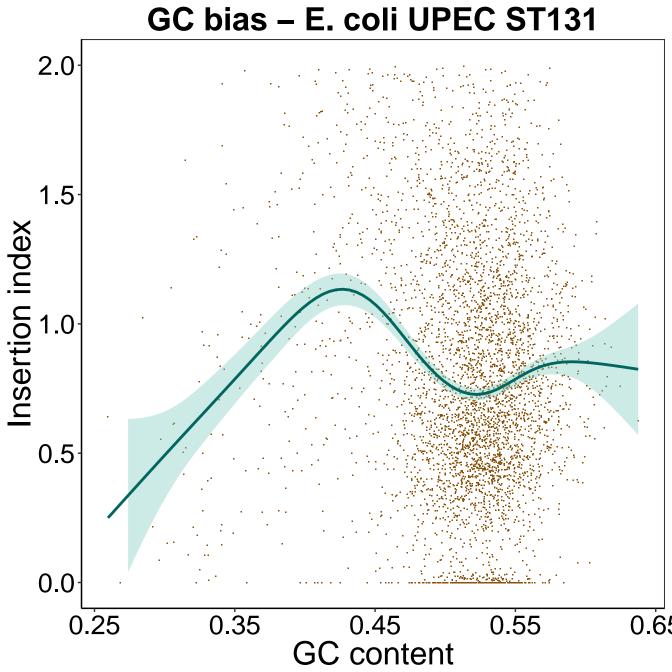
## K. pneumoniae RH201207 – normalised G

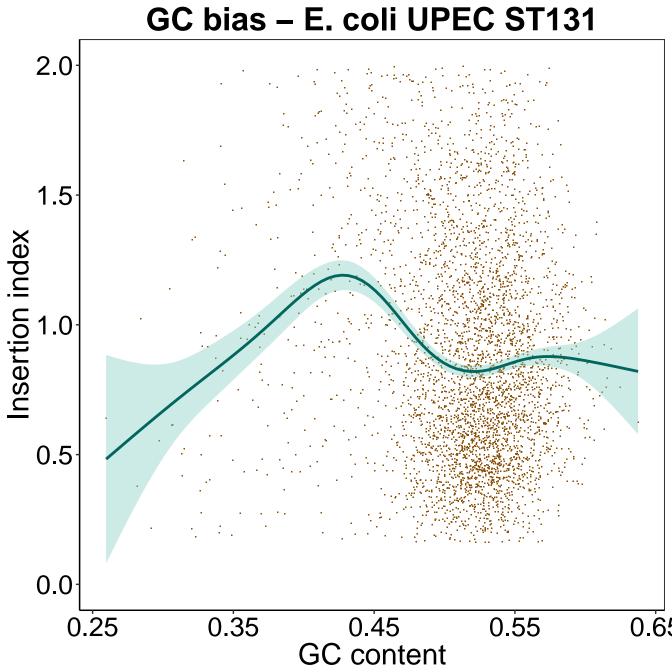




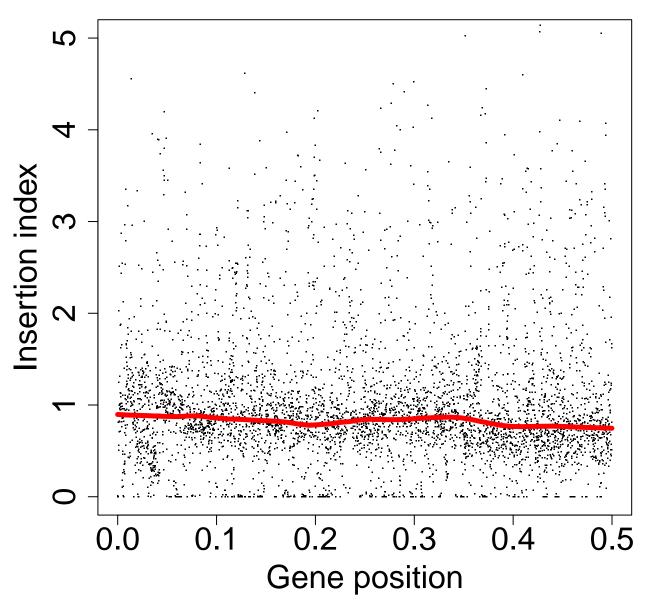
### Distance bias - E. coli UPEC ST131



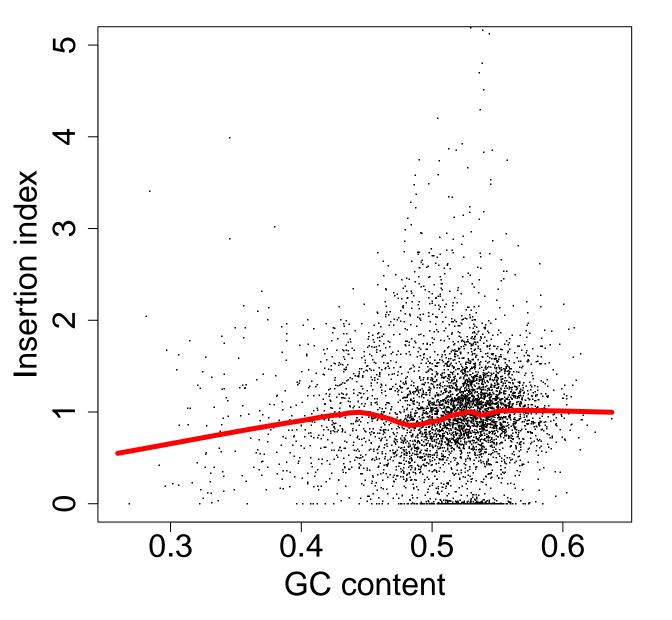


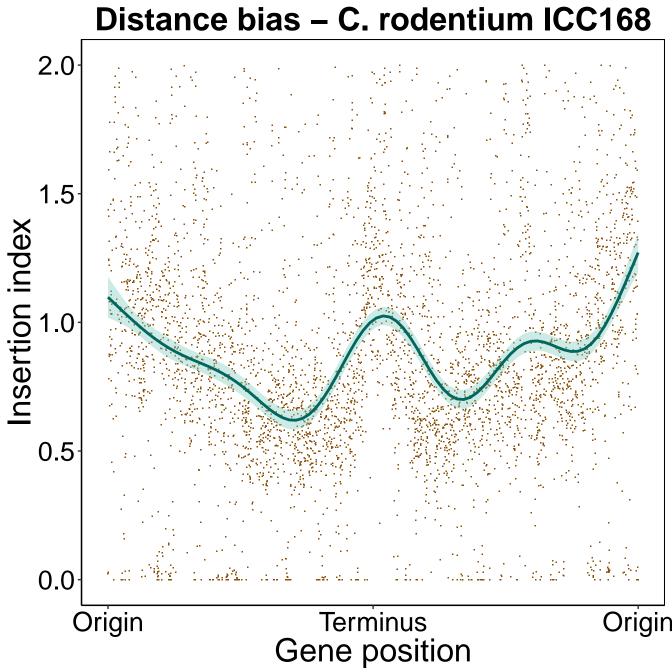


### E. coli UPEC ST131 – normalised distance

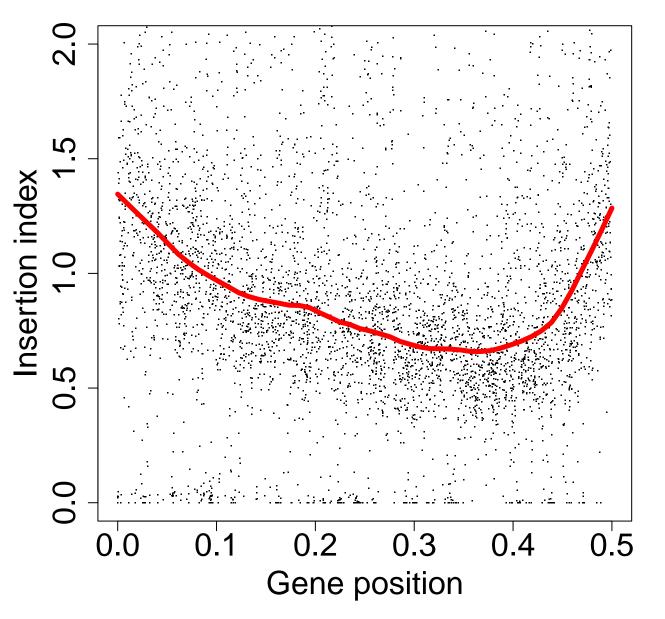


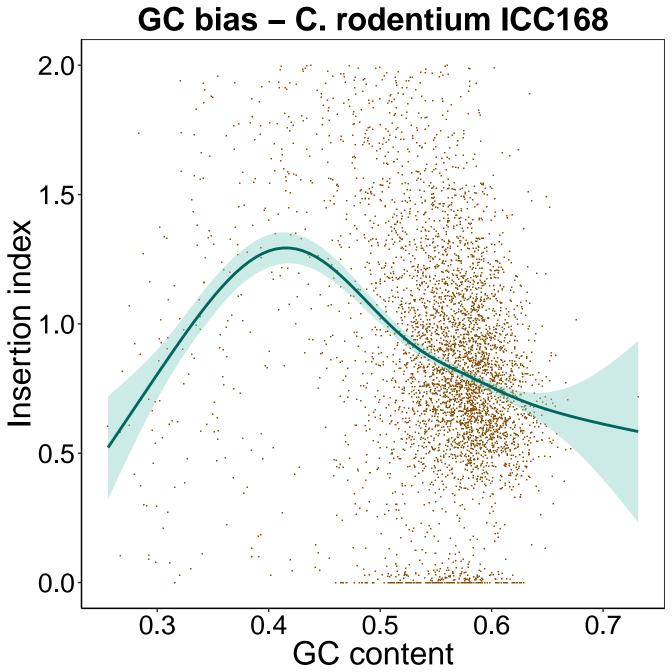
### E. coli UPEC ST131 - normalised GC

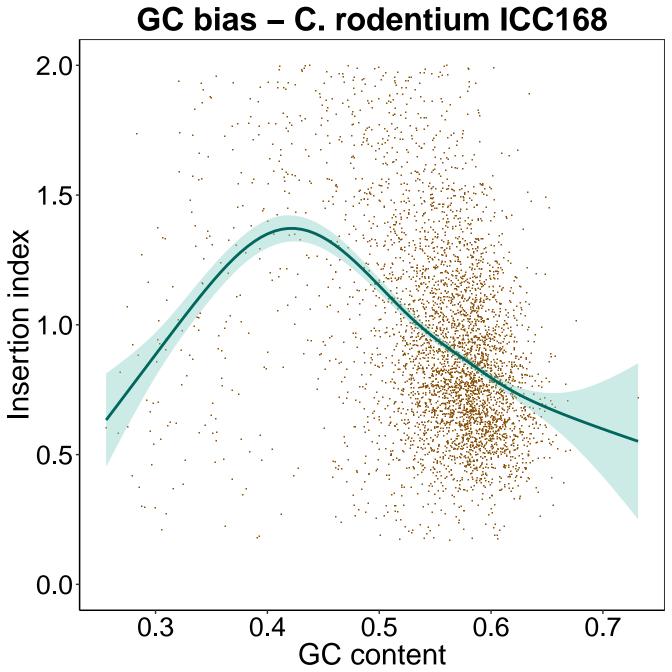




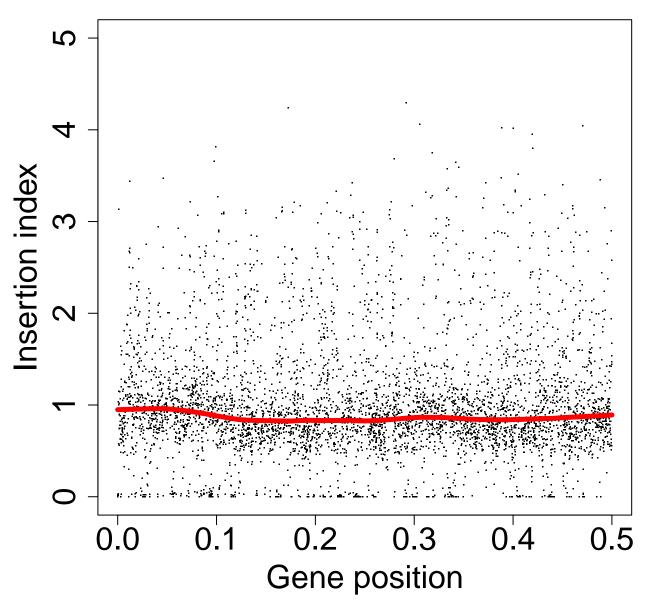
#### Distance bias - C. rodentium ICC168



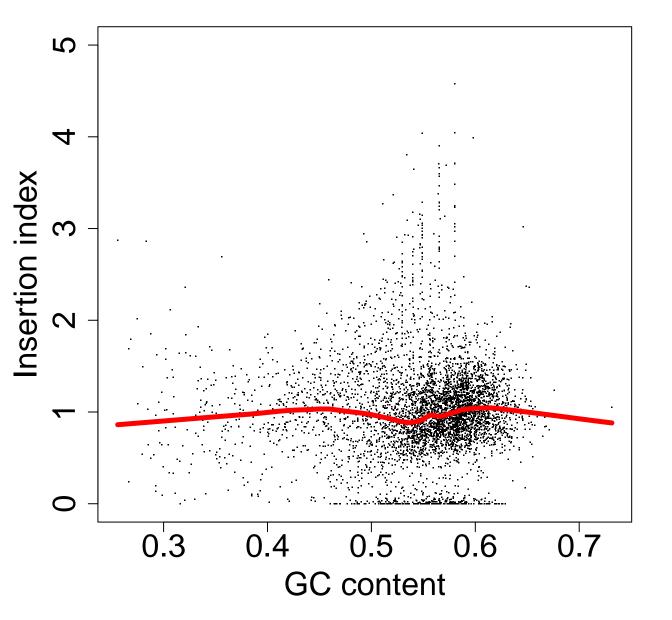


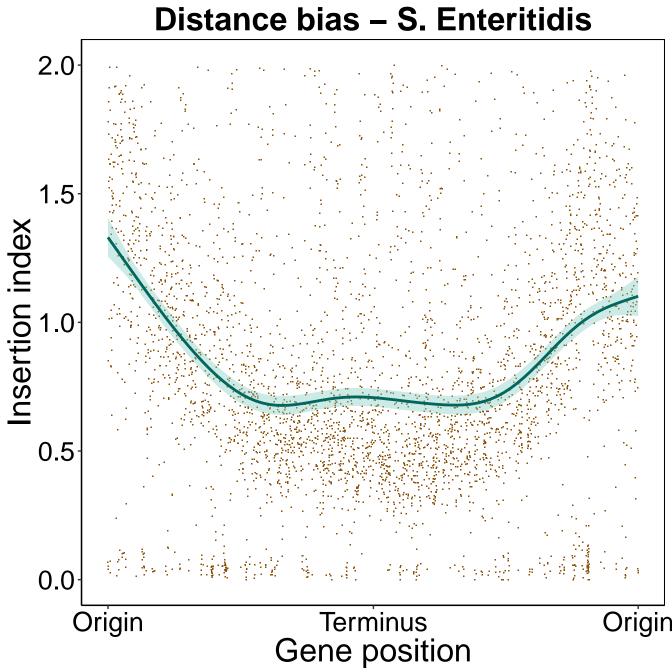


# C. rodentium ICC168 - normalised distance

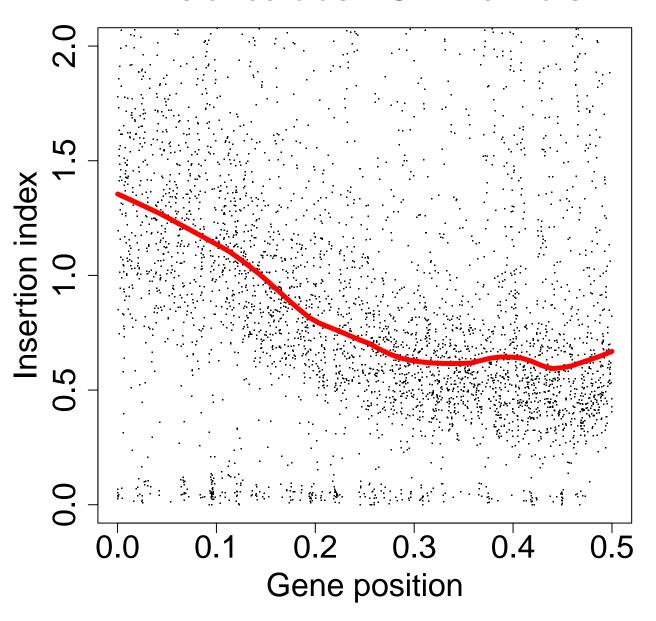


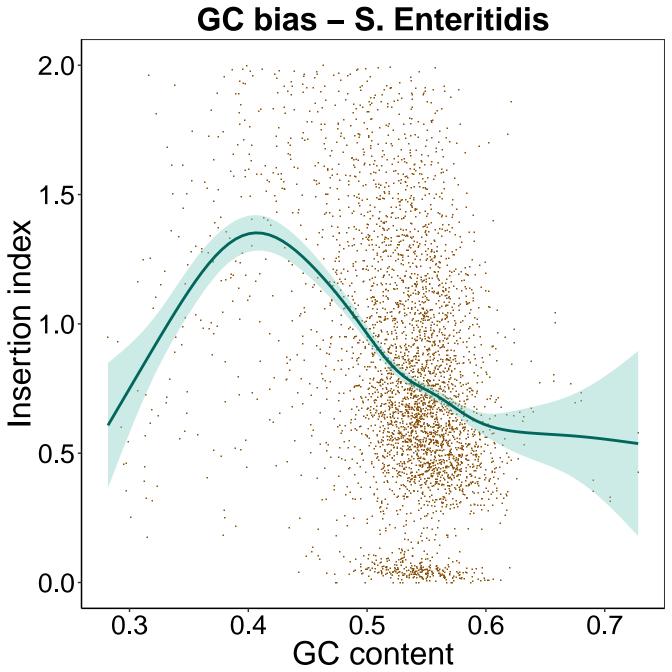
#### C. rodentium ICC168 - normalised GC

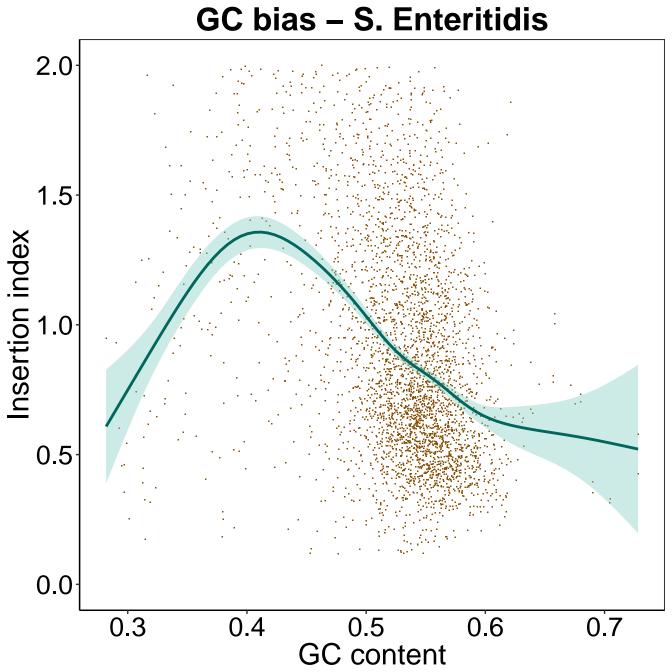




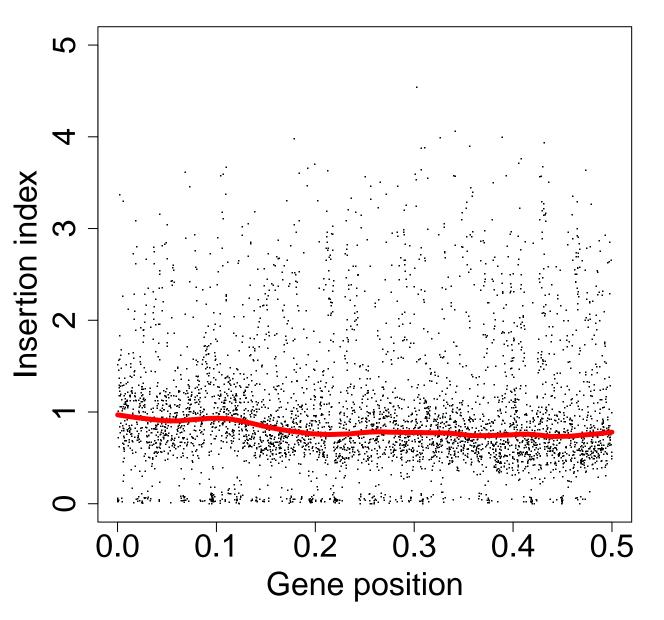
#### Distance bias - S. Enteritidis



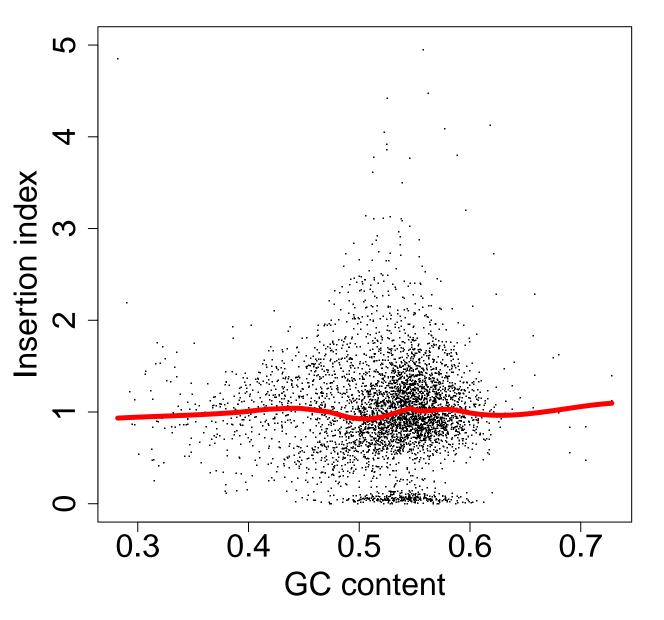




#### S. Enteritidis - normalised distance

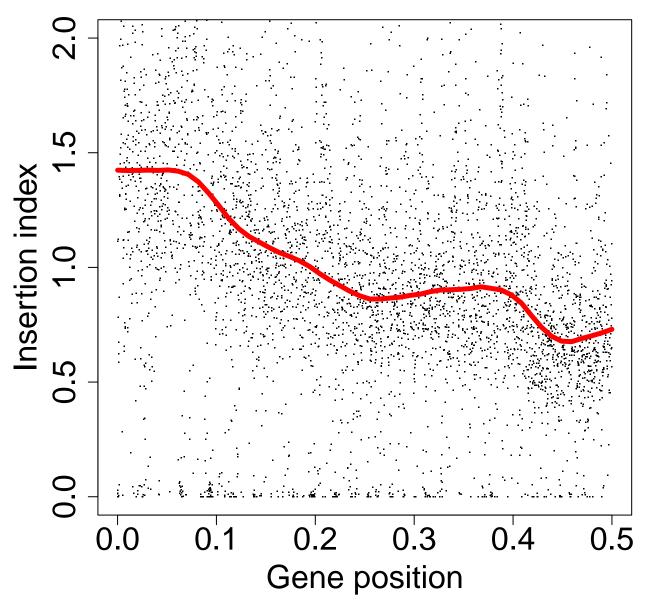


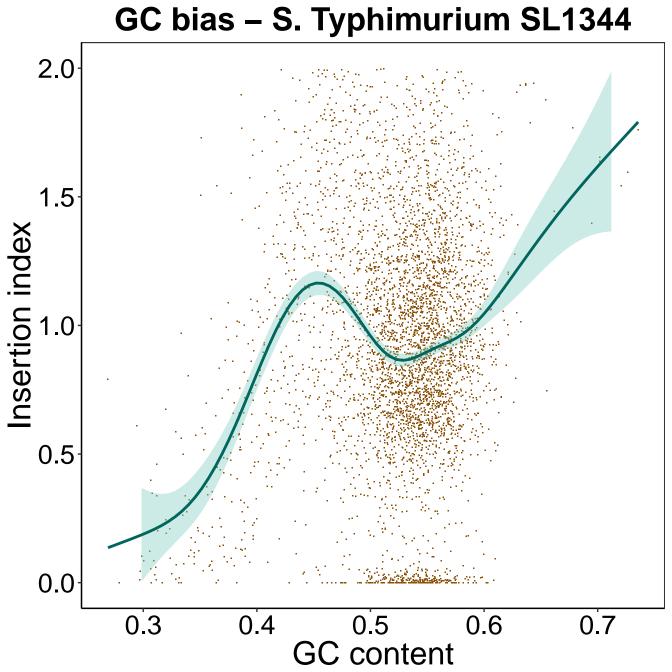
#### S. Enteritidis - normalised GC



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

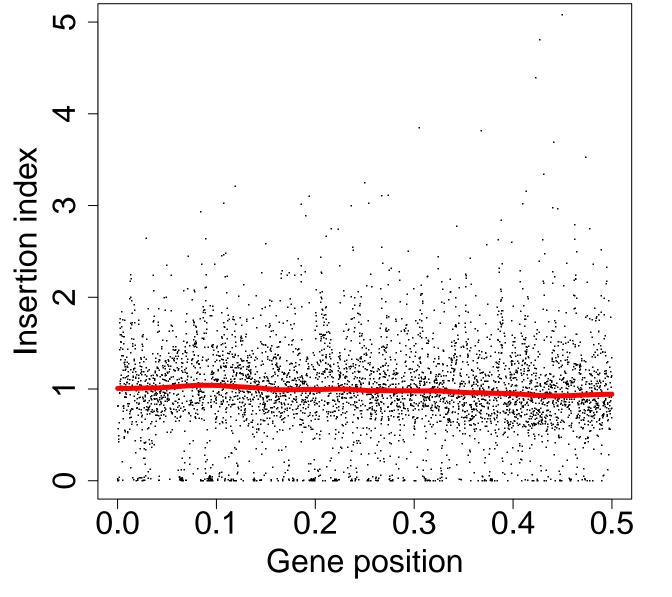
# **Distance bias – S. Typhimurium SL1344**



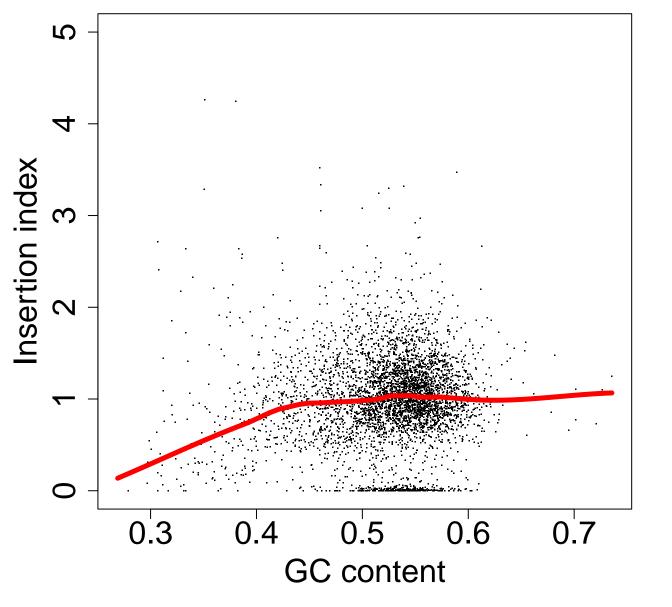


GC bias - S. Typhimurium SL1344 2.0 1.5 Insertion index 1.00 0.5 0.0 0.4 0.6 0.7 0.3 0.5 GC content

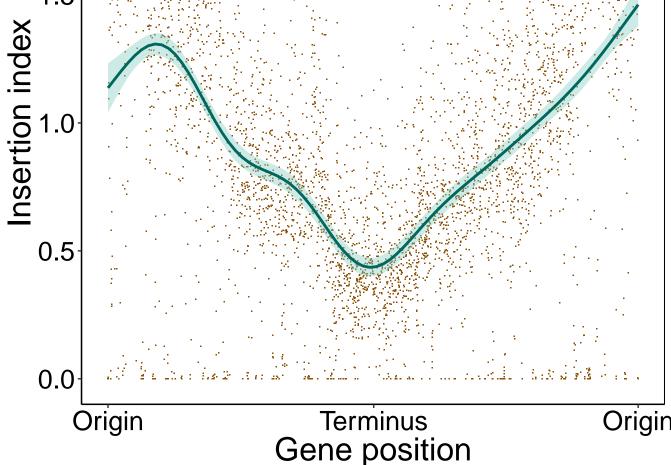
# S. Typhimurium SL1344 – normalised distar



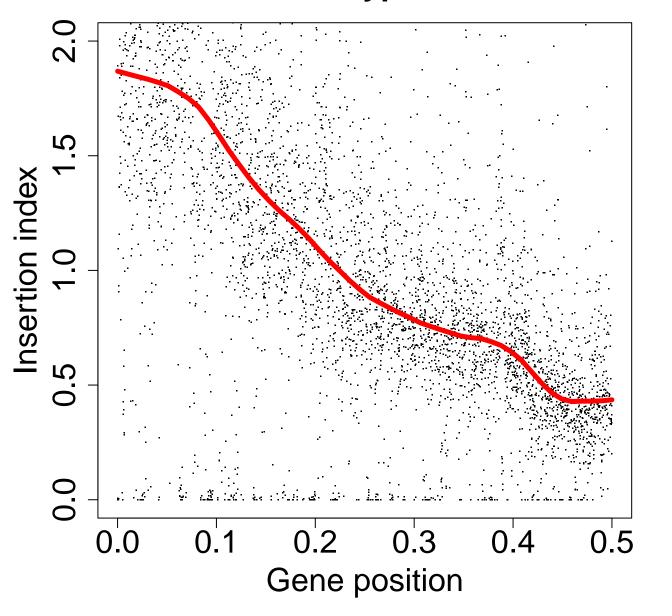
# S. Typhimurium SL1344 – normalised GC



# Distance bias – S. Typhimurium SL3261



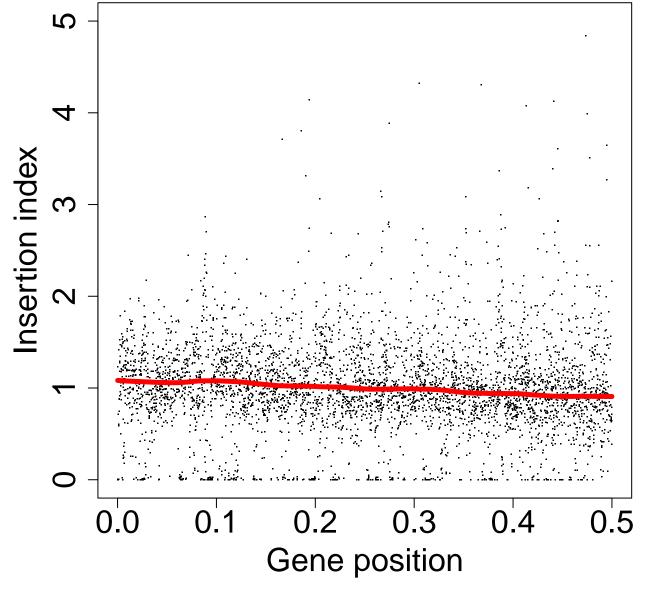
## Distance bias – S. Typhimurium SL3261



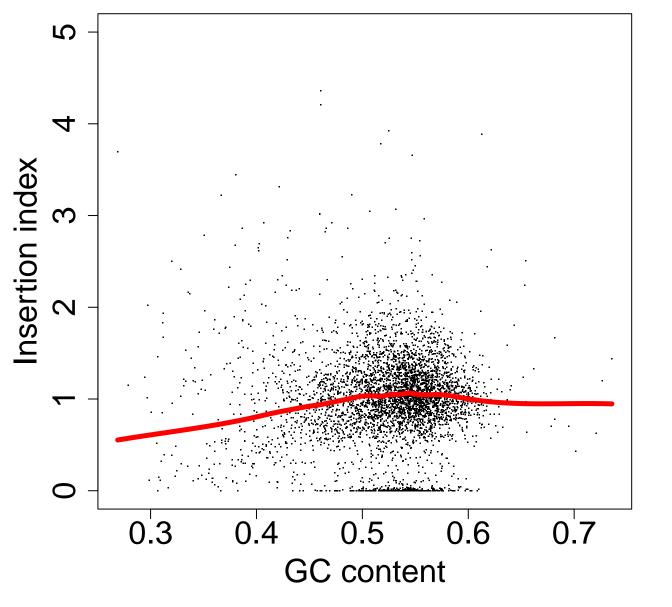
GC bias - S. Typhimurium SL3261 2.0 1.5 Insertion index 0.5 0.0 0.6 0.3 0.4 0.5 0.7 GC content

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



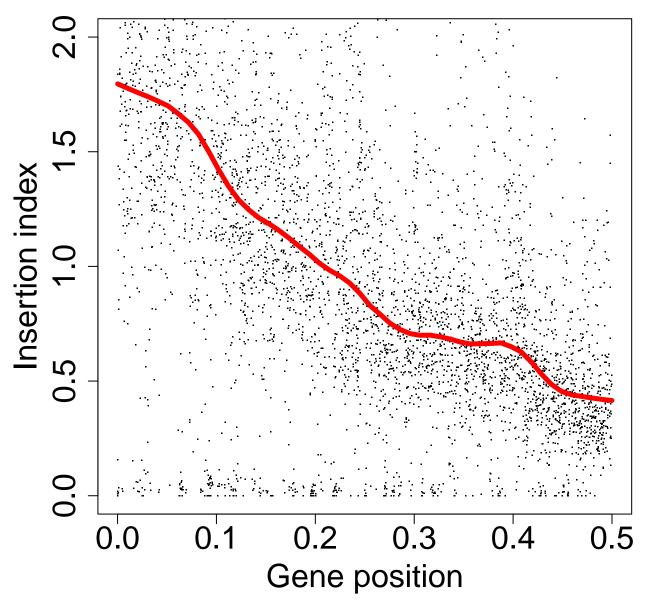
# S. Typhimurium SL3261 – normalised GC



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

Gene position

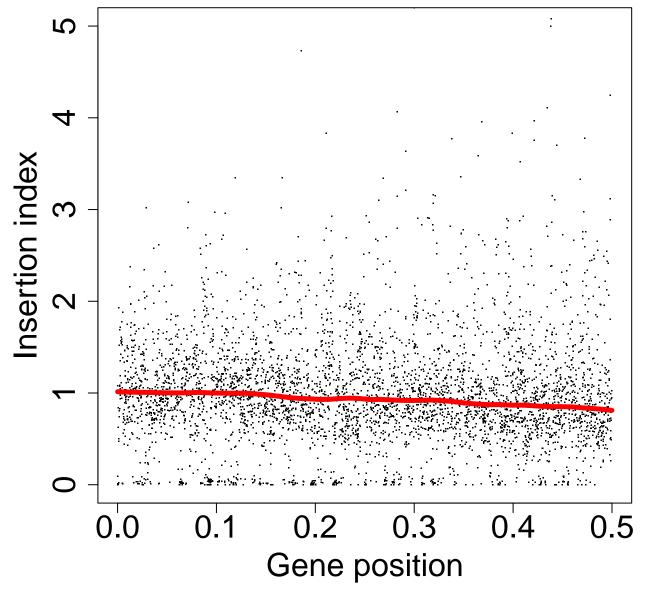
# **Distance bias – S. Typhimurium D23580**



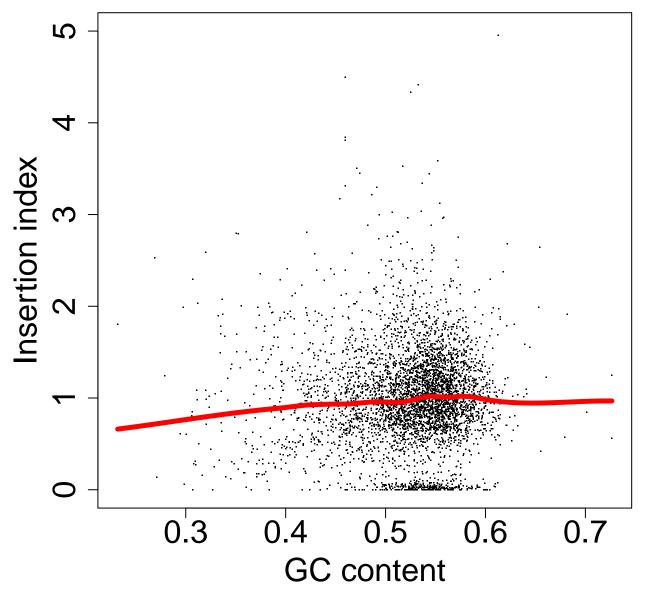
GC bias - S. Typhimurium D23580 2.0 1.5 Insertion index 0.5 0.0 0.3 0.4 0.5 0.6 0.7 GC content

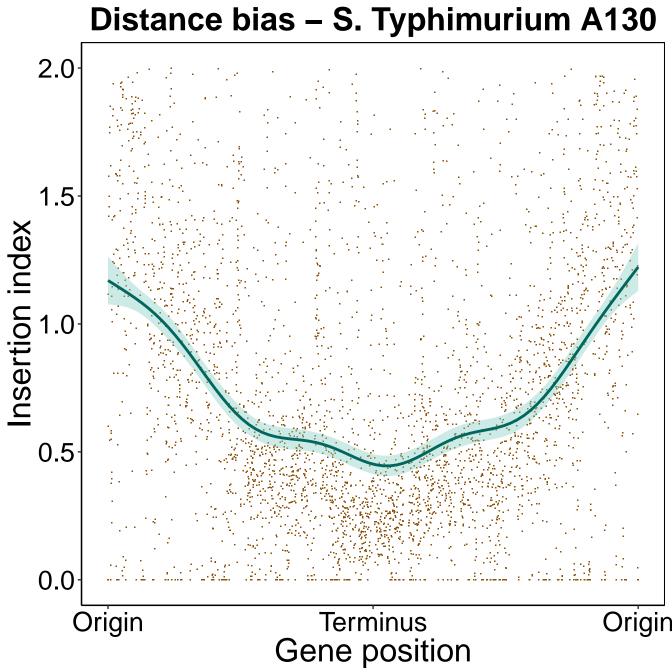
GC bias - S. Typhimurium D23580 2.0 1.5 Insertion index 1.00 0.5 0.0 0.3 0.4 0.5 0.6 0.7 GC content

# S. Typhimurium D23580 – normalised distar

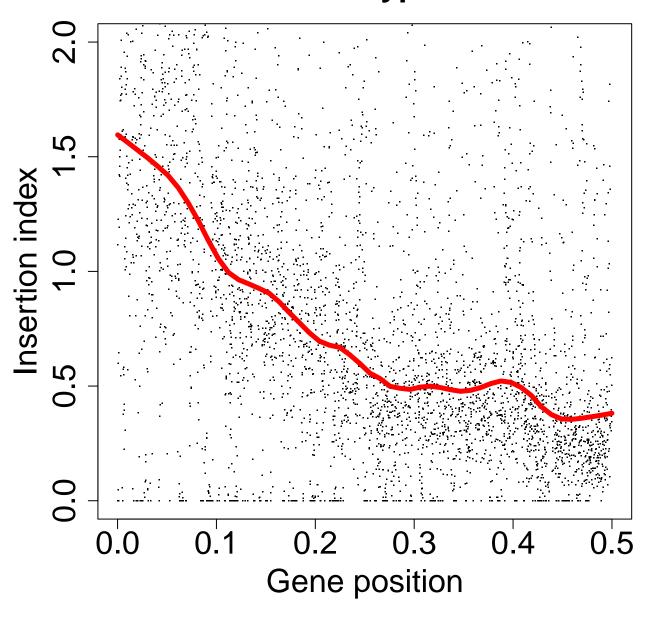


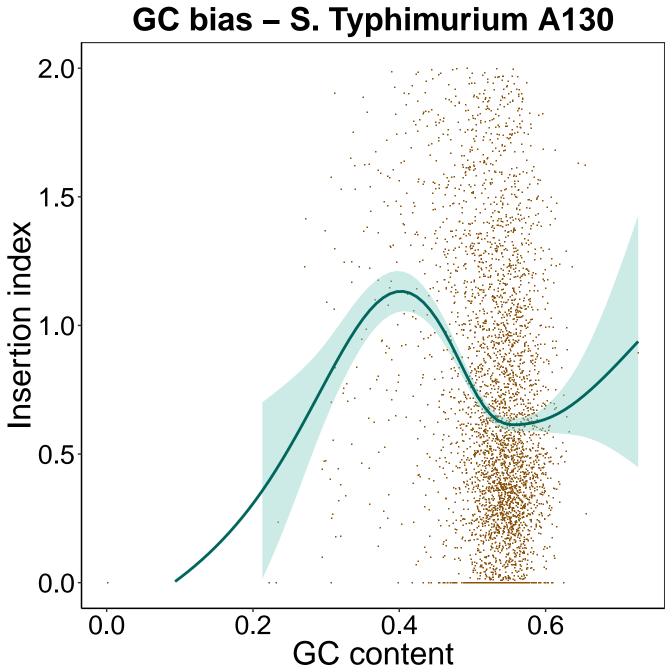
# S. Typhimurium D23580 – normalised GC

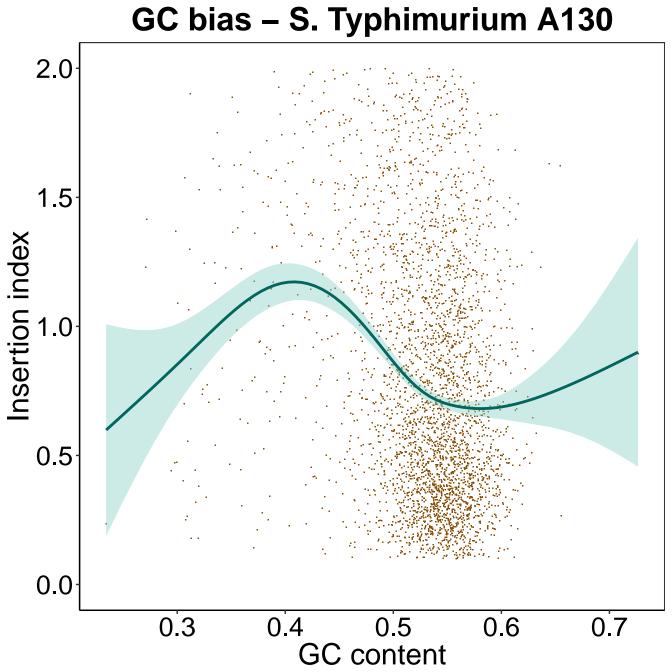




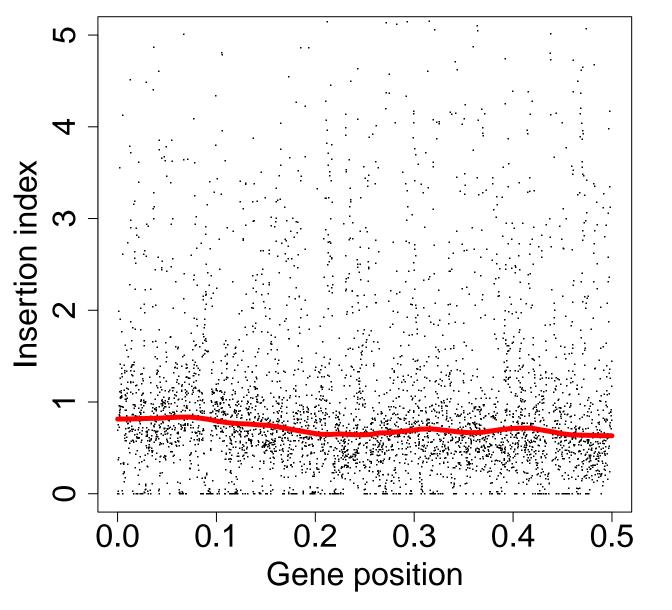
# Distance bias - S. Typhimurium A130



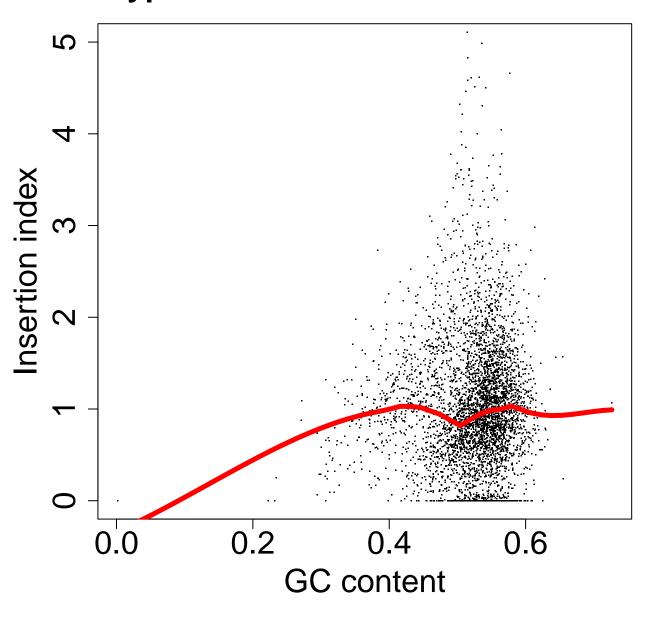


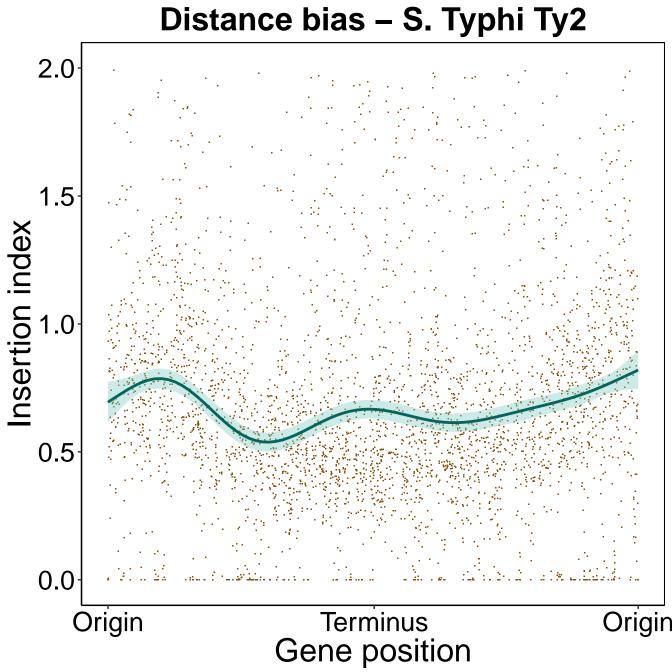


# S. Typhimurium A130 – normalised distance

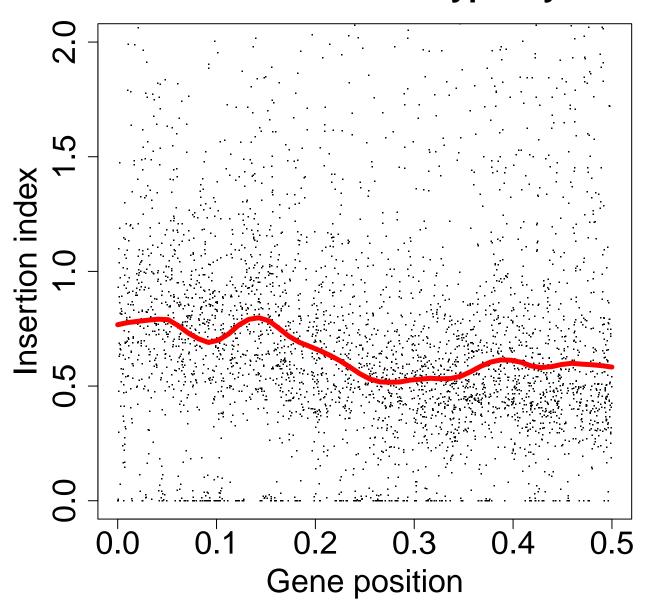


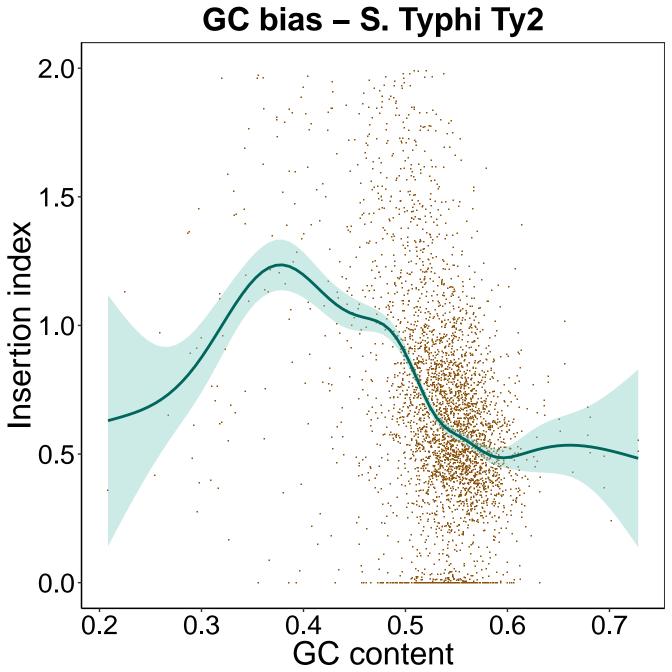
## S. Typhimurium A130 – normalised GC

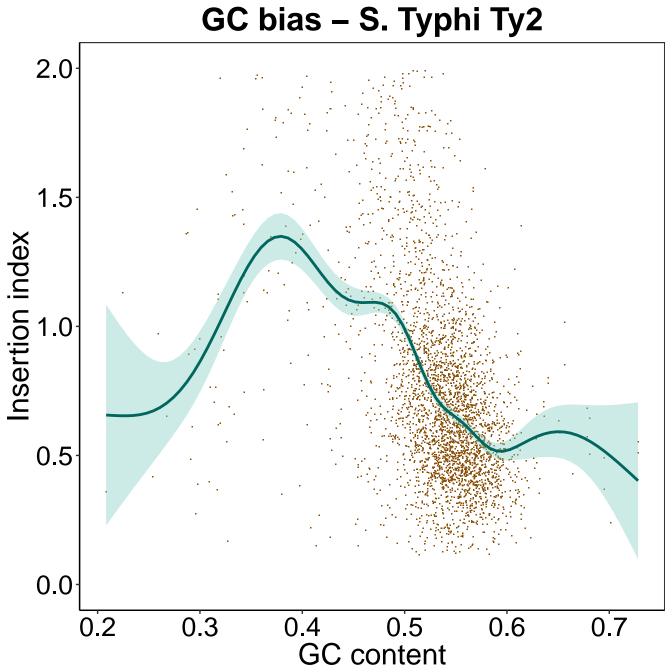




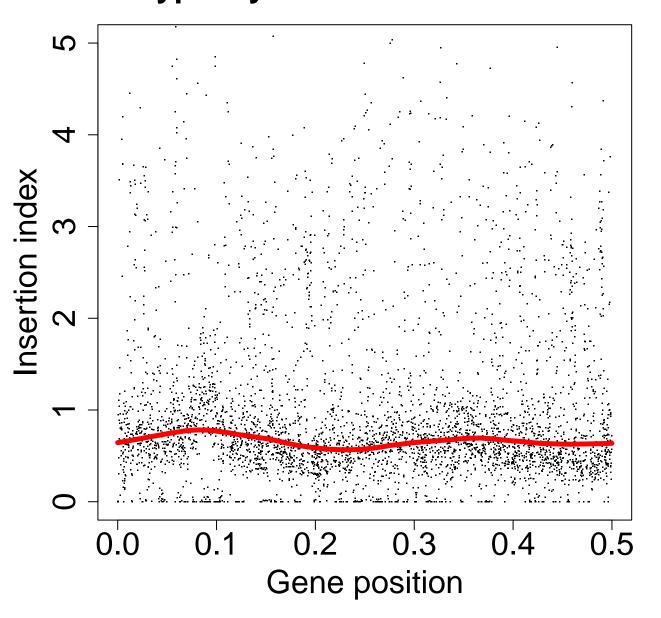
## Distance bias - S. Typhi Ty2



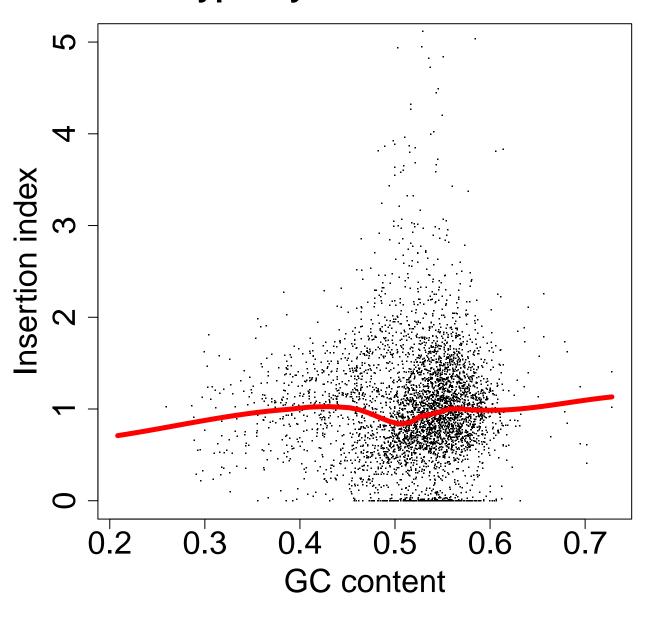




# S. Typhi Ty2 - normalised distance



# S. Typhi Ty2 – normalised GC



#### **GC** bias

