✓ Aug 21: Comprehensive Exam 10:30am

✓ Aug 26: make new list of dates for goals

Sep 4: Have all clustering testing complete for all bacteria

Sep 7: Write Up methods for clustering testing and add to substitutions paper

Sep 9: Gene expression data for the inversions project

Sep 14: Compile notes from comps papers into one document

Sep 30: New intro for Substitution paper

Sep 15-28: Apply for NSERC (if applicable)

Oct 3: NSERC Due

Oct 5-12: Apply for Mac Scholarships and Awards

Oct 31: Write out methods for gene expression paper

Sep 9: Think about/compile list of inversions in *E. coli* for new paper

Nov 15: Think about how to better look at the COG data

Nov 25: Complete any extra analysis needed for Substitution paper

Dec 4: Mac Scholarships and Awards Due

Dec 1: Write out COG methods

Dec 15: Gather papers for COG paper intro

Dec 15: Implement COG stuff

Last Week

I had my comprehensive exam which took up most of the beginning of last week. For the remainder of the week I combined all of the R scripts for the clustering testing which was the last bit that had to be made more automated. This should all run quite quickly from here on out so I am hoping to have that done by the end of the week.

I also made new goals for the next little while (see above) so let me know what you think!

I have also looked into NSERC and below is what I found:

Selection Criteria:

- 30% Academic excellence (transcript, scholarships/awards based on academic excellence)
- 50% Research ability or potential (research proposal, publications, conferences, posters, technical reports, stage of academic career to be considered, not only the number of publication and conferences but also the quality, scholarships/awards based on research ability/potential, researcher attributes (critical thinking, application of knowledge...etc), ability to complete projects within appropriate time)
- 20% Communication, interpersonal and leadership abilities (extracurriculars, professional, academic, awards for reports, posters, teaching, volunteer work, participation in publication writing, quality of presentation of application)

I currently have one paper out that was from work I did as a summer student at SickKids in which I'm second author and did all of the data collection and organization.

I could not find any info on people in the Biology department at Mac that got the NSERC Doctoral award. But I did look up some other awardees from Ontario and their publications range. Some have 2-4 first author pa-

pers accompanied by 3+ non-first author papers. However, there are some recipients who only have 2 first author papers, or 2 non-first author papers.

I trust your opinion so please let me know if you think it is worth it for me to apply!

This Week

I would like to have all of the clustering testing complete for all replicons by the end of this week.

Next Week

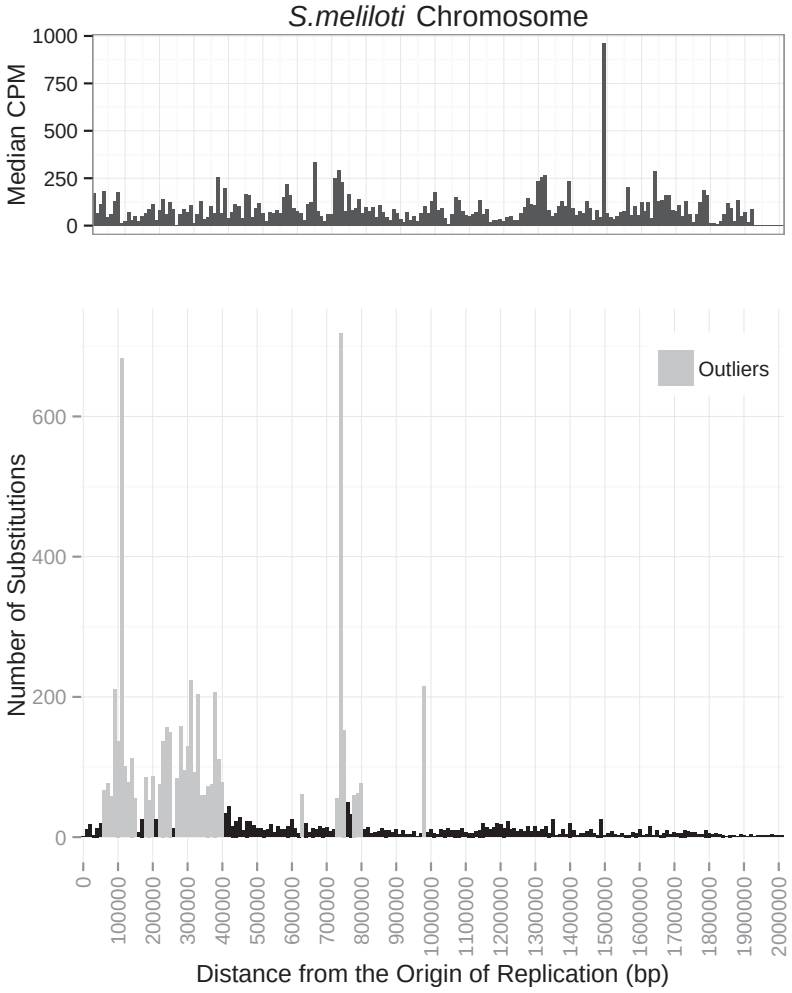
I plan on writing out methods for the clustering analysis and adding this to the substitutions paper. I would also like to go back to gathering gene expression data for the expression and inversions analysis.

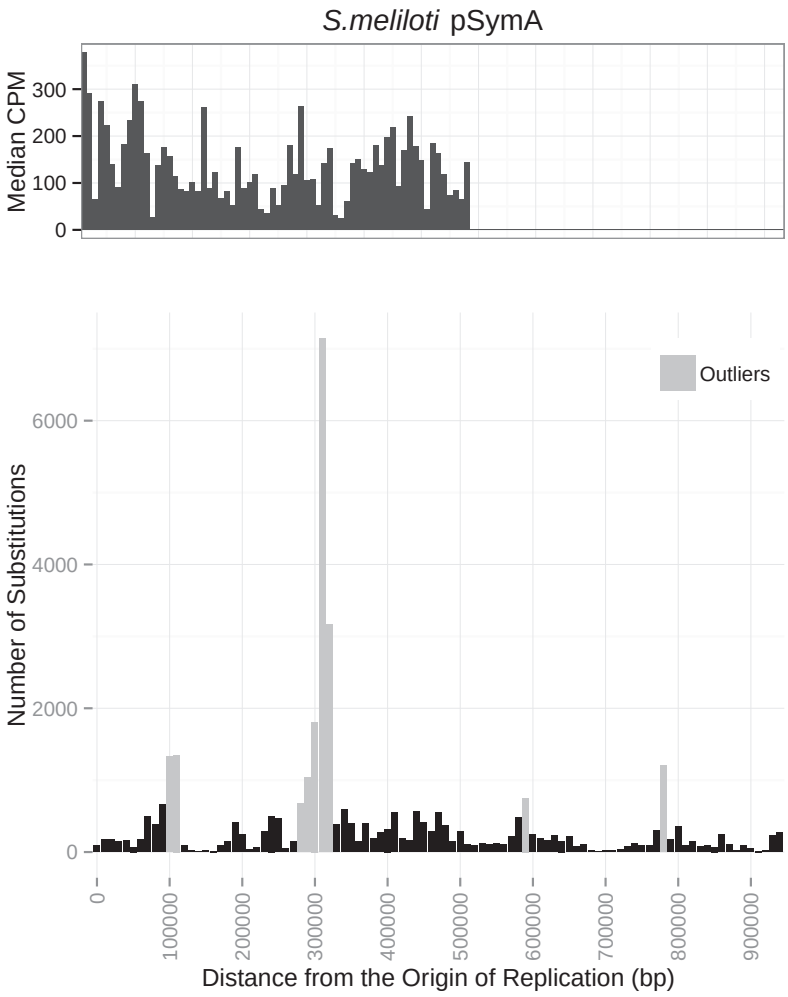
Bacteria and Replicon	Coefficient Estimate	Standard Error	P-value
E. coli Chromosome	-6.41×10^{-5}	1.65×10^{-5}	1.1×10^{-4}
B. subtilis Chromosome	-9.9×10^{-5}	2.18×10^{-5}	6×10^{-6}
Streptomyces Chromosome	-1.5×10^{-6}	1.4×10^{-7}	$<2\times10^{-16}$
S. meliloti Chromosome	3.19×10^{-5}	3.57×10^{-5}	3.7×10^{-1}
S. meliloti pSymA	-5.36×10^{-5}	6.34×10^{-4}	9.33×10^{-1}
S. meliloti pSymB	5.05×10^{-4}	2.6×10^{-4}	5.3×10^{-2}

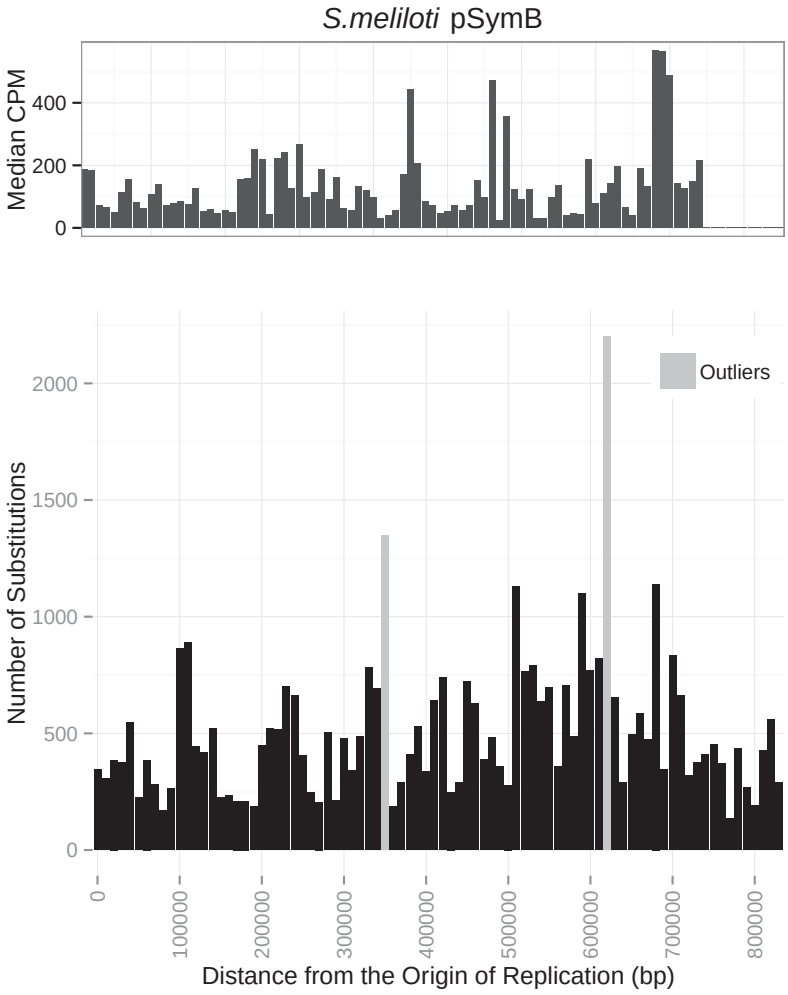
Table 1: Linear regression analysis of the median counts per million expression data along the genome of the respective bacteria replicons. Grey coloured boxes indicate statistically significant results at the 0.5 significance level. Linear regression was calculated after the origin of replication was moved to the beginning of the genome and all subsequent positions were scaled around the origin accounting for bidirectionality of replication.

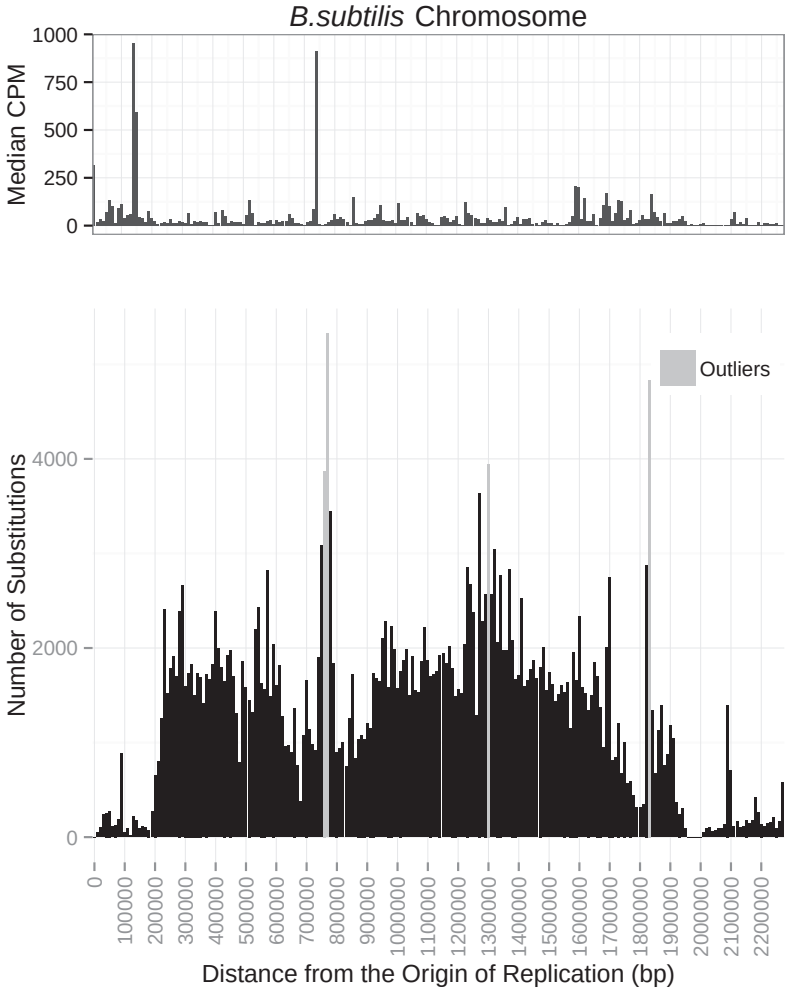
Bacteria and Replicon	Coefficient Estimate	Standard Error	P-value
E. coli Chromosome	-1.394×10^{-7}	2.425×10^{-9}	$<2\times10^{-16}$
B. subtilis Chromosome	-1.265×10^{-8}	1.562×10^{-9}	5.430×10^{-16}
Streptomyces Chromosome	1.736×10^{-8}	7.231×10^{-10}	$<2\times10^{-16}$
S. meliloti Chromosome	-1.541×10^{-6}	3.042×10^{-8}	$<2\times10^{-16}$
S. meliloti pSymA	-9.130×10^{-7}	1.975×10^{-8}	$<2\times10^{-16}$
S. meliloti pSymB	2.488×10^{-7}	1.964×10^{-8}	$<2\times10^{-16}$

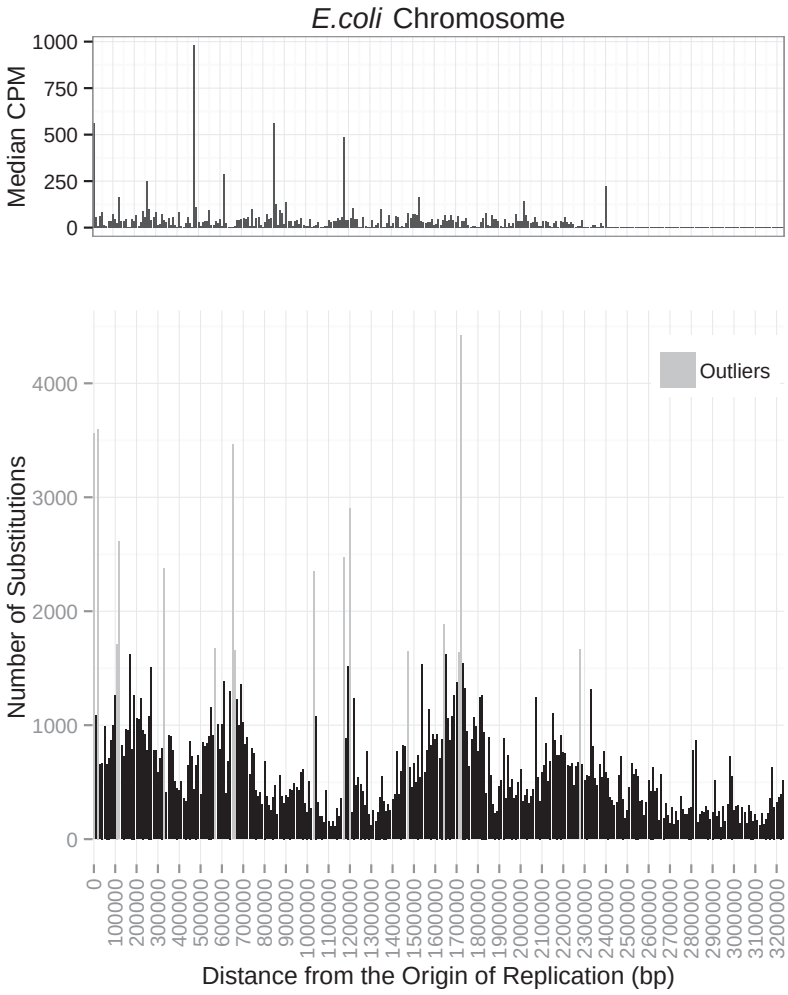
Table 2: Logistic regression analysis of the number of substitutions along the genome of the respective bacteria replicons. Grey coloured boxes indicate a negative logistic regression coefficient estimate. All results are statistically significant. Logistic regression was calculated after the origin of replication was moved to the beginning of the genome and all subsequent positions were scaled around the origin accounting for bidirectionality of replication.

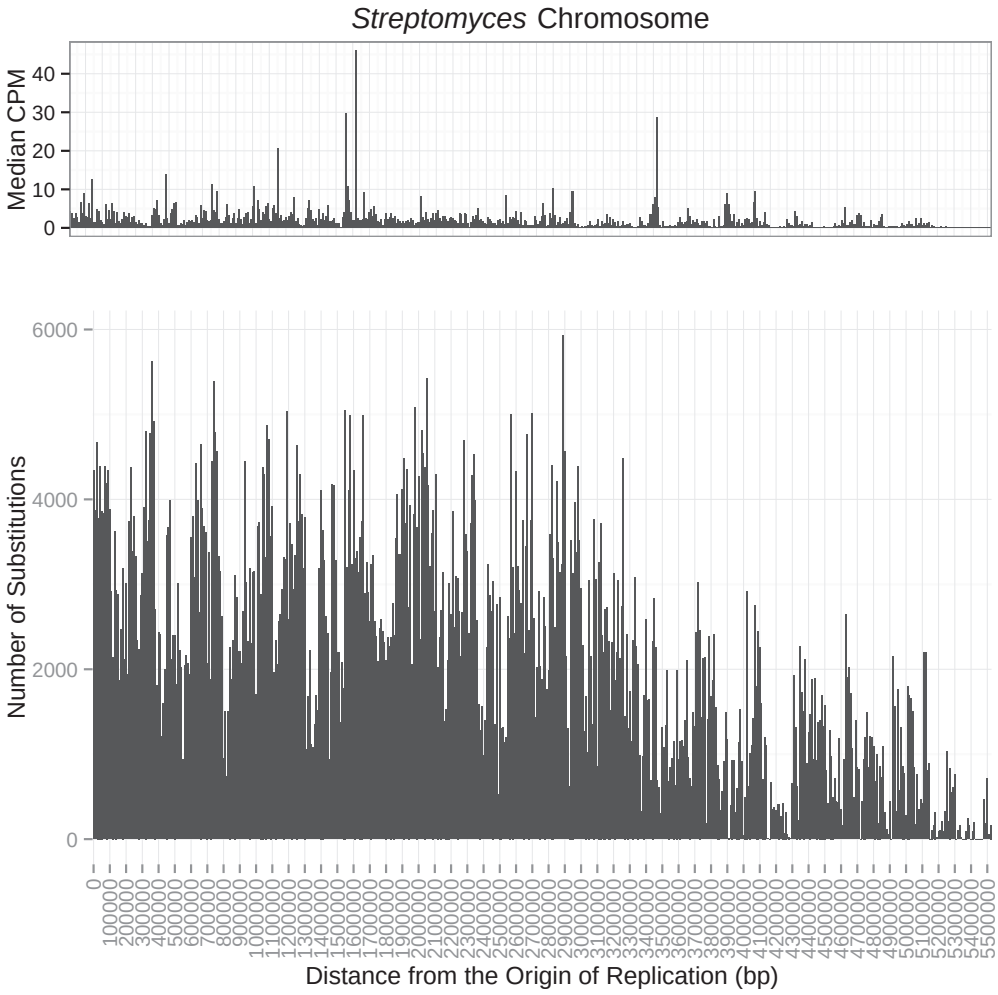

S.meliloti Chromosome
Median CPM
1000
750
500
250
0
Outliers
Number of Substitutions
600
400
200
0
0
100000
200000
300000
400000
500000
600000
700000
800000
900000
1000000
1100000
1200000
1300000
1400000
1500000
1600000
1700000
1800000
1900000
2000000
Distance from the Origin of Replication (bp)


S.meliloti pSymA
Median CPM
300
200
100
0
Outliers
Number of Substitutions
6000
4000
2000
0
0
100000
200000
300000
400000
500000
600000
700000
800000
900000
Distance from the Origin of Replication (bp)


S.meliloti pSymB
Median CPM
400
200
0
Outliers
2000
1500
1000
500
0
Number of Substitutions
0
100000
200000
300000
400000
500000
600000
700000
800000
Distance from the Origin of Replication (bp)


B.subtilis Chromosome
Median CPM
1000
750
500
250
0
Outliers
Number of Substitutions
4000
2000
0
0
100000
200000
300000
400000
500000
600000
700000
800000
900000
1000000
1100000
1200000
1300000
1400000
1500000
1600000
1700000
1800000
1900000
2000000
2100000
2200000
Distance from the Origin of Replication (bp)


E.coli Chromosome
Median CPM
1000
750
500
250
0
Outliers
Number of Substitutions
4000
3000
2000
1000
0
0
100000
200000
300000
400000
500000
600000
700000
800000
900000
1000000
1100000
1200000
1300000
1400000
1500000
1600000
1700000
1800000
1900000
2000000
2100000
2200000
2300000
2400000
2500000
2600000
2700000
2800000
2900000
3000000
3100000
3200000
Distance from the Origin of Replication (bp)


Streptomyces Chromosome
Median CPM
0
10
20
30
40
Number of Substitutions
0
2000
4000
6000
0
100000
200000
300000
400000
500000
600000
700000
800000
900000
1000000
1100000
1200000
1300000
1400000
1500000
1600000
1700000
1800000
1900000
2000000
2100000
2200000
2300000
2400000
2500000
2600000
2700000
2800000
2900000
3000000
3100000
3200000
3300000
3400000
3500000
3600000
3700000
3800000
3900000
4000000
4100000
4200000
4300000
4400000
4500000
4600000
4700000
4800000
4900000
5000000
5100000
5200000
5300000
5400000
5500000
Distance from the Origin of Replication (bp)

Origin Location	*E. coli* Chromosome	*B. subtilis* Chromosome	*Streptomyces* Chromosome	*S. meliloti* Chromosome	*S. meliloti* pSymA	*S. meliloti* pSymB
Moved 100kb Left	$-1.445\times10^{-7***}$	$4.374\times10^{-9*}$	$6.909\times10^{-9***}$	$-1.316\times10^{-6***}$	$-1.058\times10^{-6***}$	$-2.009\times10^{-7***}$
Moved 90kb Left	$-1.544\times10^{-7***}$	$-1.036\times10^{-7***}$	$5.677\times10^{-9***}$	$-1.32\times10^{-6***}$	$-1.246\times10^{-6***}$	$-1.357\times10^{-7***}$
Moved 80kb Left	$-1.65\times10^{-7***}$	$-1.072\times10^{-7***}$	$8.11\times10^{-9***}$	$-1.338\times10^{-6***}$	$-1.398\times10^{-6***}$	$-6.57\times10^{-8***}$
Moved 70kb Left	$-1.667\times10^{-7***}$	$-1.102\times10^{-7***}$	$6.716\times10^{-9***}$	$-1.363\times10^{-6***}$	$-1.405\times10^{-6***}$	9.83×10^{-8}
Moved 60kb Left	$-1.64\times10^{-7***}$	$-1.19\times10^{-7***}$	$8.7\times10^{-9***}$	$-1.324\times10^{-6***}$	$-1.394\times10^{-6***}$	$1.129\times10^{-7***}$
Moved 50kb Left	$-1.446\times10^{-7***}$	$-1.211\times10^{-7***}$	$1.045\times10^{-8***}$	$-1.36\times10^{-6***}$	$-1.403\times10^{-6***}$	$1.521\times10^{-7***}$
Moved 40kb Left	$-1.4\times10^{-7***}$	$-1.299\times10^{-7***}$	$1.214\times10^{-8***}$	$-1.255\times10^{-6***}$	$-1.422\times10^{-6***}$	$1.543\times10^{-7***}$
Moved 30kb Left	$-1.498\times10^{-7***}$	$-1.292\times10^{-7***}$	$1.24\times10^{-8***}$	$-1.26\times10^{-6***}$	$-1.392\times10^{-6***}$	$1.63\times10^{-7***}$
Moved 20kb Left	$-1.51\times10^{-7***}$	$-1.1\times10^{-7***}$	$1.395\times10^{-8***}$	$-1.525\times10^{-6***}$	$-1.412\times10^{-6***}$	$1.603\times10^{-7***}$
Moved 10kb Left	$-1.262\times10^{-7***}$	-2.602×10^{-9}	$1.563\times10^{-8***}$	$-1.599\times10^{-6***}$	$-9.499\times10^{-7***}$	$2.973\times10^{-7***}$
Moved 10kb Right	$-1.305\times10^{-7***}$	$-2.045\times10^{-8***}$	$1.578\times10^{-8***}$	$1.614\times10^{-6***}$	$-1.026\times10^{-6***}$	$3.505\times10^{-7***}$
Moved 20kb Right	$-1.454\times10^{-7***}$	$-1.006\times10^{-7***}$	$1.903\times10^{-8***}$	$-1.634\times10^{-6***}$	$-1.475\times10^{-6***}$	$1.649\times10^{-7***}$
Moved 30kb Right	$-1.548\times10^{-7***}$	$-8.596\times10^{-8***}$	$2.046\times10^{-8***}$	$-1.698\times10^{-6***}$	$-1.417\times10^{-6***}$	$1.526\times10^{-7***}$
Moved 40kb Right	$-1.632\times10^{-7***}$	$-8.378\times10^{-8***}$	$2.125\times10^{-8***}$	$-1.719\times10^{-6***}$	$-1.367\times10^{-6***}$	$1.589\times10^{-7***}$
Moved 50kb Right	$-1.856\times10^{-7***}$	$-7.879\times10^{-8***}$	$1.957\times10^{-8***}$	$-1.735\times10^{-6***}$	$-1.277\times10^{-6***}$	$1.654\times10^{-7***}$
Moved 60kb Right	$-1.91\times10^{-7***}$	$-6.98\times10^{-8***}$	$1.974\times10^{-8***}$	$-1.788\times10^{-6***}$	$-1.169\times10^{-6***}$	$1.645\times10^{-7***}$
Moved 70kb Right	$-1.892\times10^{-7***}$	$-6.634\times10^{-8***}$	$1.934\times10^{-8***}$	$-1.854\times10^{-6***}$	$-1.059\times10^{-6***}$	$1.843\times10^{-7***}$
Moved 80kb Right	$-1.879\times10^{-7**}$	$-5.814\times10^{-8***}$	$2.313\times10^{-8***}$	$-1.891\times10^{-6***}$	$-9.07\times10^{-7***}$	$1.90\times10^{-7***}$
Moved 90kb Right	$-1.862\times10^{-7***}$	$-4.314\times10^{-8***}$	$2.304\times10^{-8***}$	$-1.865\times10^{-6***}$	$-7.171\times10^{-7***}$	$2.415\times10^{-7***}$
Moved 100kb Right	$-1.799\times10^{-7***}$	$-2.597\times10^{-8***}$	$1.945\times10^{-8***}$	$-1.525\times10^{-6***}$	$-6.572\times10^{-7***}$	$3.095\times10^{-7***}$

Table 3: Logistic regression analysis of the number of substitutions along the genome of the respective bacteria replicons. All results are marked with significance codes as followed: < 0.001 = '***', $0.001 < 0.01$ = '**', $0.01 < 0.05$ = '*', $0.05 < 0.1$ = '.', > 0.1 = ' '. Logistic regression was calculated after the origin of replication was moved to the beginning of the genome and all subsequent positions were scaled around the origin accounting for bidirectionality of replication.