

# Report of *Agrobacterium tumefaciens* in T11.1.1

## Mapping stats of Illumina reads

21625023 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

9707 + 0 supplementary

0 + 0 duplicates

21574840 + 0 mapped (99.77% : N/A)

21615316 + 0 paired in sequencing

10807658 + 0 read1

10807658 + 0 read2

21469466 + 0 properly paired (99.33% : N/A)

21556000 + 0 with itself and mate mapped

9133 + 0 singletons (0.04% : N/A)

37962 + 0 with mate mapped to a different chr

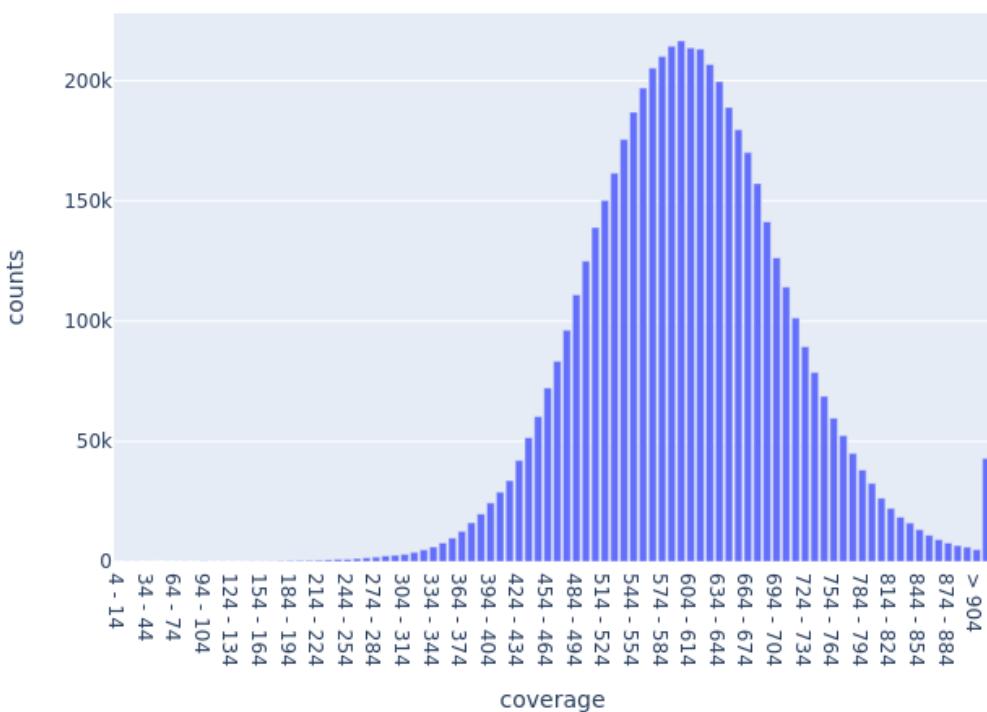
36743 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 606.4909256663539

Agrobacterium tumefaciens in T11.1.1

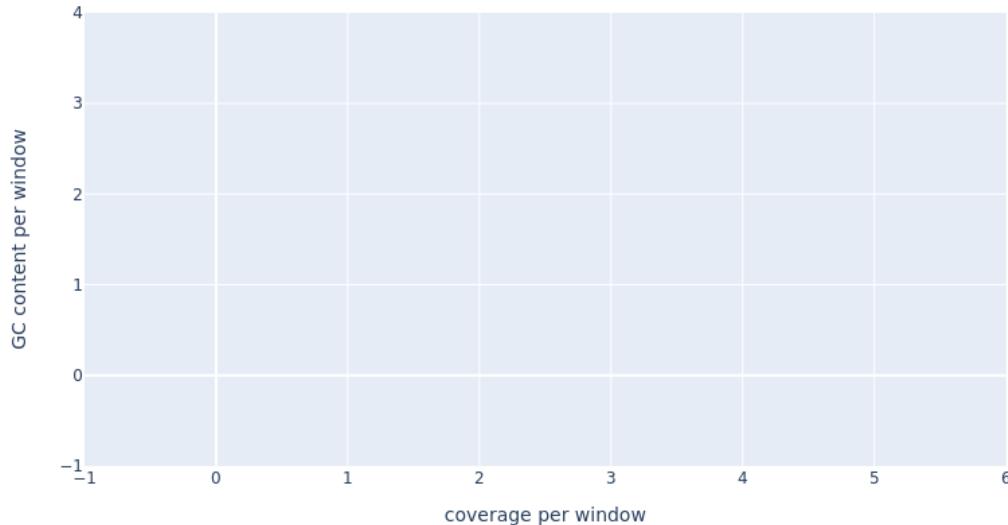


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T11.1.1



# Report of *Agrobacterium tumefaciens* in T11.1.2

## Mapping stats of Illumina reads

20369109 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

8587 + 0 supplementary

0 + 0 duplicates

20326150 + 0 mapped (99.79% : N/A)

20360522 + 0 paired in sequencing

10180261 + 0 read1

10180261 + 0 read2

20202802 + 0 properly paired (99.23% : N/A)

20308160 + 0 with itself and mate mapped

9403 + 0 singletons (0.05% : N/A)

52448 + 0 with mate mapped to a different chr

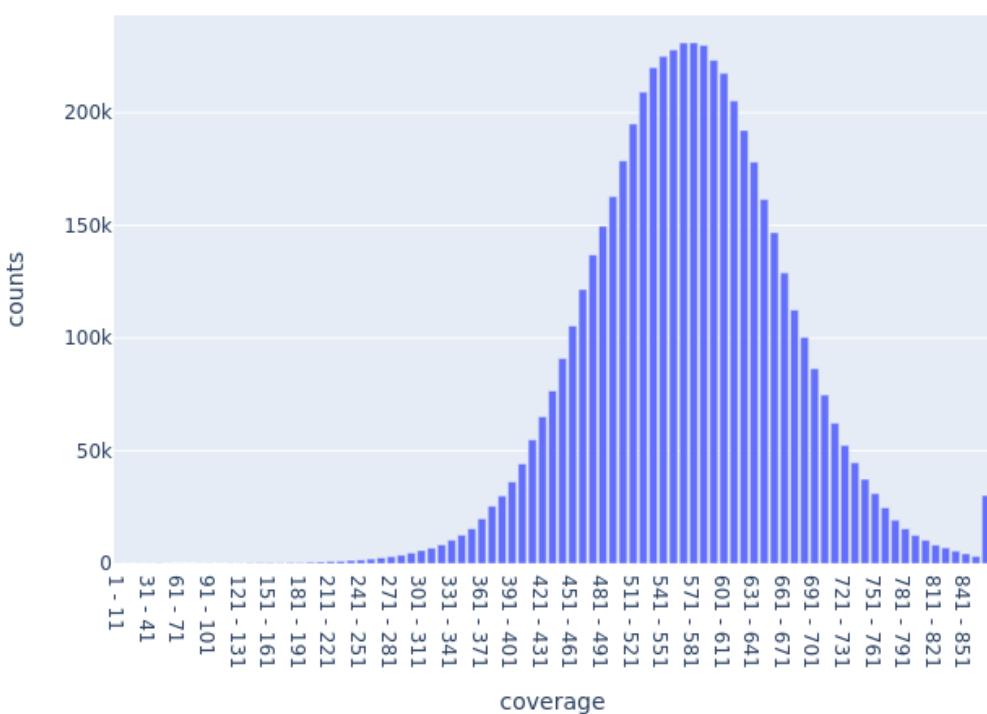
50886 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 571.2777954461277

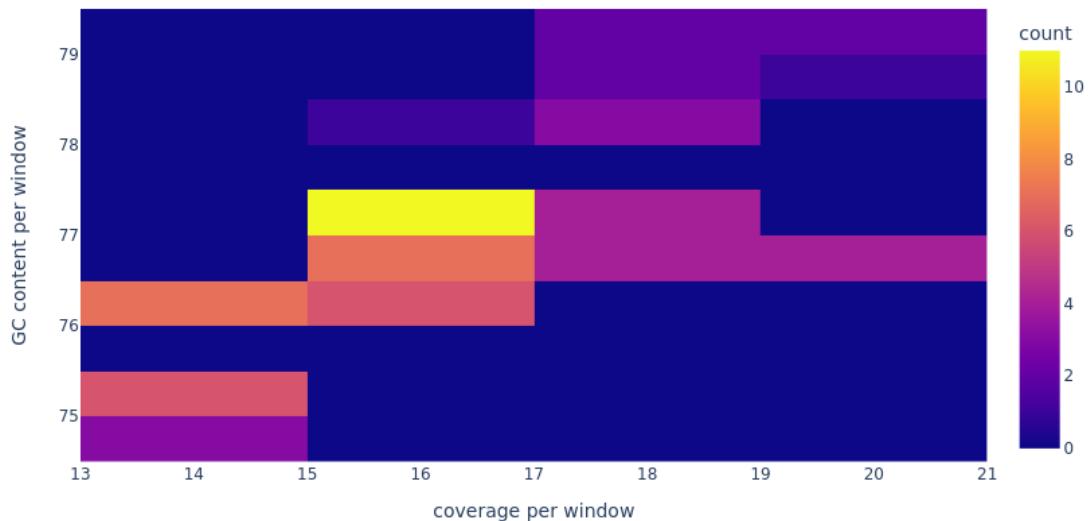
Agrobacterium tumefaciens in T11.1.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T11.1.2



# Report of Comamonas testosterone in T11.2.1

## Mapping stats of Illumina reads

18418345 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

53 + 0 supplementary

0 + 0 duplicates

797480 + 0 mapped (4.33% : N/A)

18418292 + 0 paired in sequencing

9209146 + 0 read1

9209146 + 0 read2

768134 + 0 properly paired (4.17% : N/A)

768826 + 0 with itself and mate mapped

28601 + 0 singletons (0.16% : N/A)

22 + 0 with mate mapped to a different chr

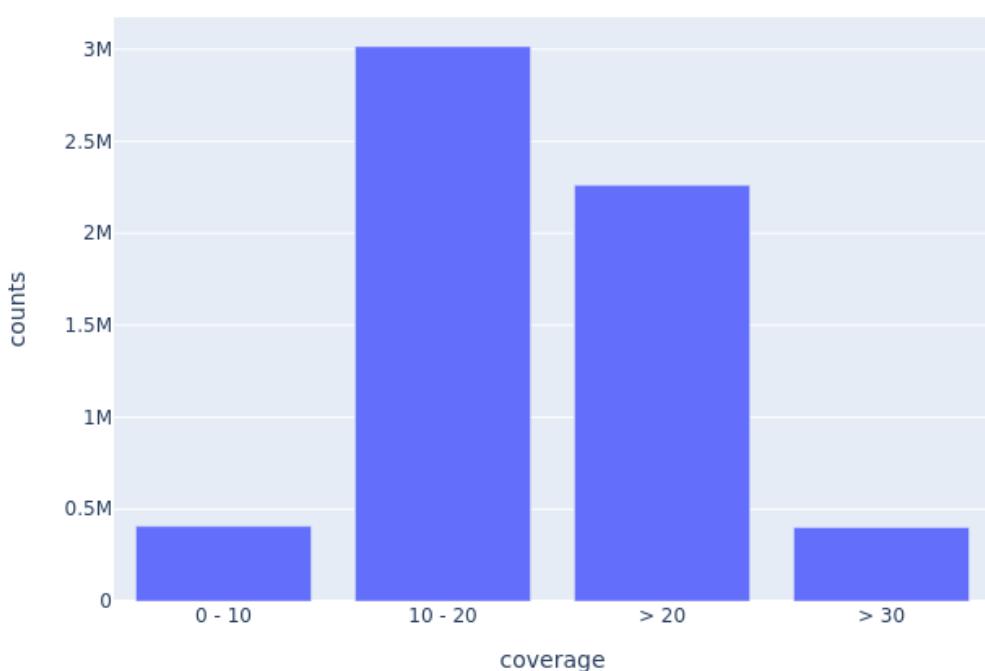
20 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 19.29465759186088

Comamonas testosterone in T11.2.1

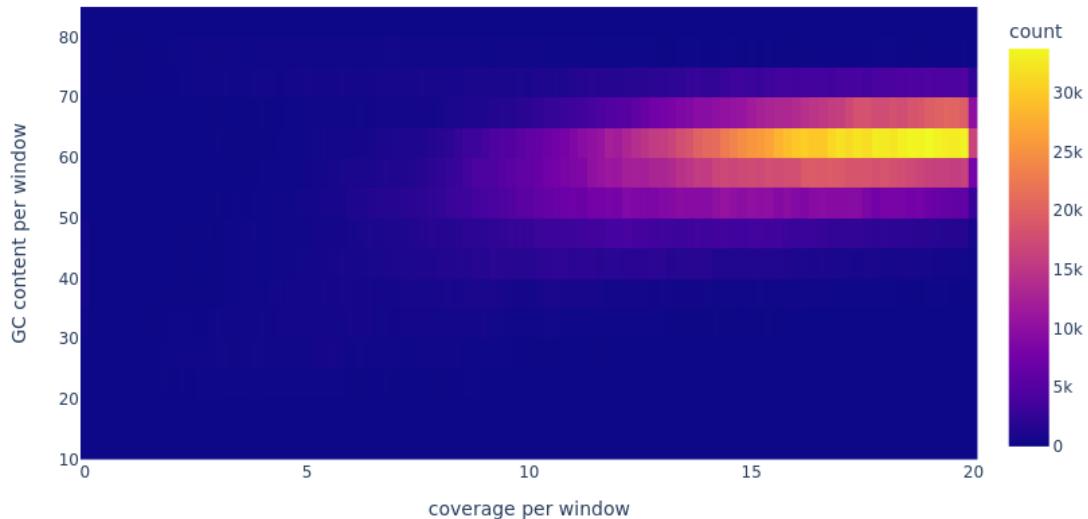


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.2.1



# Report of *Comamonas testosteronei* in T11.2.2.rep

## Mapping stats of Illumina reads

19797657 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

6207 + 0 supplementary

0 + 0 duplicates

19735902 + 0 mapped (99.69% : N/A)

19791450 + 0 paired in sequencing

9895725 + 0 read1

9895725 + 0 read2

19636778 + 0 properly paired (99.22% : N/A)

19721028 + 0 with itself and mate mapped

8667 + 0 singletons (0.04% : N/A)

4770 + 0 with mate mapped to a different chr

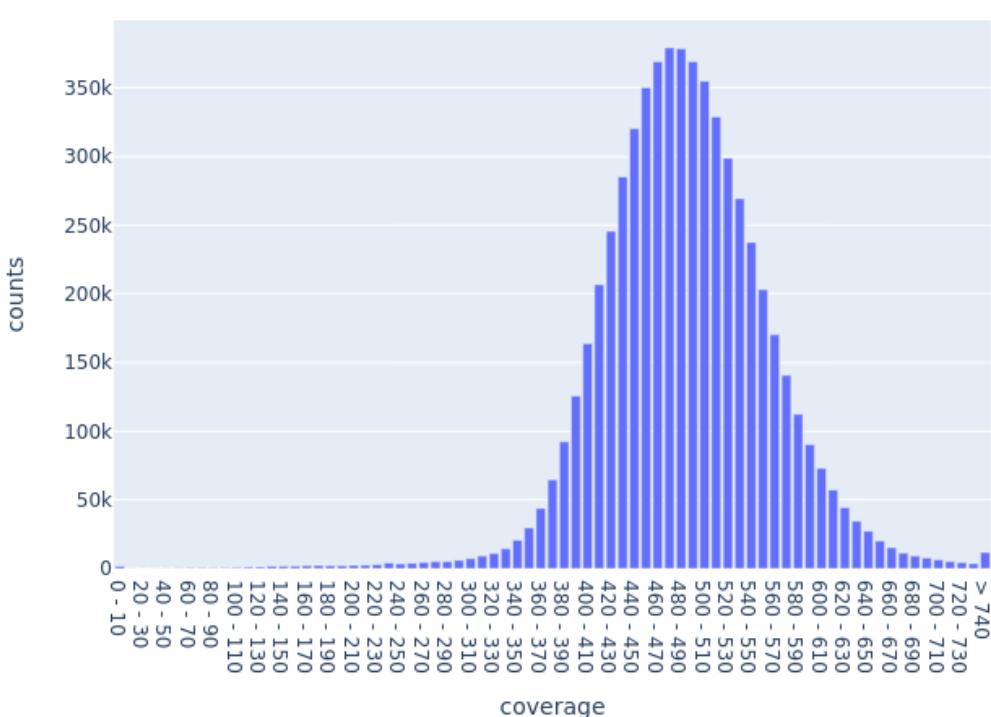
4570 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 487.75044766189416

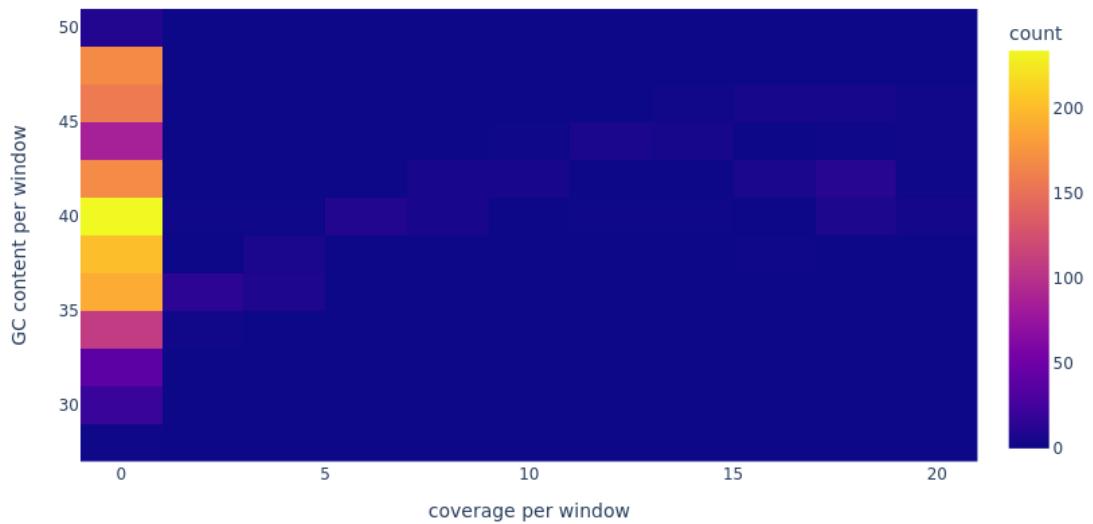
Comamonas testosteronei in T11.2.2.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.2.2.rep



# Report of Comamonas testosterone in T11.2.3

## Mapping stats of Illumina reads

21134068 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

86 + 0 supplementary

0 + 0 duplicates

879188 + 0 mapped (4.16% : N/A)

21133982 + 0 paired in sequencing

10566991 + 0 read1

10566991 + 0 read2

844588 + 0 properly paired (4.00% : N/A)

845404 + 0 with itself and mate mapped

33698 + 0 singletons (0.16% : N/A)

10 + 0 with mate mapped to a different chr

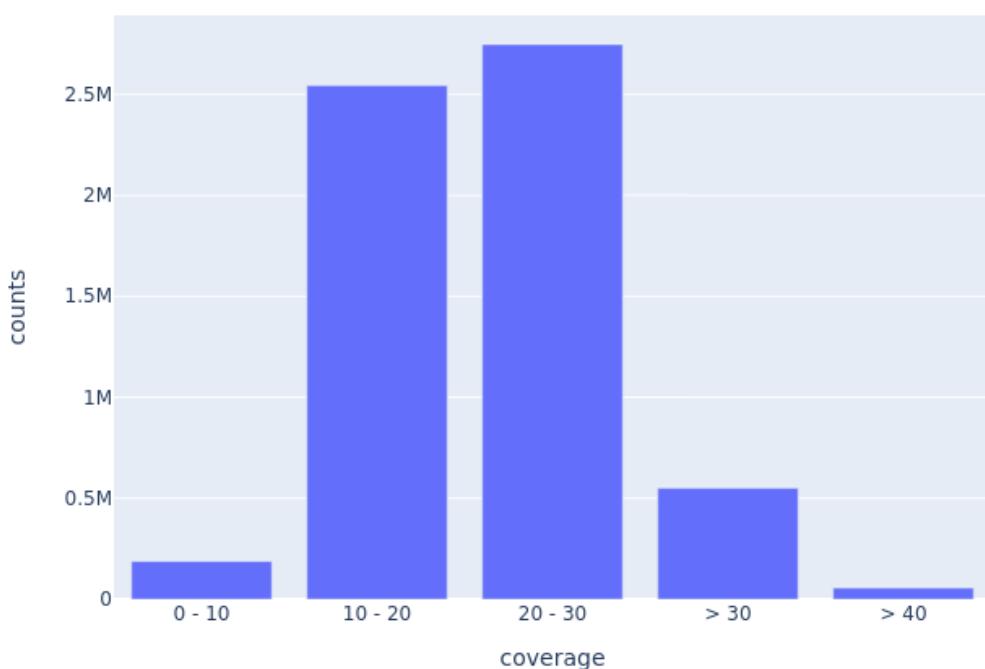
9 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 21.234067468708044

Comamonas testosterone in T11.2.3

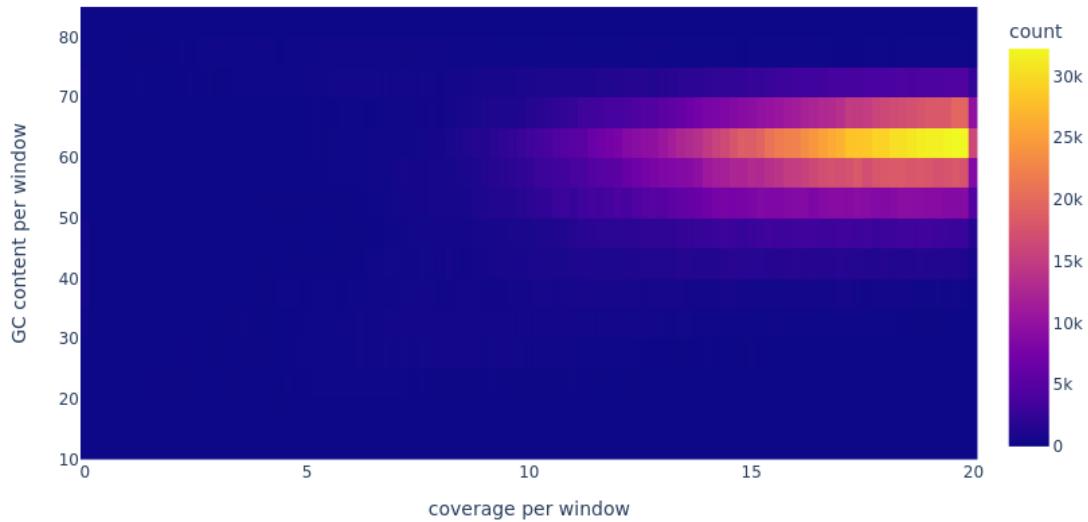


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.2.3



# Report of *Comamonas testosteronei* in T11.2.4.rep

## Mapping stats of Illumina reads

17865444 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

10130 + 0 supplementary

0 + 0 duplicates

17762106 + 0 mapped (99.42% : N/A)

17855314 + 0 paired in sequencing

8927657 + 0 read1

8927657 + 0 read2

17699828 + 0 properly paired (99.13% : N/A)

17744892 + 0 with itself and mate mapped

7084 + 0 singletons (0.04% : N/A)

892 + 0 with mate mapped to a different chr

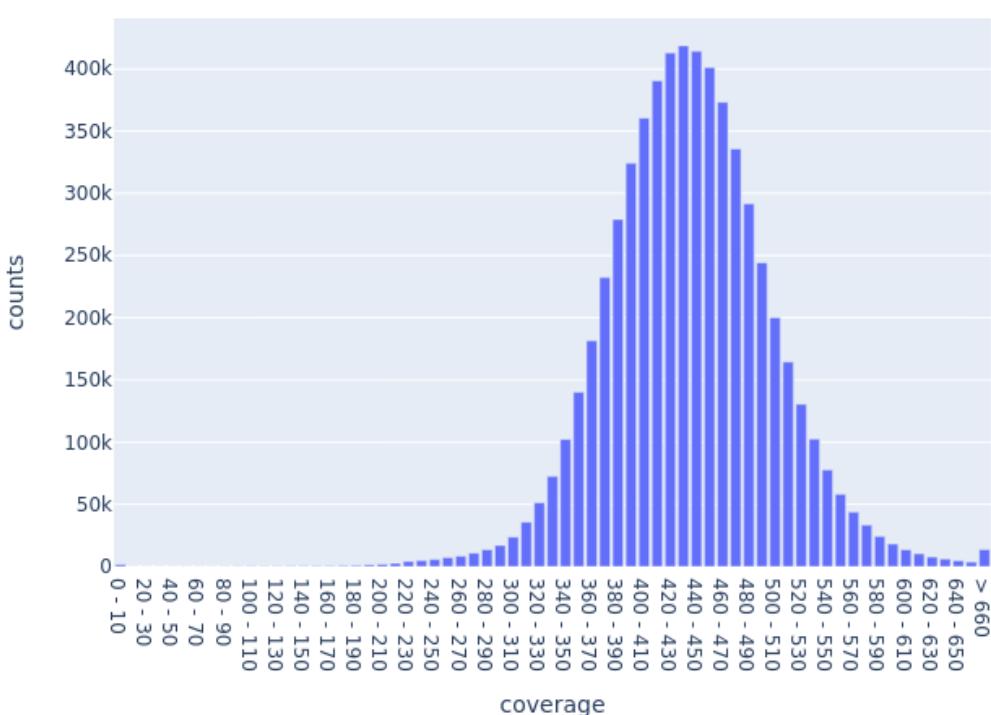
818 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 439.0240786629262

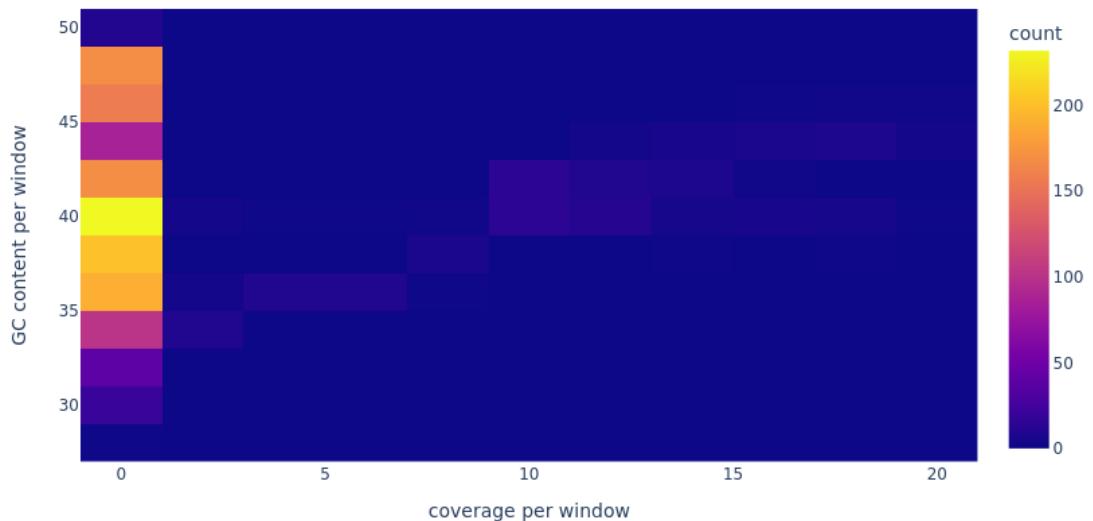
Comamonas testosteronei in T11.2.4.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.2.4.rep



# Report of *Comamonas testosteronei* in T11.2.5.rep

## Mapping stats of Illumina reads

20187321 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

7379 + 0 supplementary

0 + 0 duplicates

20134684 + 0 mapped (99.74% : N/A)

20179942 + 0 paired in sequencing

10089971 + 0 read1

10089971 + 0 read2

20011754 + 0 properly paired (99.17% : N/A)

20118024 + 0 with itself and mate mapped

9281 + 0 singletons (0.05% : N/A)

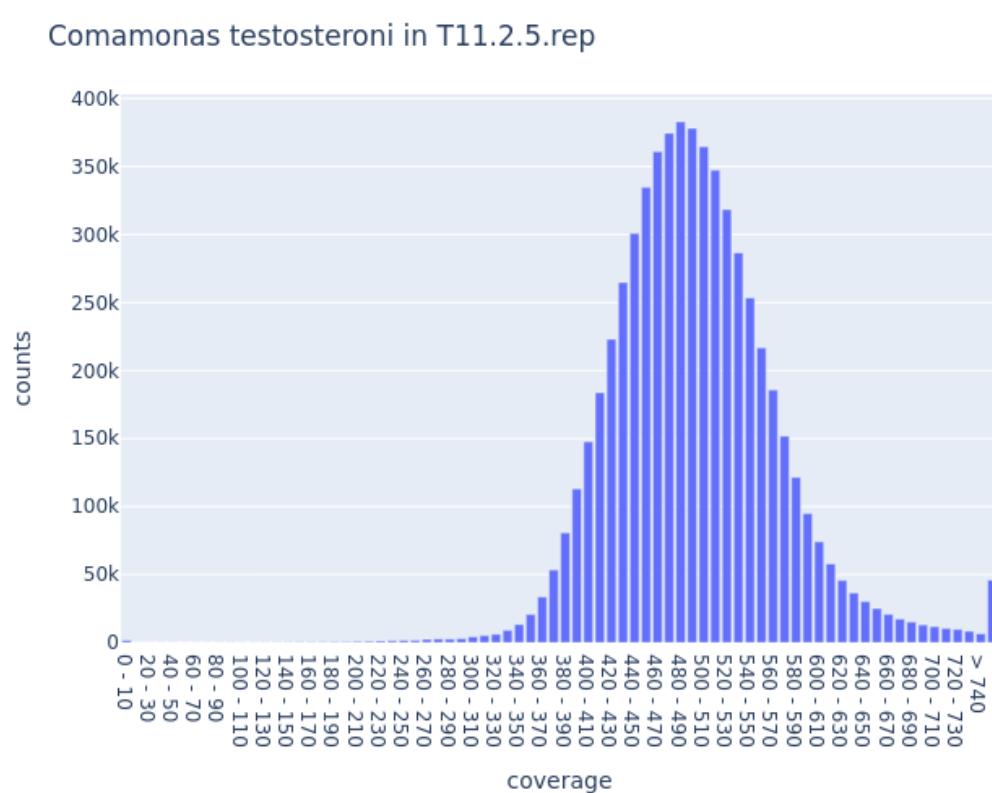
6506 + 0 with mate mapped to a different chr

6300 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

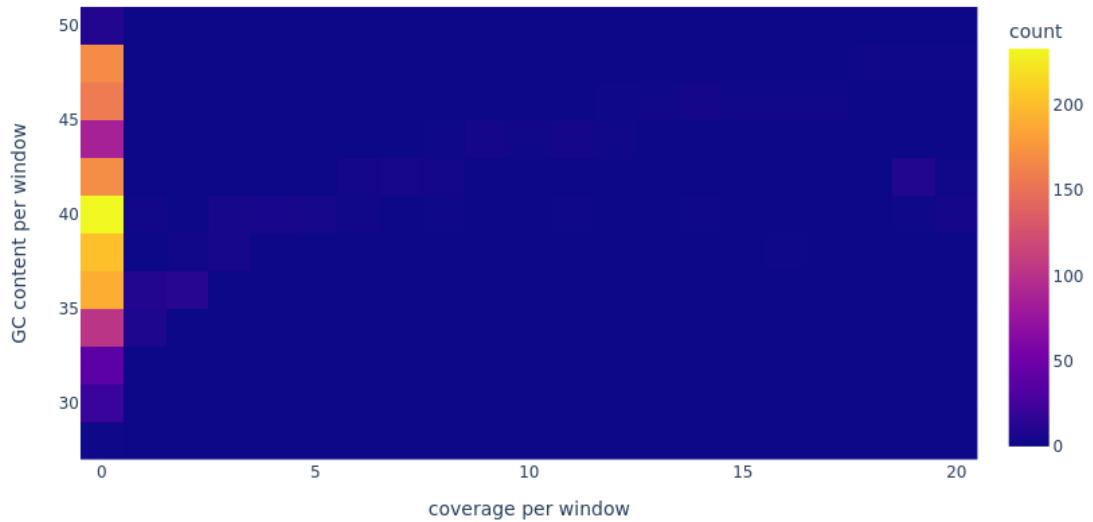
Average coverage: 497.5601735654398



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.2.5.rep



# Report of *Agrobacterium tumefaciens* in T11.3.1

## Mapping stats of Illumina reads

178826272 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

39794 + 0 supplementary

0 + 0 duplicates

172373238 + 0 mapped (96.39% : N/A)

178786478 + 0 paired in sequencing

89393239 + 0 read1

89393239 + 0 read2

171742140 + 0 properly paired (96.06% : N/A)

172249030 + 0 with itself and mate mapped

84414 + 0 singletons (0.05% : N/A)

180366 + 0 with mate mapped to a different chr

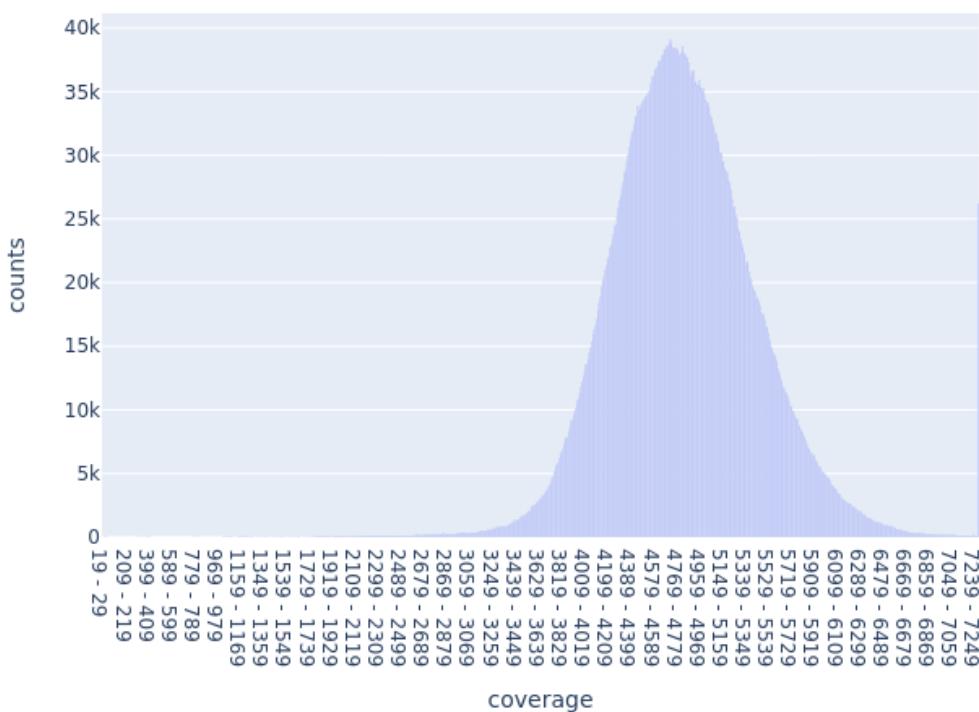
172280 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 4841.837044715135

Agrobacterium tumefaciens in T11.3.1

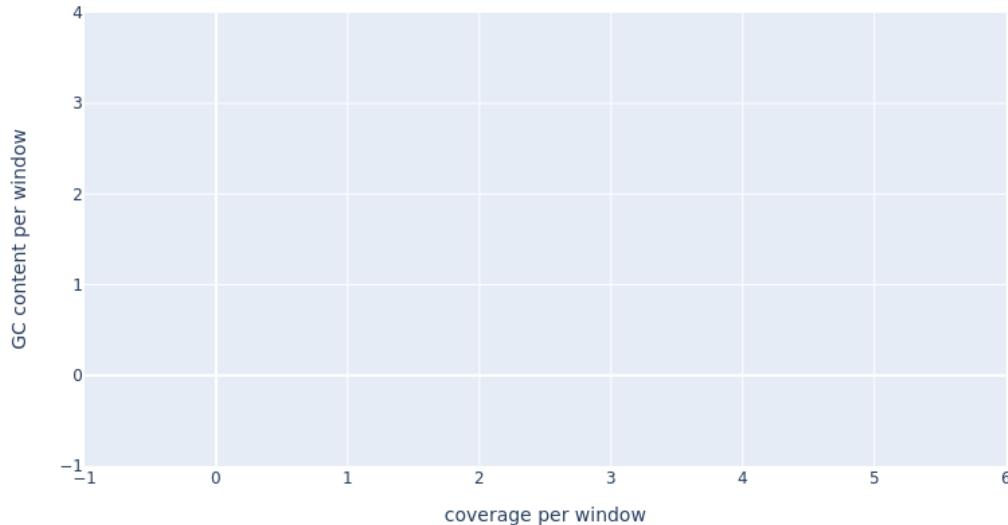


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T11.3.1



# Report of Comamonas testosterone in T11.3.1

## Mapping stats of Illumina reads

178786842 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

364 + 0 supplementary

0 + 0 duplicates

4377034 + 0 mapped (2.45% : N/A)

178786478 + 0 paired in sequencing

89393239 + 0 read1

89393239 + 0 read2

4125932 + 0 properly paired (2.31% : N/A)

4131330 + 0 with itself and mate mapped

245340 + 0 singletons (0.14% : N/A)

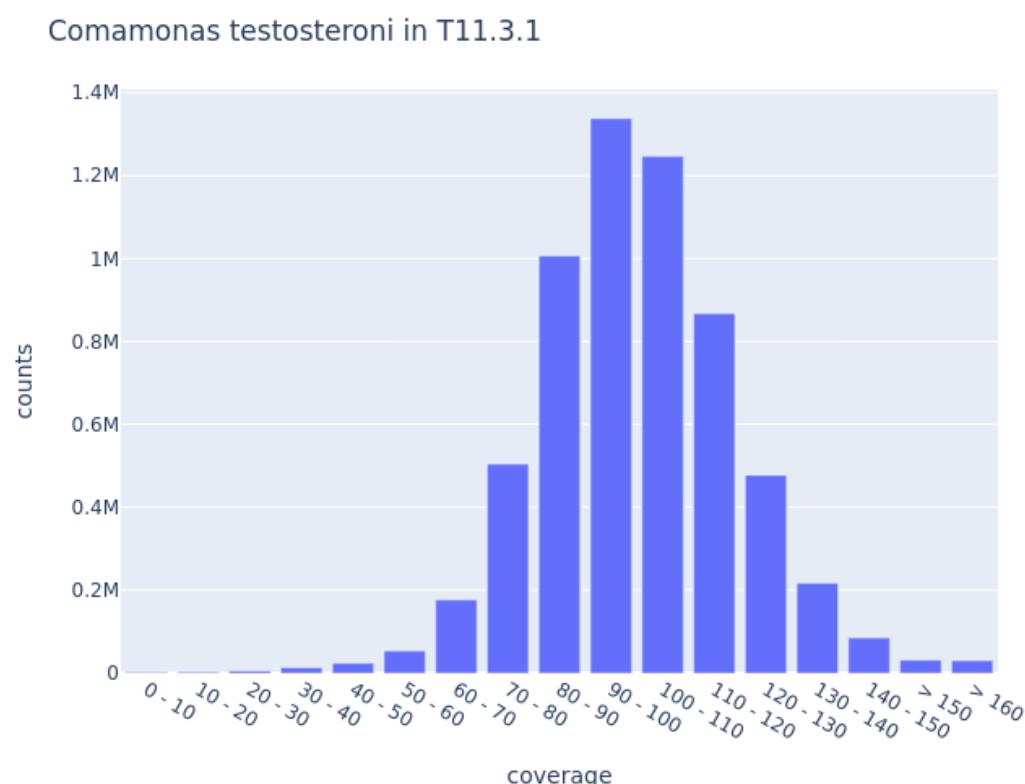
14 + 0 with mate mapped to a different chr

11 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

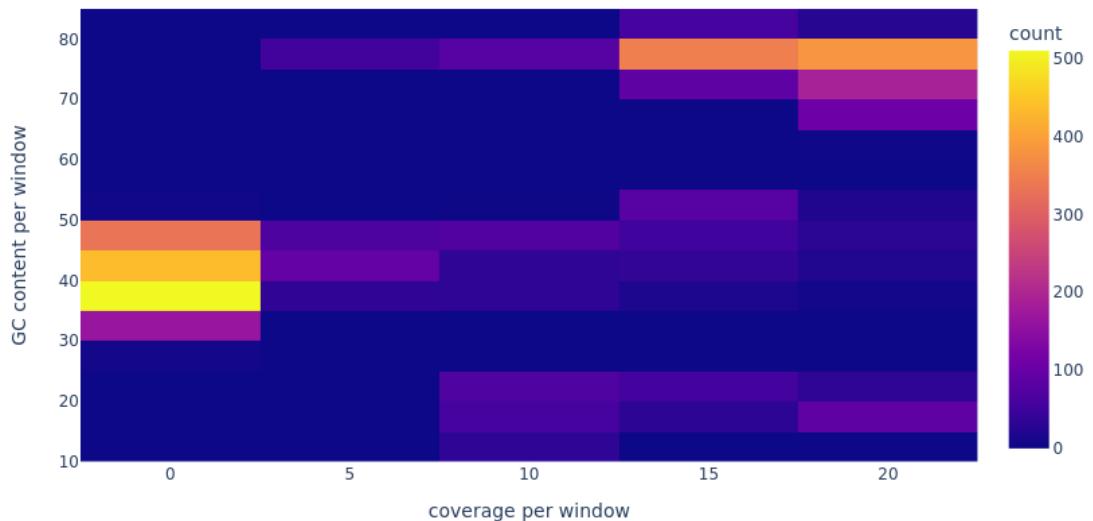
Average coverage: 103.88807113152328



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.3.1



# Report of *Microbacterium saperdae* in T11.3.1

## Mapping stats of Illumina reads

178786736 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

258 + 0 supplementary

0 + 0 duplicates

2239457 + 0 mapped (1.25% : N/A)

178786478 + 0 paired in sequencing

89393239 + 0 read1

89393239 + 0 read2

2148986 + 0 properly paired (1.20% : N/A)

2153374 + 0 with itself and mate mapped

85825 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

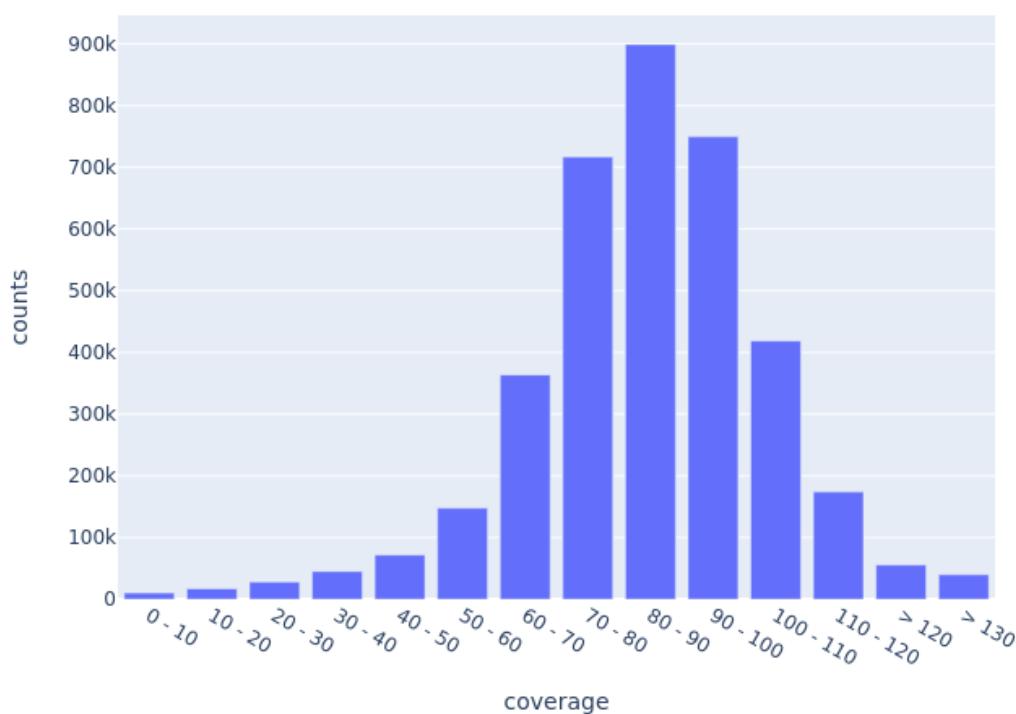
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 86.60121399968641

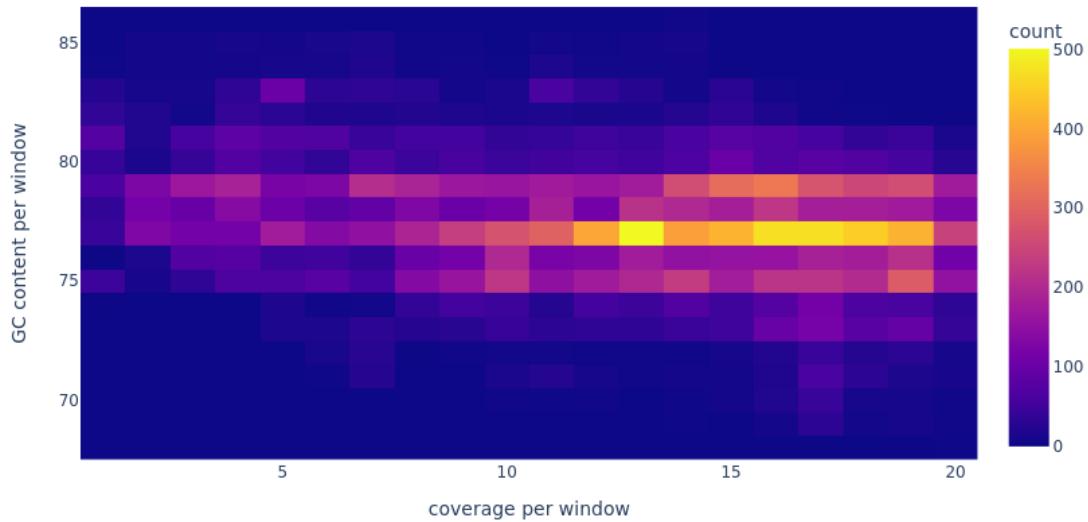
Microbacterium saperdae in T11.3.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T11.3.1



# Report of *Agrobacterium tumefaciens* in T11.3.2

## Mapping stats of Illumina reads

213142792 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

50750 + 0 supplementary

0 + 0 duplicates

206879135 + 0 mapped (97.06% : N/A)

213092042 + 0 paired in sequencing

106546021 + 0 read1

106546021 + 0 read2

205791772 + 0 properly paired (96.57% : N/A)

206699928 + 0 with itself and mate mapped

128457 + 0 singletons (0.06% : N/A)

432930 + 0 with mate mapped to a different chr

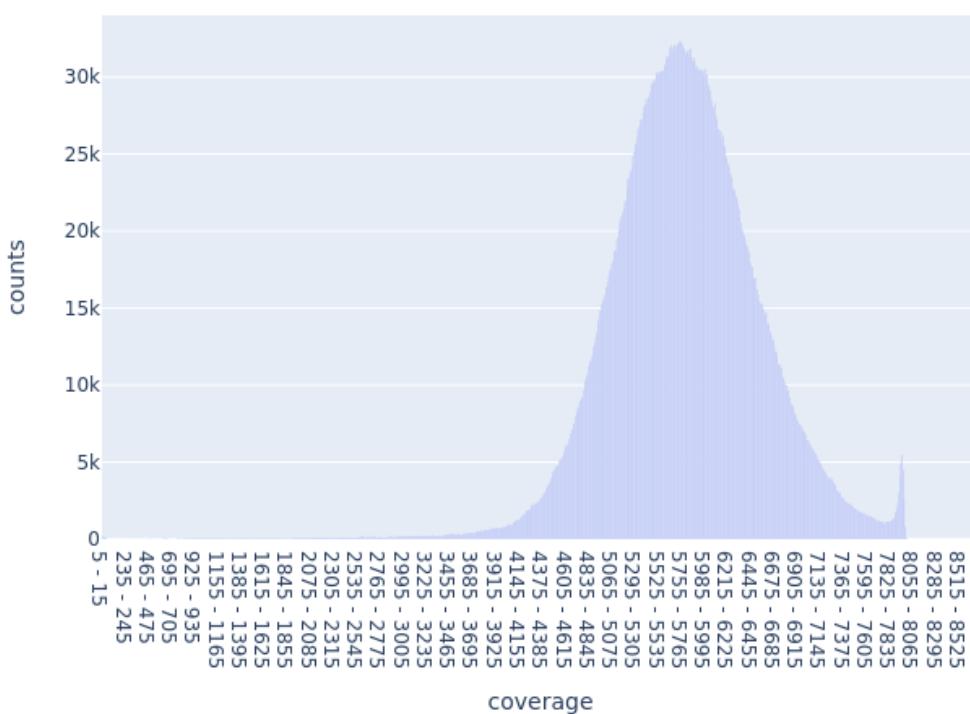
418015 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

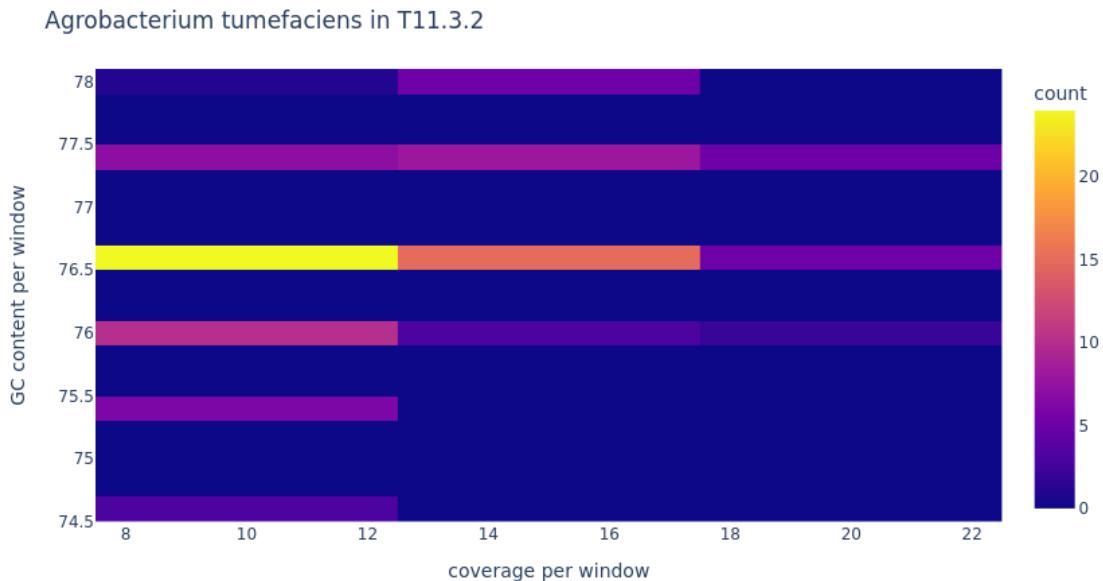
Average coverage: 5800.784663760083

Agrobacterium tumefaciens in T11.3.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.



# Report of Comamonas testosterone in T11.3.2

## Mapping stats of Illumina reads

213092553 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

511 + 0 supplementary

0 + 0 duplicates

5866919 + 0 mapped (2.75% : N/A)

213092042 + 0 paired in sequencing

106546021 + 0 read1

106546021 + 0 read2

5530828 + 0 properly paired (2.60% : N/A)

5535068 + 0 with itself and mate mapped

331340 + 0 singletons (0.16% : N/A)

48 + 0 with mate mapped to a different chr

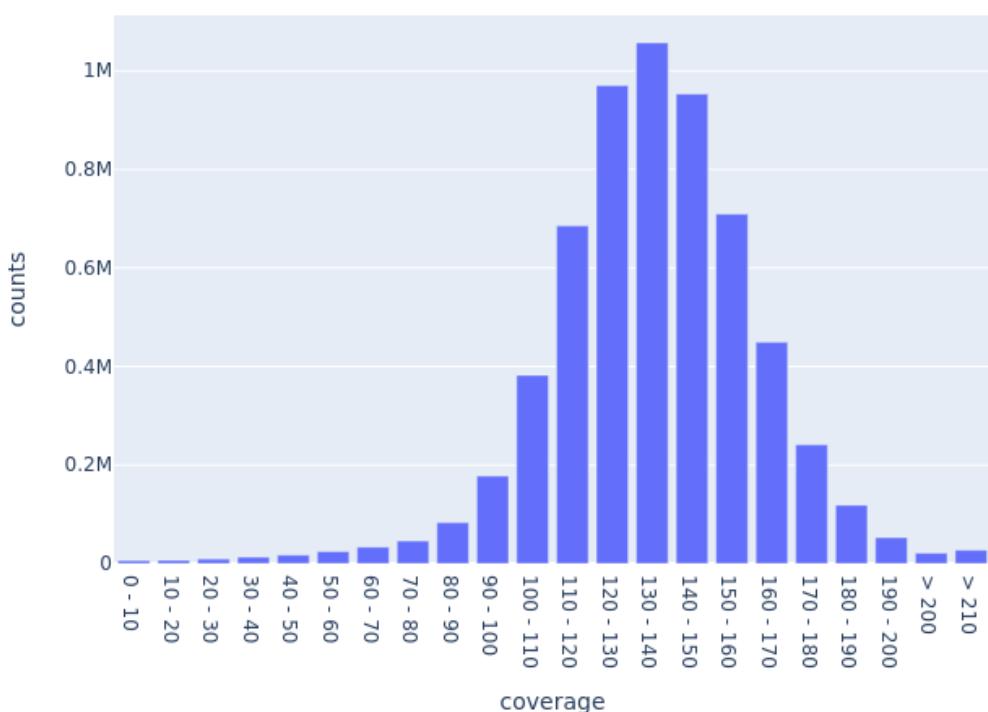
32 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 139.8541042151959

Comamonas testosterone in T11.3.2

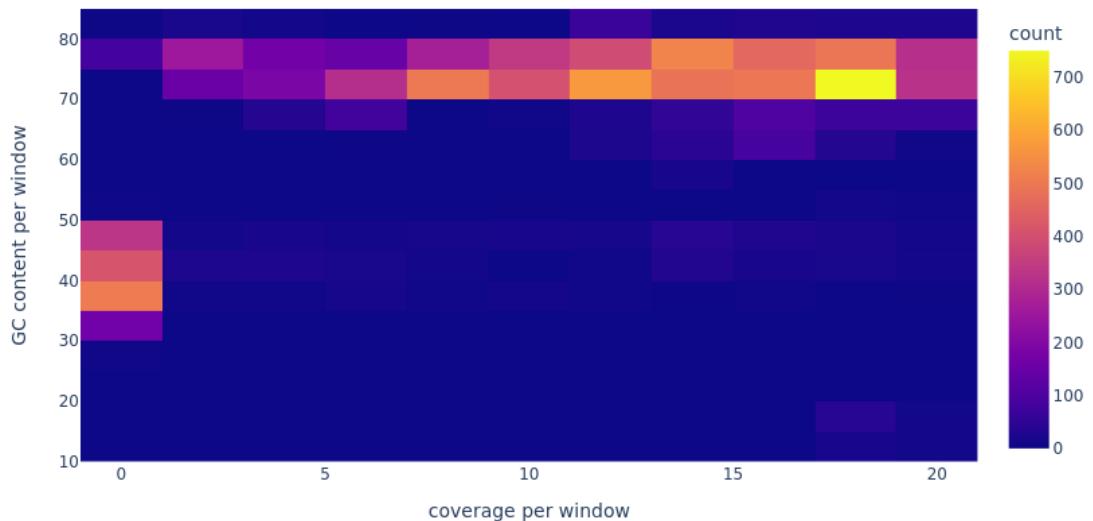


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.3.2



# Report of *Microbacterium saperdae* in T11.3.2

## Mapping stats of Illumina reads

213092095 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

53 + 0 supplementary

0 + 0 duplicates

521112 + 0 mapped (0.24% : N/A)

213092042 + 0 paired in sequencing

106546021 + 0 read1

106546021 + 0 read2

408056 + 0 properly paired (0.19% : N/A)

410124 + 0 with itself and mate mapped

110935 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

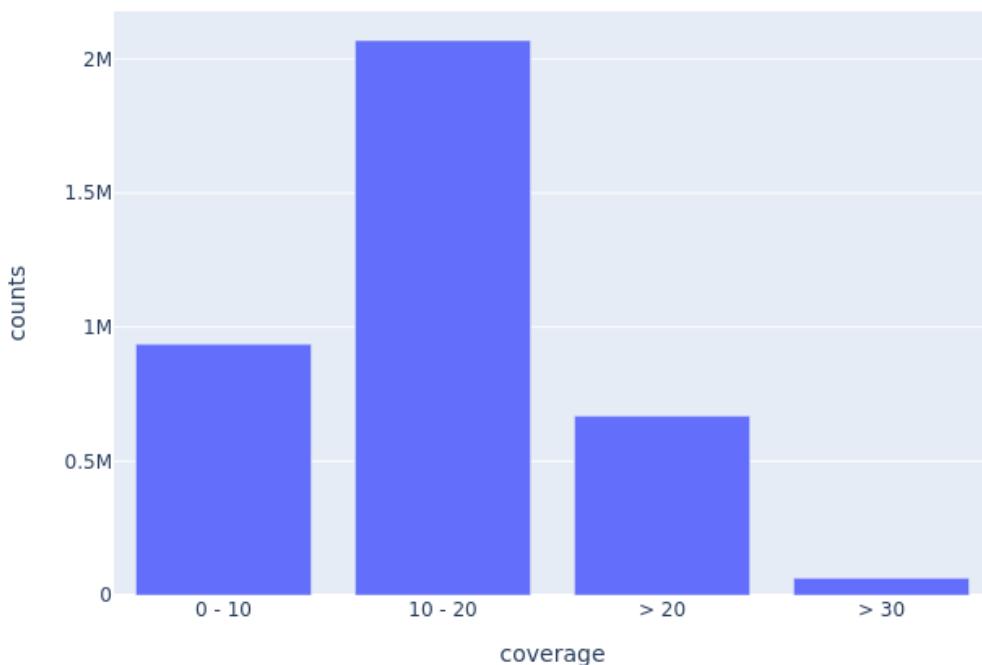
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 16.73078810445128

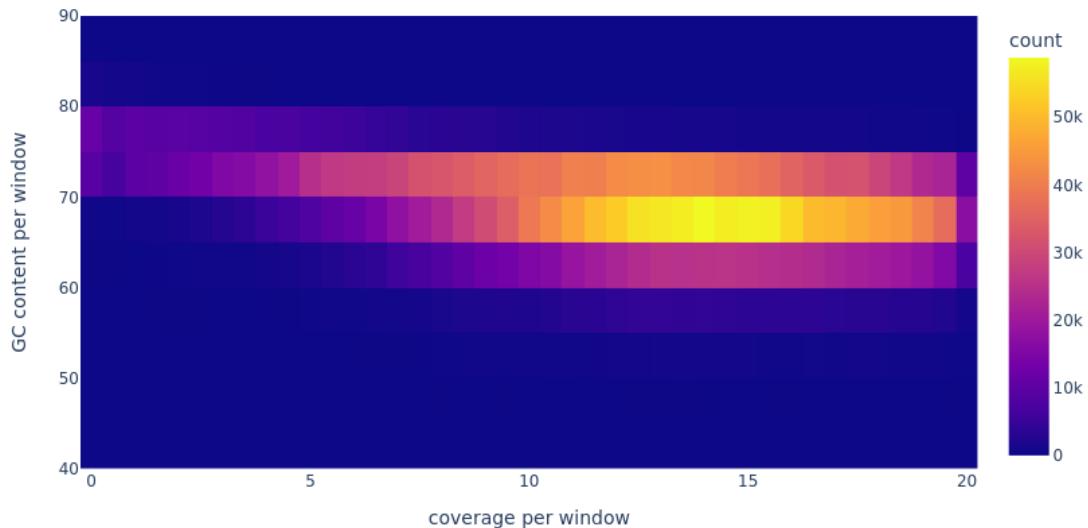
Microbacterium saperdae in T11.3.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T11.3.2



# Report of *Agrobacterium tumefaciens* in T11.3.3

## Mapping stats of Illumina reads

195263694 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

64788 + 0 supplementary

0 + 0 duplicates

190029351 + 0 mapped (97.32% : N/A)

195198906 + 0 paired in sequencing

97599453 + 0 read1

97599453 + 0 read2

189078750 + 0 properly paired (96.86% : N/A)

189864074 + 0 with itself and mate mapped

100489 + 0 singletons (0.05% : N/A)

386956 + 0 with mate mapped to a different chr

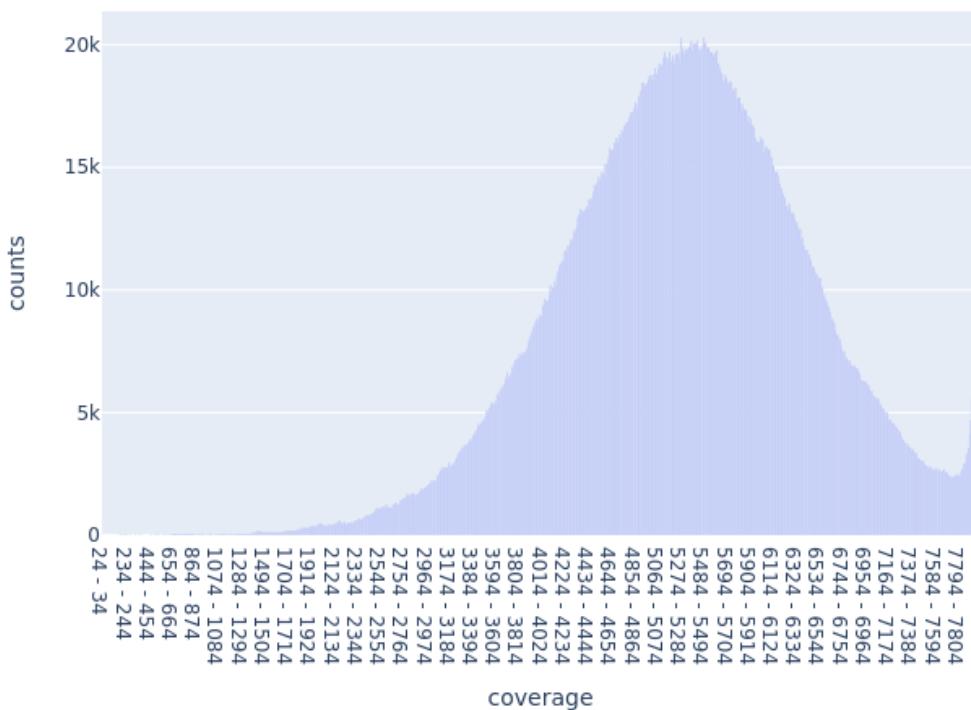
374265 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 5322.899869254211

Agrobacterium tumefaciens in T11.3.3

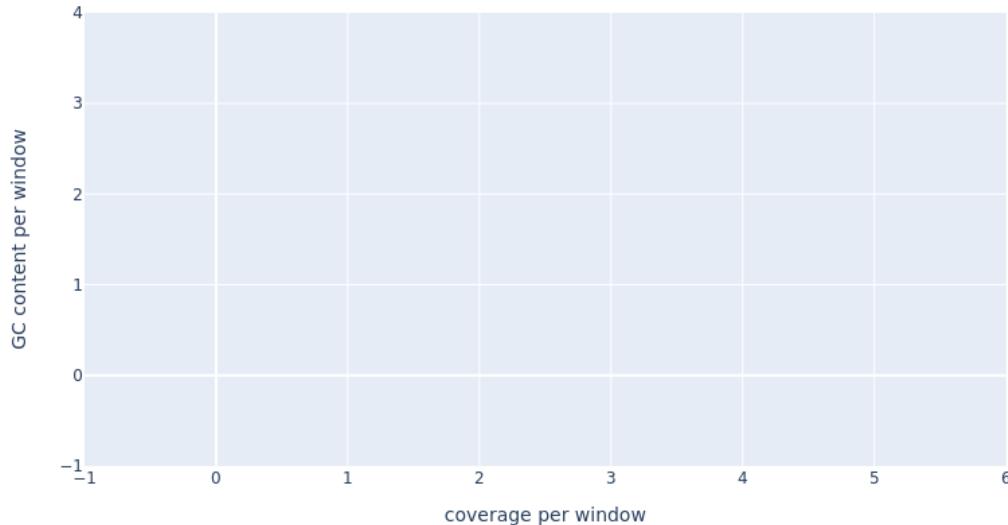


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T11.3.3



# Report of Comamonas testosterone in T11.3.3

## Mapping stats of Illumina reads

195199367 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

461 + 0 supplementary

0 + 0 duplicates

4893772 + 0 mapped (2.51% : N/A)

195198906 + 0 paired in sequencing

97599453 + 0 read1

97599453 + 0 read2

4603394 + 0 properly paired (2.36% : N/A)

4606720 + 0 with itself and mate mapped

286591 + 0 singletons (0.15% : N/A)

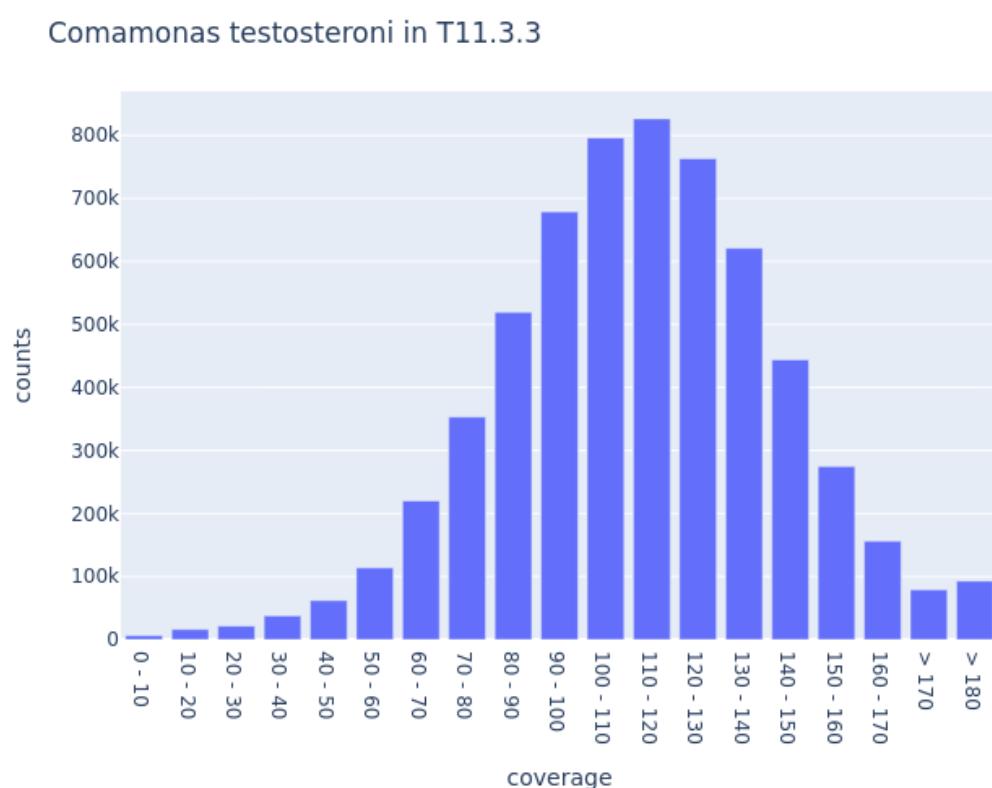
72 + 0 with mate mapped to a different chr

52 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 116.33623775986783

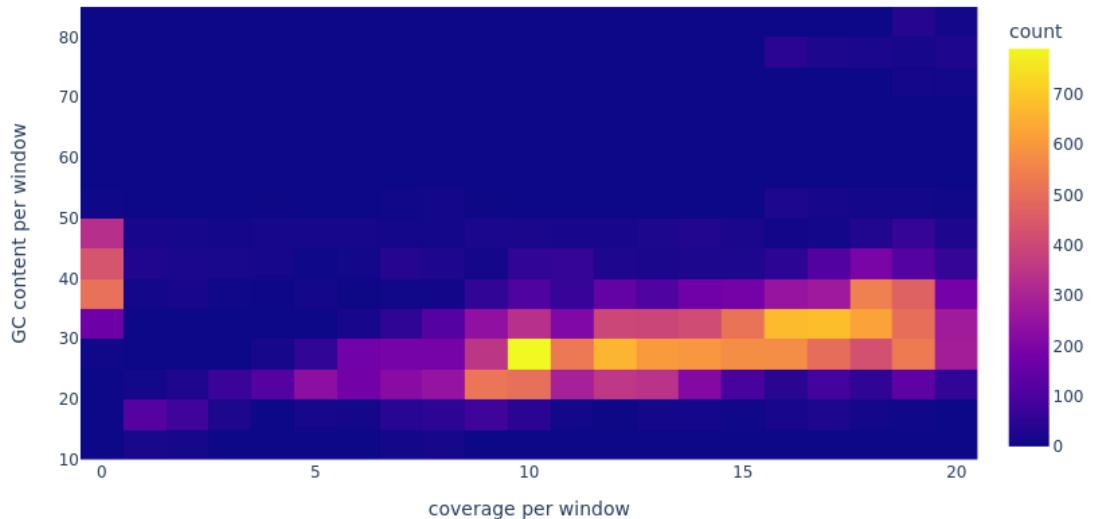


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.3.3



# Report of *Microbacterium saperdae* in T11.3.3

## Mapping stats of Illumina reads

195198951 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

45 + 0 supplementary

0 + 0 duplicates

561254 + 0 mapped (0.29% : N/A)

195198906 + 0 paired in sequencing

97599453 + 0 read1

97599453 + 0 read2

459772 + 0 properly paired (0.24% : N/A)

461948 + 0 with itself and mate mapped

99261 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

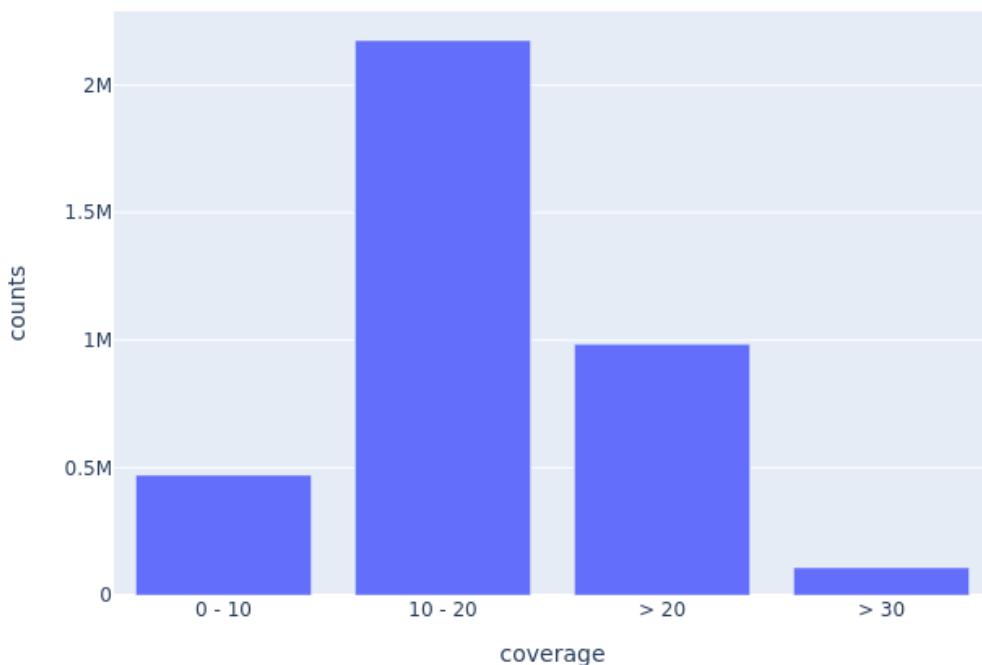
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 18.948204606520367

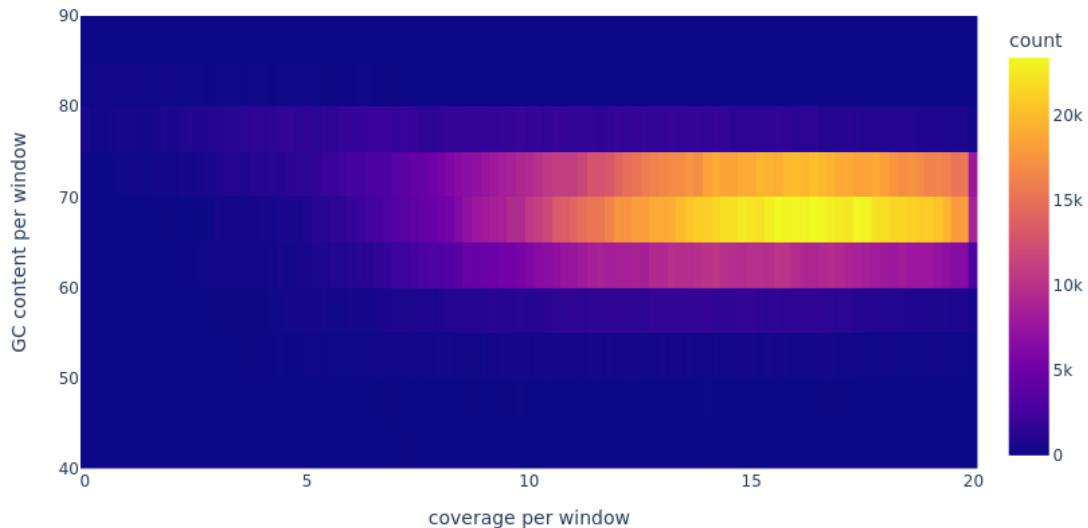
Microbacterium saperdae in T11.3.3



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T11.3.3



# Report of *Agrobacterium tumefaciens* in T11.3.4

## Mapping stats of Illumina reads

219332270 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

64522 + 0 supplementary

0 + 0 duplicates

214576591 + 0 mapped (97.83% : N/A)

219267748 + 0 paired in sequencing

109633874 + 0 read1

109633874 + 0 read2

213270782 + 0 properly paired (97.27% : N/A)

214374190 + 0 with itself and mate mapped

137879 + 0 singletons (0.06% : N/A)

514908 + 0 with mate mapped to a different chr

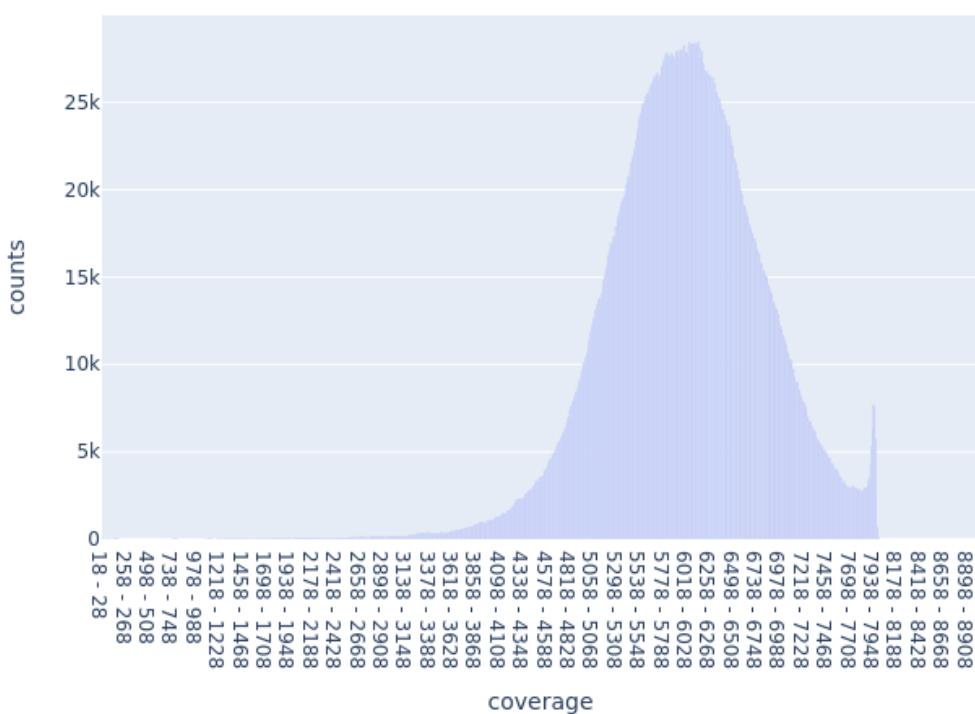
497549 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 6010.654097832551

Agrobacterium tumefaciens in T11.3.4

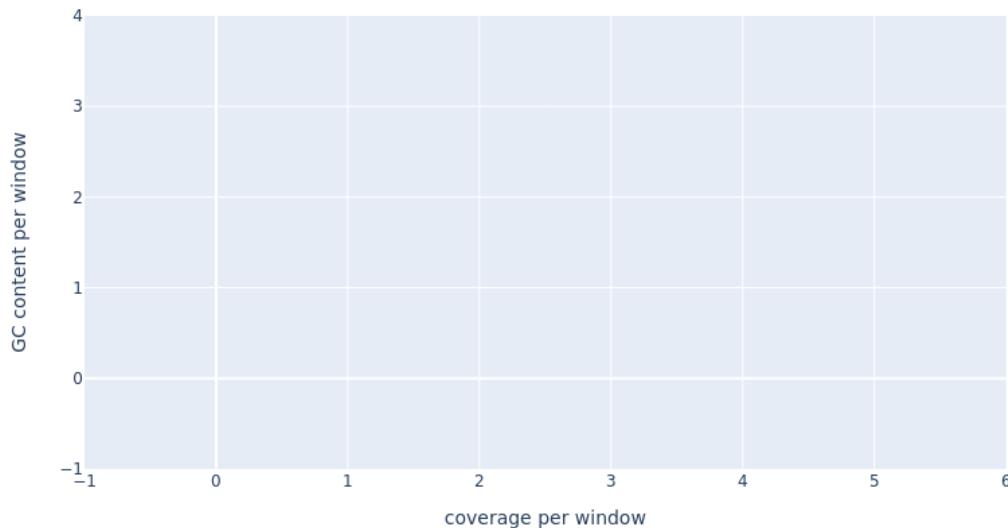


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T11.3.4



# Report of Comamonas testosterone in T11.3.4

## Mapping stats of Illumina reads

219268222 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

474 + 0 supplementary

0 + 0 duplicates

4129543 + 0 mapped (1.88% : N/A)

219267748 + 0 paired in sequencing

109633874 + 0 read1

109633874 + 0 read2

3787808 + 0 properly paired (1.73% : N/A)

3791714 + 0 with itself and mate mapped

337355 + 0 singletons (0.15% : N/A)

36 + 0 with mate mapped to a different chr

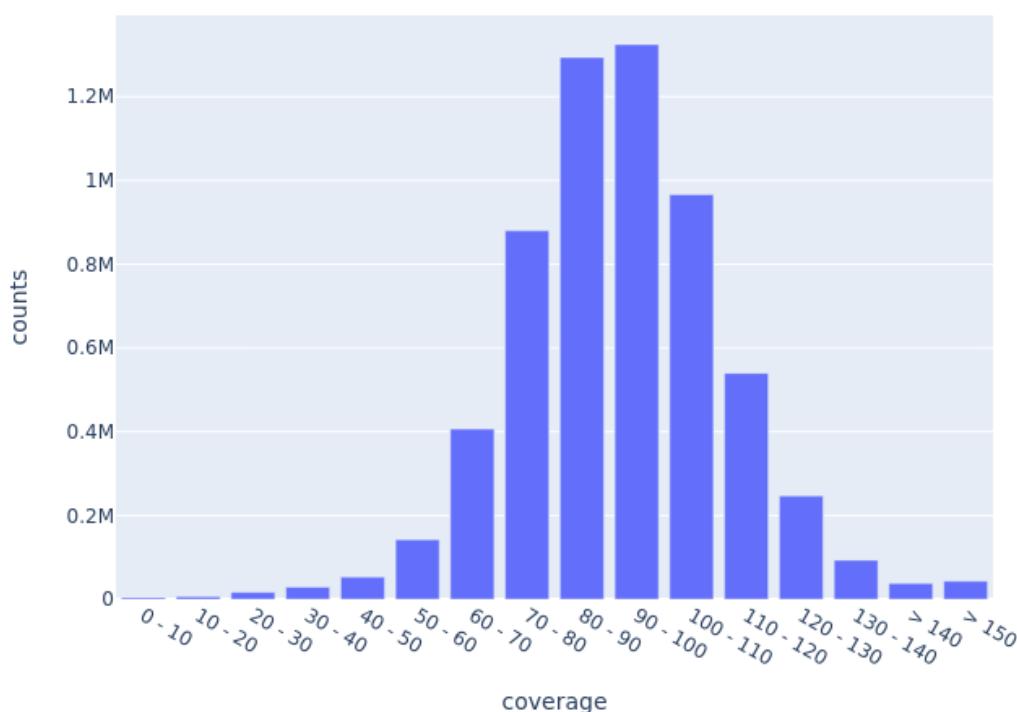
26 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 96.76962377993131

Comamonas testosterone in T11.3.4

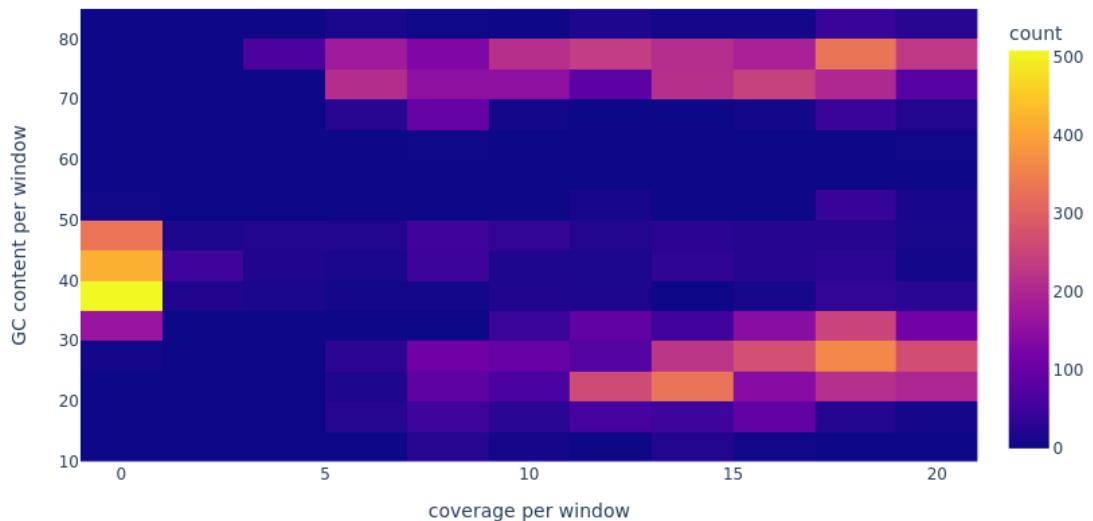


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.3.4



# Report of *Microbacterium saperdae* in T11.3.4

## Mapping stats of Illumina reads

219267813 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

65 + 0 supplementary

0 + 0 duplicates

763330 + 0 mapped (0.35% : N/A)

219267748 + 0 paired in sequencing

109633874 + 0 read1

109633874 + 0 read2

645246 + 0 properly paired (0.29% : N/A)

647464 + 0 with itself and mate mapped

115801 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

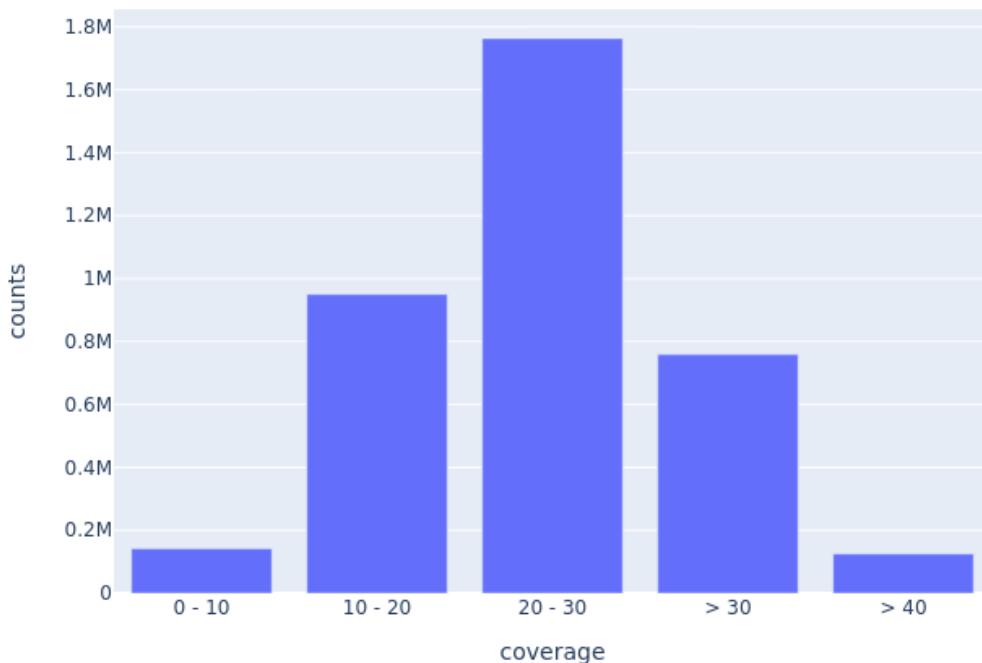
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 26.51355836333192

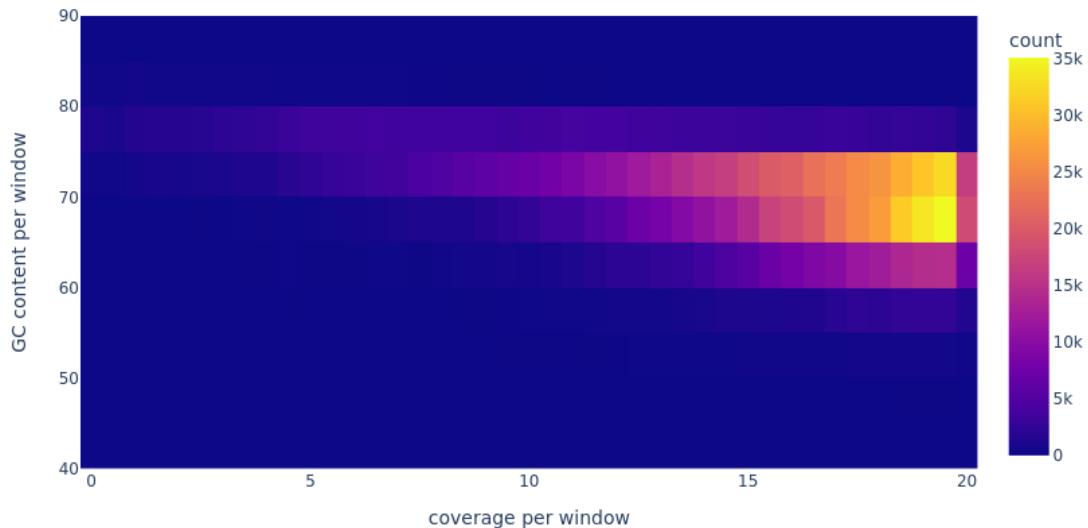
Microbacterium saperdae in T11.3.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T11.3.4



# Report of *Agrobacterium tumefaciens* in T11.3.5

## Mapping stats of Illumina reads

209192784 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

48312 + 0 supplementary

0 + 0 duplicates

204603202 + 0 mapped (97.81% : N/A)

209144472 + 0 paired in sequencing

104572236 + 0 read1

104572236 + 0 read2

204041342 + 0 properly paired (97.56% : N/A)

204466326 + 0 with itself and mate mapped

88564 + 0 singletons (0.04% : N/A)

134152 + 0 with mate mapped to a different chr

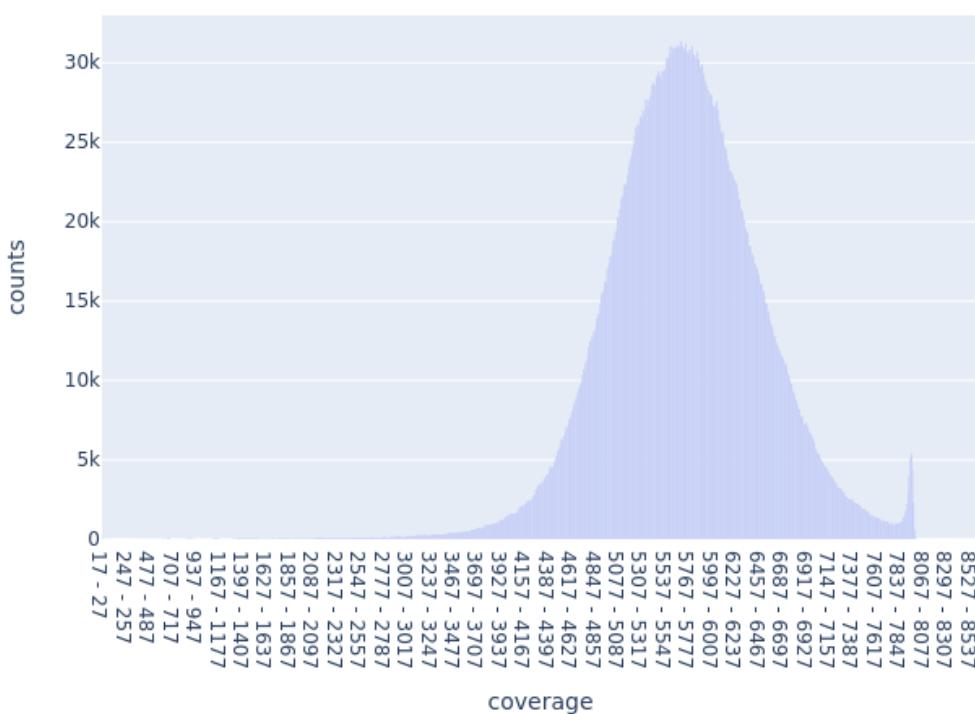
127856 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 5736.976981785894

Agrobacterium tumefaciens in T11.3.5

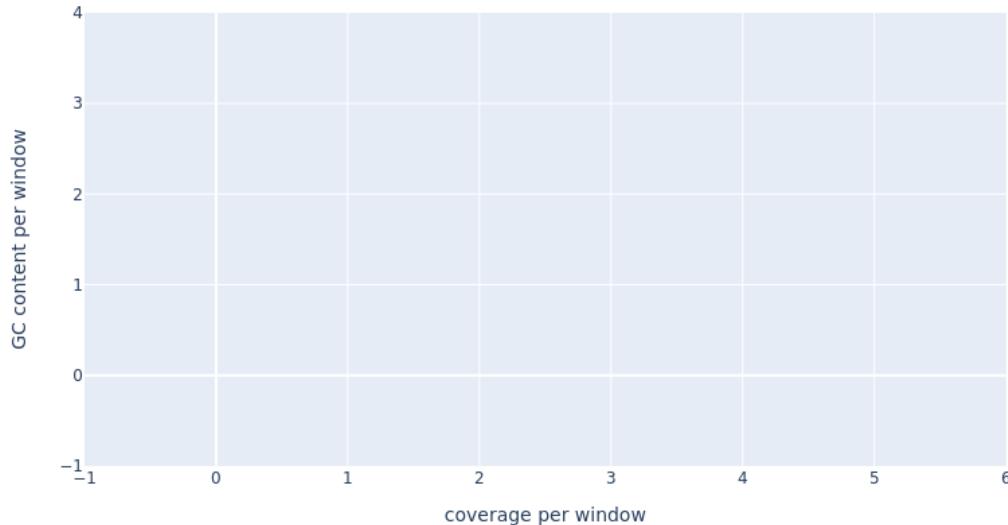


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T11.3.5



# Report of Comamonas testosterone in T11.3.5

## Mapping stats of Illumina reads

209144977 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

505 + 0 supplementary

0 + 0 duplicates

3709343 + 0 mapped (1.77% : N/A)

209144472 + 0 paired in sequencing

104572236 + 0 read1

104572236 + 0 read2

3417112 + 0 properly paired (1.63% : N/A)

3421562 + 0 with itself and mate mapped

287276 + 0 singletons (0.14% : N/A)

8 + 0 with mate mapped to a different chr

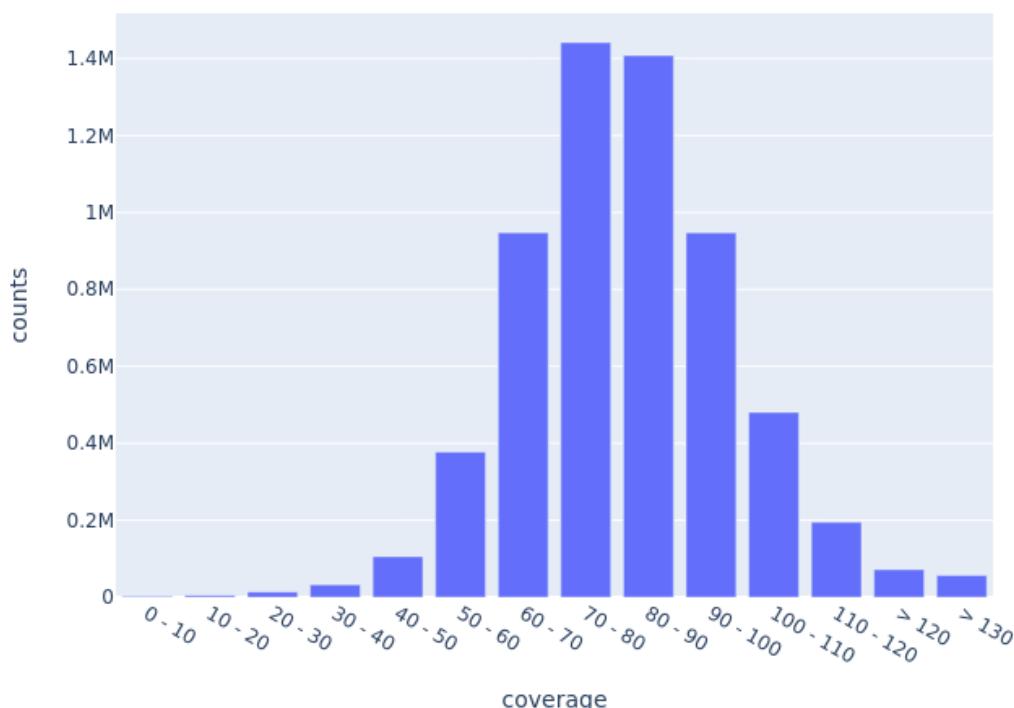
5 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 86.41483182129485

Comamonas testosterone in T11.3.5

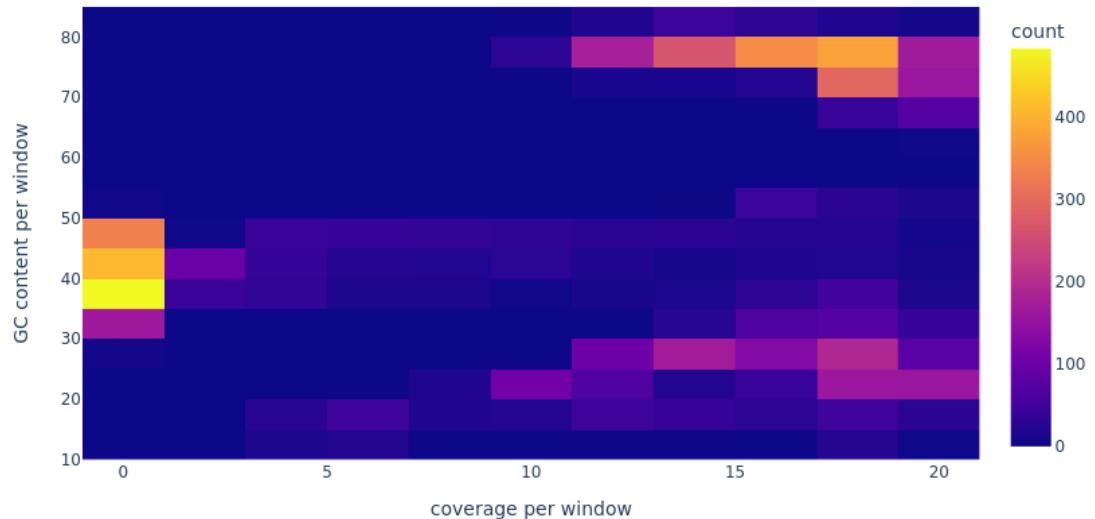


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.3.5



# Report of *Microbacterium saperdae* in T11.3.5

## Mapping stats of Illumina reads

209144540 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

68 + 0 supplementary

0 + 0 duplicates

964640 + 0 mapped (0.46% : N/A)

209144472 + 0 paired in sequencing

104572236 + 0 read1

104572236 + 0 read2

863970 + 0 properly paired (0.41% : N/A)

867444 + 0 with itself and mate mapped

97128 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

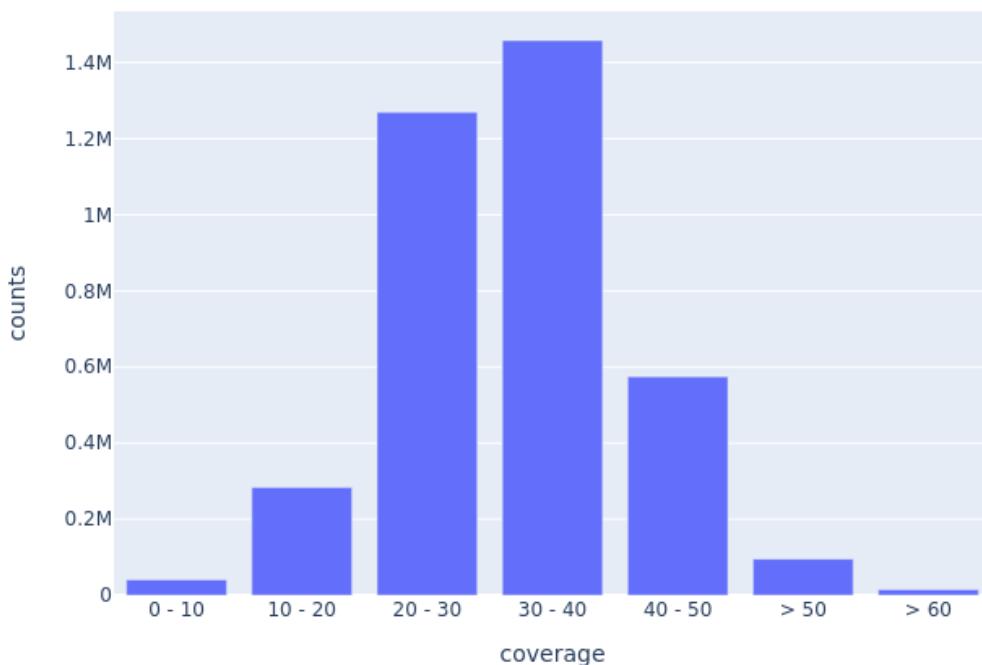
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 34.44282466036531

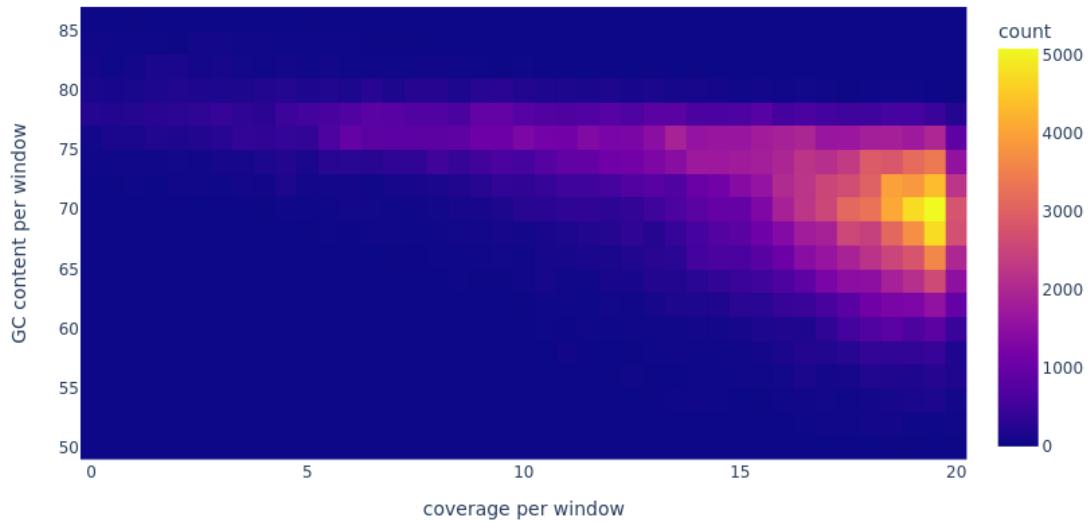
Microbacterium saperdae in T11.3.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T11.3.5



# Report of *Agrobacterium tumefaciens* in T11.4.1

## Mapping stats of Illumina reads

198352098 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

56926 + 0 supplementary

0 + 0 duplicates

170555308 + 0 mapped (85.99% : N/A)

198295172 + 0 paired in sequencing

99147586 + 0 read1

99147586 + 0 read2

169549432 + 0 properly paired (85.50% : N/A)

170162350 + 0 with itself and mate mapped

336032 + 0 singletons (0.17% : N/A)

294400 + 0 with mate mapped to a different chr

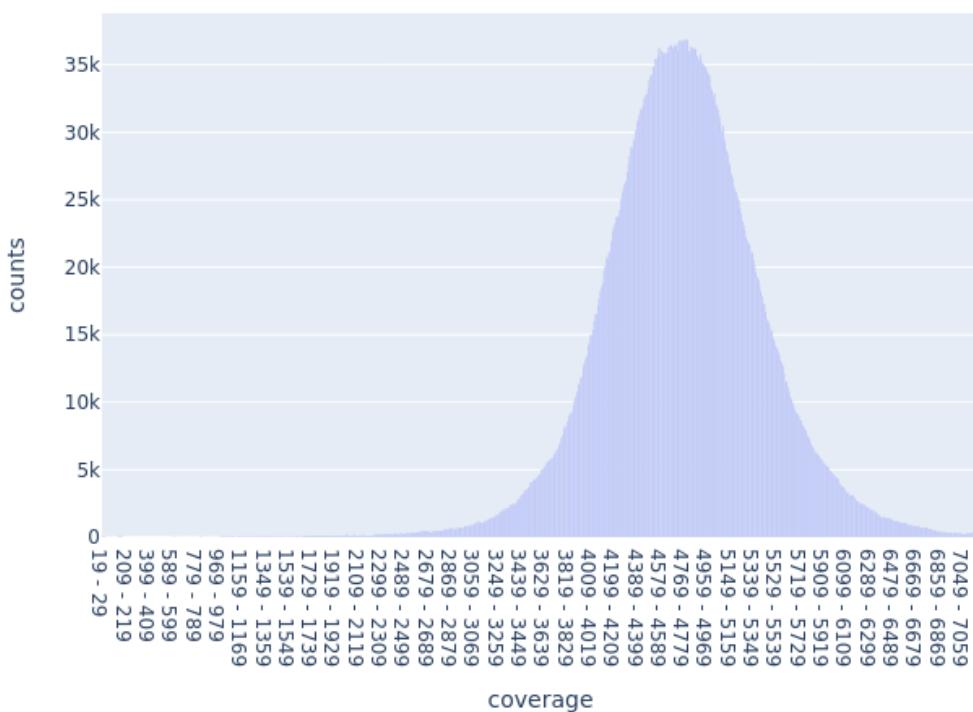
284128 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 4784.489666071926

Agrobacterium tumefaciens in T11.4.1

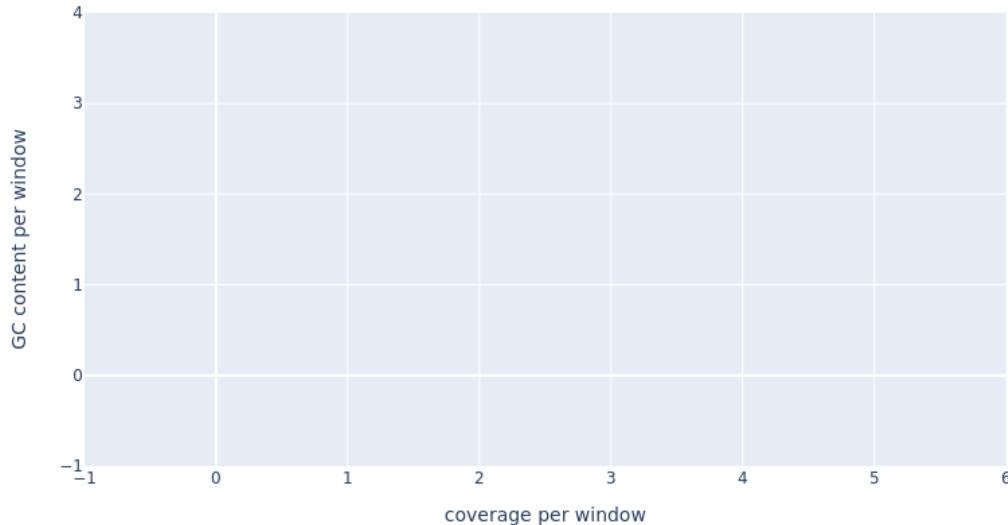


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T11.4.1



# Report of Comamonas testosterone in T11.4.1

## Mapping stats of Illumina reads

198296899 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1727 + 0 supplementary

0 + 0 duplicates

11709093 + 0 mapped (5.90% : N/A)

198295172 + 0 paired in sequencing

99147586 + 0 read1

99147586 + 0 read2

11389158 + 0 properly paired (5.74% : N/A)

11398208 + 0 with itself and mate mapped

309158 + 0 singletons (0.16% : N/A)

254 + 0 with mate mapped to a different chr

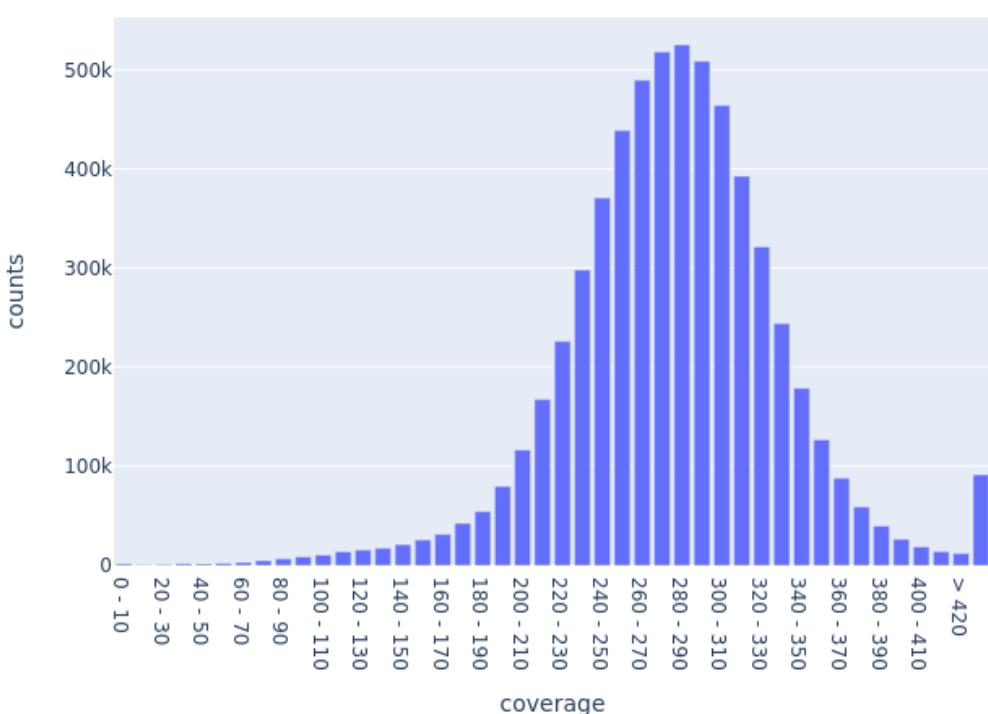
225 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 284.9261502096101

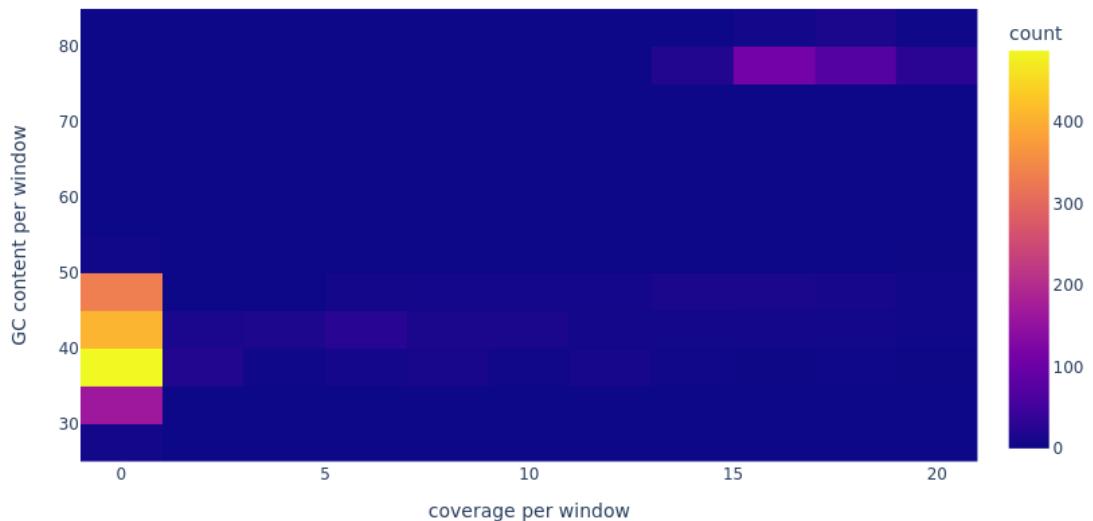
Comamonas testosterone in T11.4.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.4.1



# Report of *Microbacterium saperdae* in T11.4.1

## Mapping stats of Illumina reads

198295186 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

14 + 0 supplementary

0 + 0 duplicates

164307 + 0 mapped (0.08% : N/A)

198295172 + 0 paired in sequencing

99147586 + 0 read1

99147586 + 0 read2

63234 + 0 properly paired (0.03% : N/A)

65078 + 0 with itself and mate mapped

99215 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

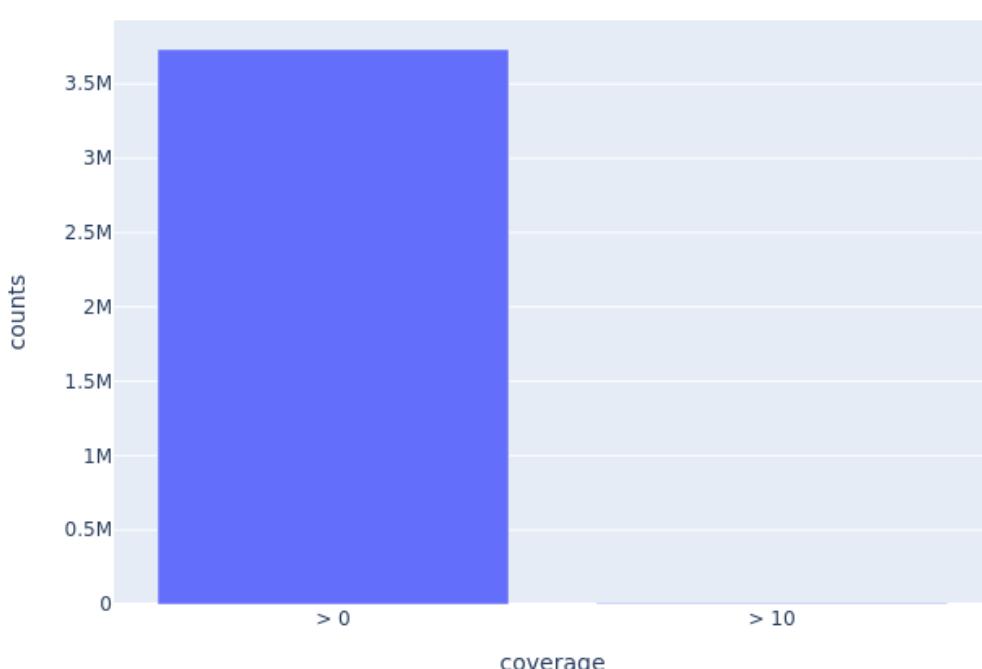
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 2.963161001316959

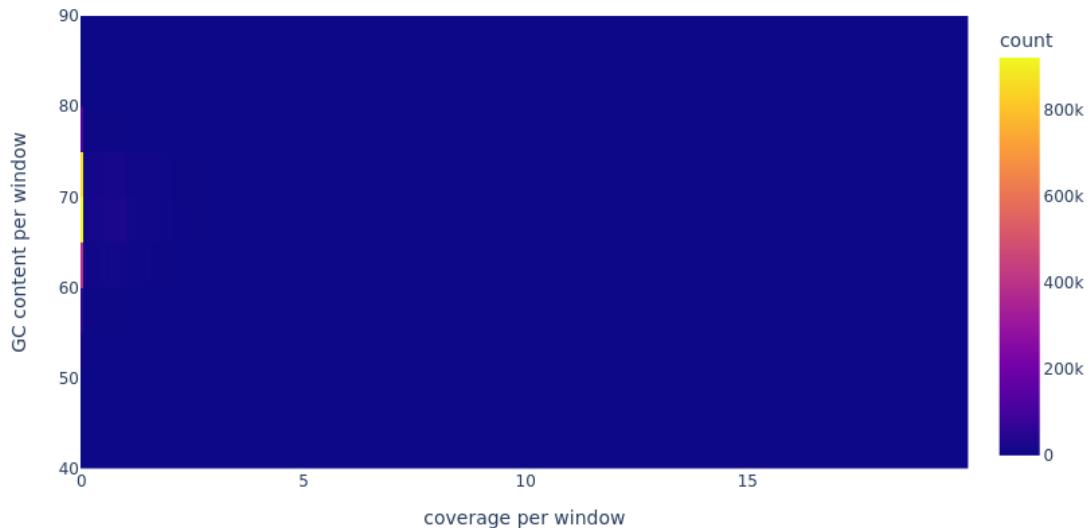
Microbacterium saperdae in T11.4.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T11.4.1



# Report of *Ochrobactrum anthropi* in T11.4.1

## Mapping stats of Illumina reads

198299852 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

4680 + 0 supplementary

0 + 0 duplicates

19308242 + 0 mapped (9.74% : N/A)

198295172 + 0 paired in sequencing

99147586 + 0 read1

99147586 + 0 read2

17662558 + 0 properly paired (8.91% : N/A)

17706622 + 0 with itself and mate mapped

1596940 + 0 singletons (0.81% : N/A)

23488 + 0 with mate mapped to a different chr

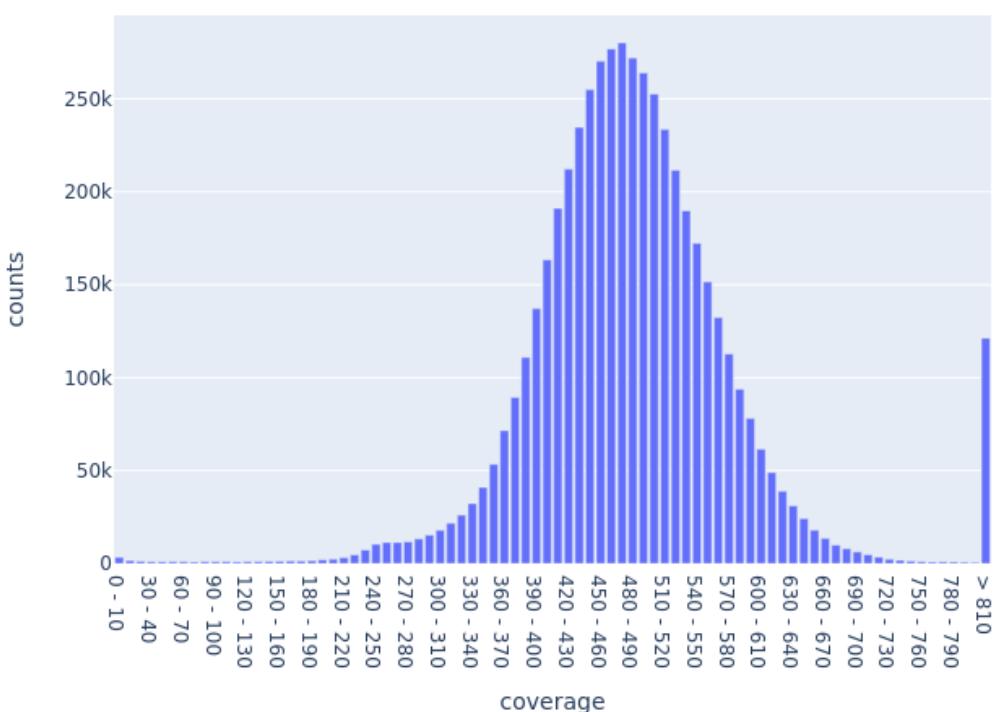
16457 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 535.8028447432893

Ochrobactrum anthropi in T11.4.1

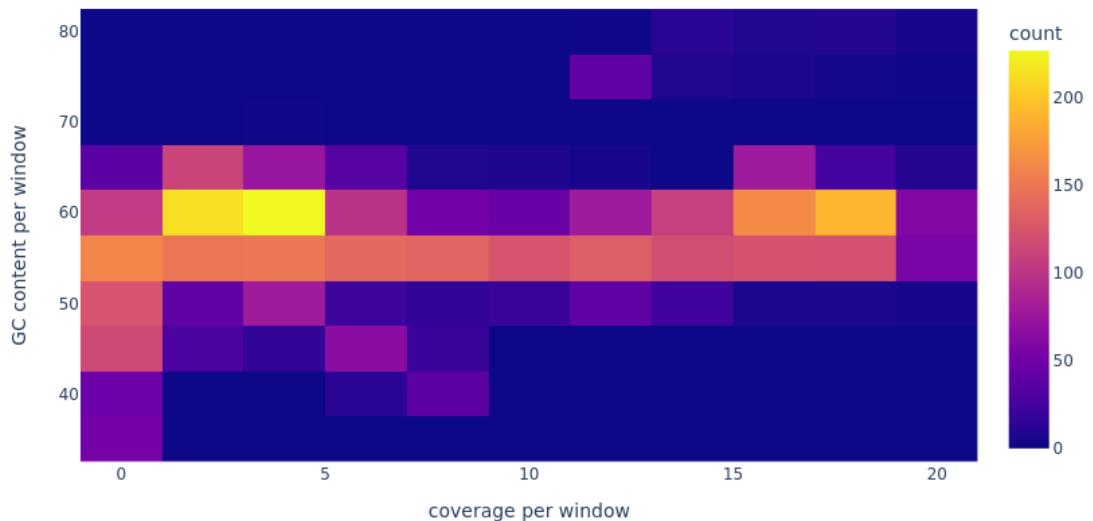


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T11.4.1



# Report of *Agrobacterium tumefaciens* in T11.4.2

## Mapping stats of Illumina reads

207294399 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

25285 + 0 supplementary

0 + 0 duplicates

183261483 + 0 mapped (88.41% : N/A)

207269114 + 0 paired in sequencing

103634557 + 0 read1

103634557 + 0 read2

182256012 + 0 properly paired (87.93% : N/A)

182946440 + 0 with itself and mate mapped

289758 + 0 singletons (0.14% : N/A)

335956 + 0 with mate mapped to a different chr

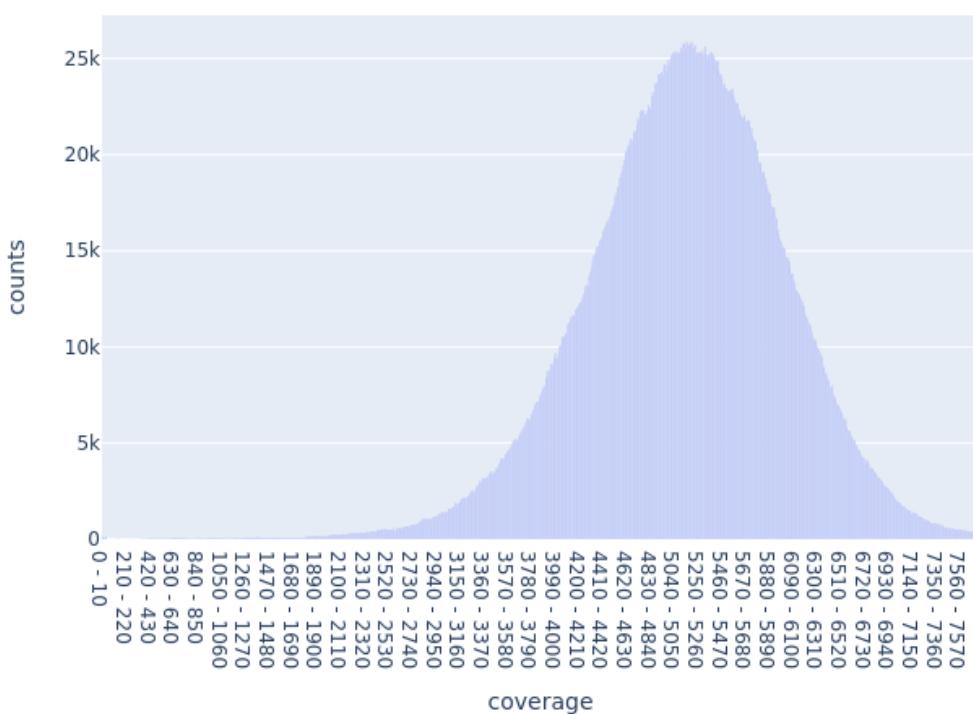
325002 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

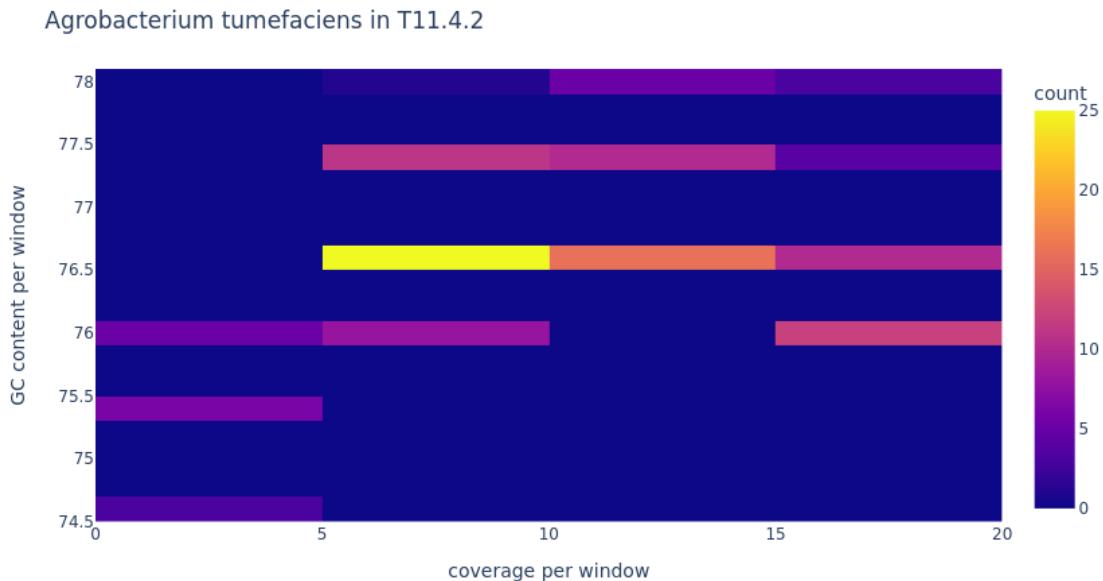
Average coverage: 5144.0048871216795

Agrobacterium tumefaciens in T11.4.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.



# Report of Comamonas testosterone in T11.4.2

## Mapping stats of Illumina reads

207269788 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

674 + 0 supplementary

0 + 0 duplicates

9752750 + 0 mapped (4.71% : N/A)

207269114 + 0 paired in sequencing

103634557 + 0 read1

103634557 + 0 read2

9439078 + 0 properly paired (4.55% : N/A)

9445198 + 0 with itself and mate mapped

306878 + 0 singletons (0.15% : N/A)

146 + 0 with mate mapped to a different chr

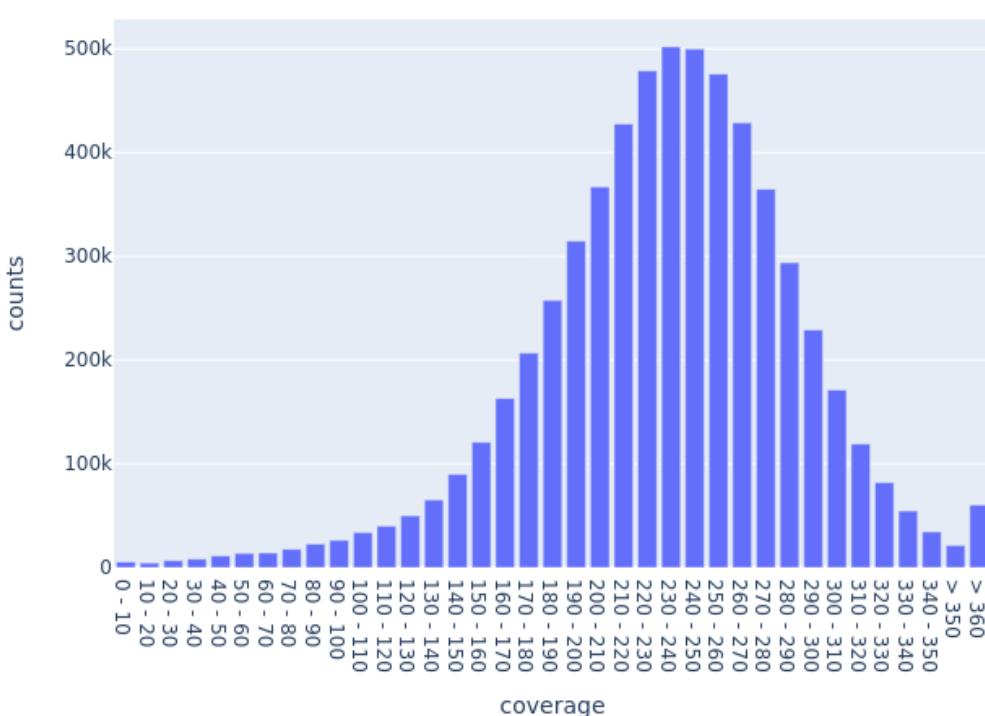
127 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 236.44991552975475

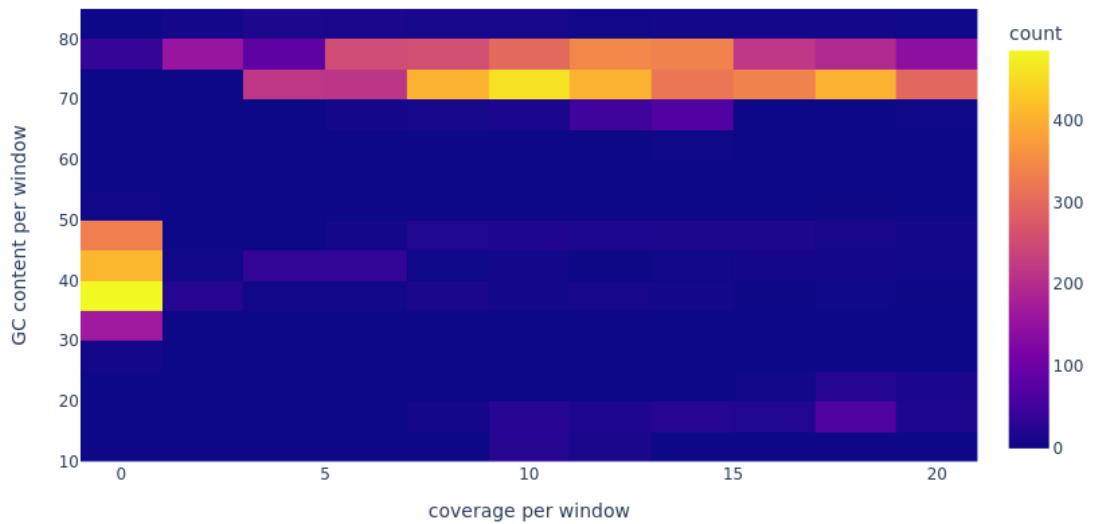
Comamonas testosterone in T11.4.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.4.2



# Report of *Microbacterium saperdae* in T11.4.2

## Mapping stats of Illumina reads

207269264 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

150 + 0 supplementary

0 + 0 duplicates

2681272 + 0 mapped (1.29% : N/A)

207269114 + 0 paired in sequencing

103634557 + 0 read1

103634557 + 0 read2

2565846 + 0 properly paired (1.24% : N/A)

2568900 + 0 with itself and mate mapped

112222 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

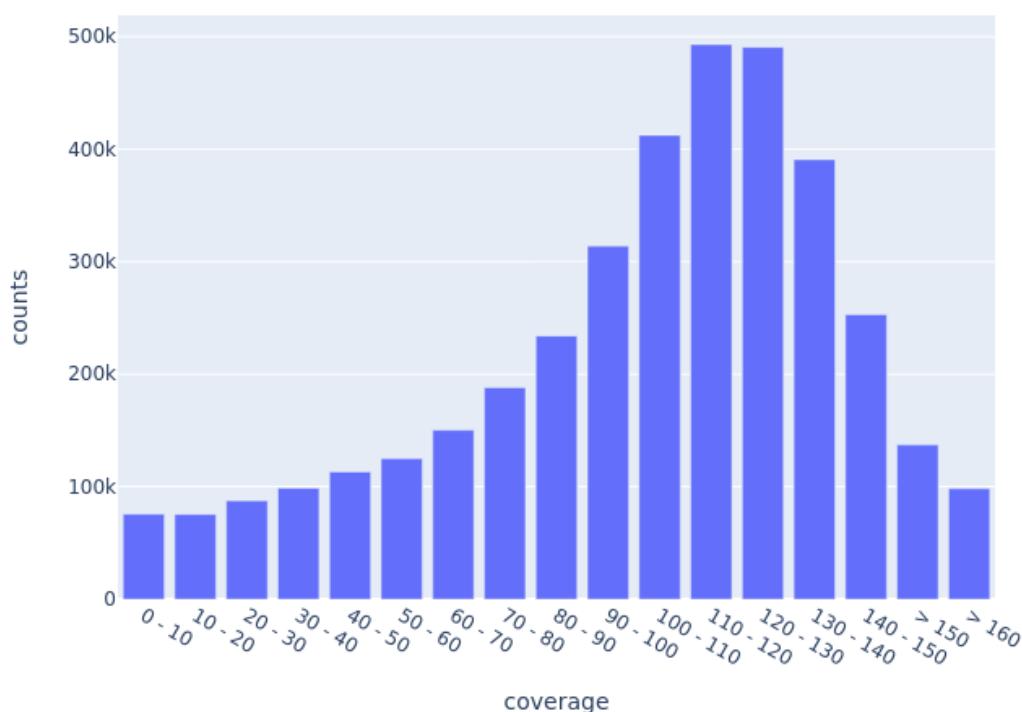
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 104.0639953250898

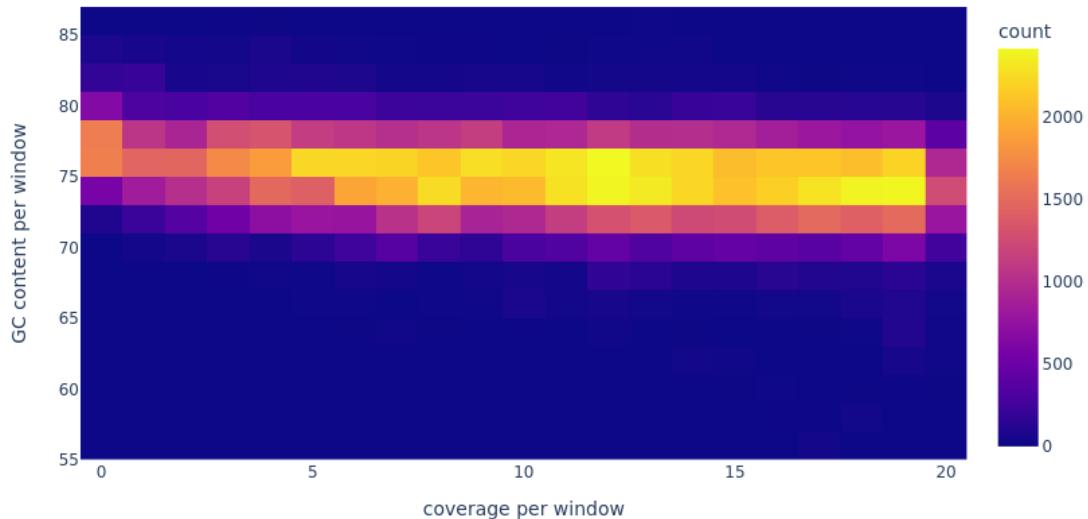
Microbacterium saperdae in T11.4.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T11.4.2



# Report of *Ochrobactrum anthropi* in T11.4.2

## Mapping stats of Illumina reads

207273376 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

4262 + 0 supplementary

0 + 0 duplicates

15254599 + 0 mapped (7.36% : N/A)

207269114 + 0 paired in sequencing

103634557 + 0 read1

103634557 + 0 read2

13502672 + 0 properly paired (6.51% : N/A)

13547088 + 0 with itself and mate mapped

1703249 + 0 singletons (0.82% : N/A)

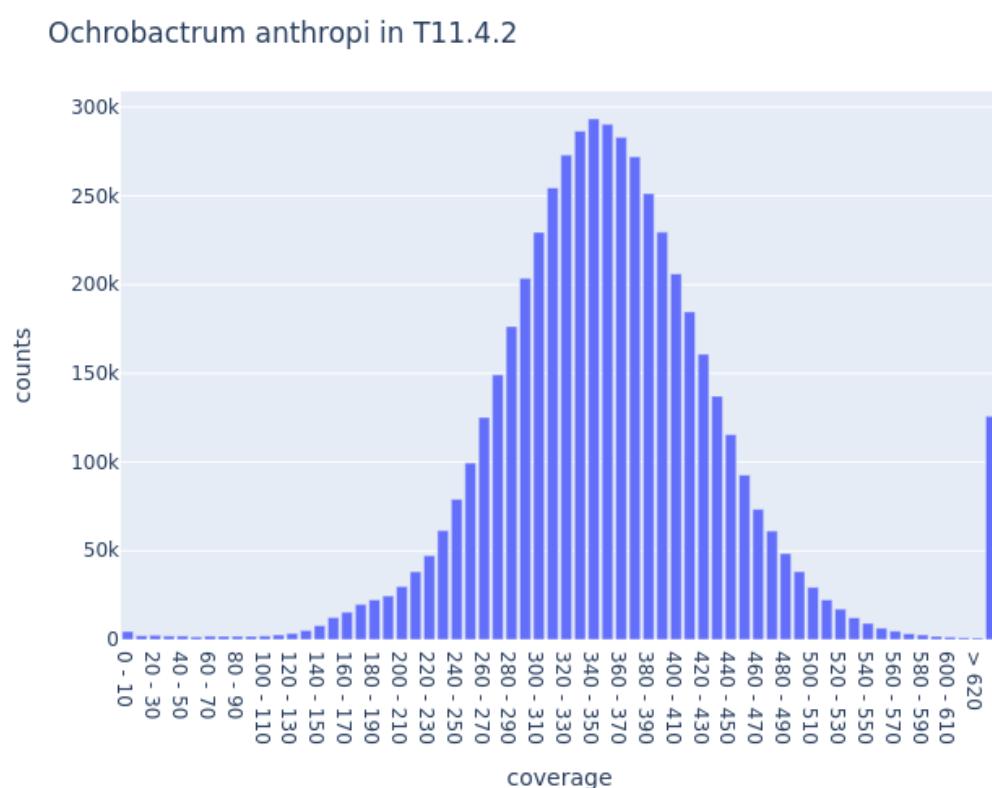
24840 + 0 with mate mapped to a different chr

17285 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 415.5930483109216

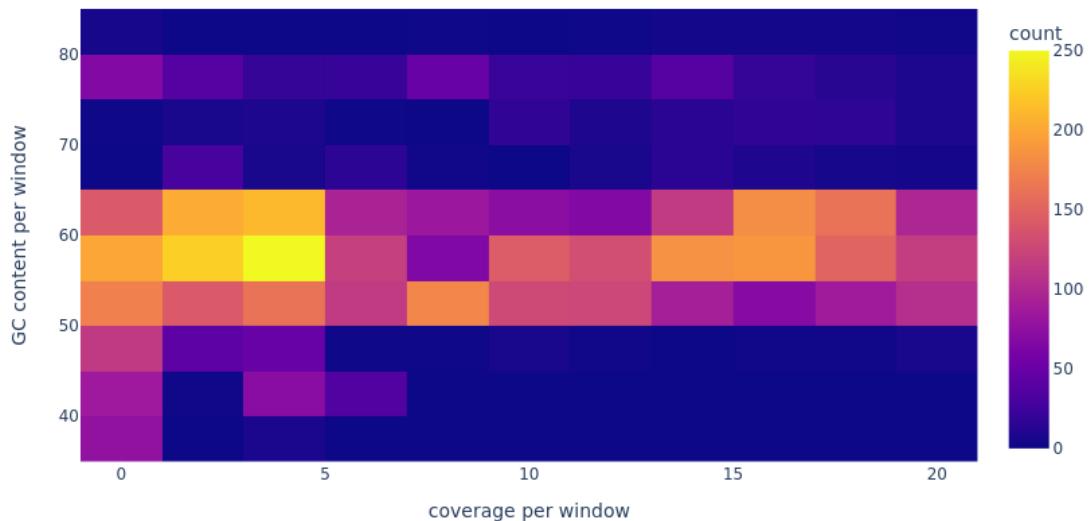


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T11.4.2



# Report of *Agrobacterium tumefaciens* in T11.4.3

## Mapping stats of Illumina reads

235639751 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

36787 + 0 supplementary

0 + 0 duplicates

189577665 + 0 mapped (80.45% : N/A)

235602964 + 0 paired in sequencing

117801482 + 0 read1

117801482 + 0 read2

188412126 + 0 properly paired (79.97% : N/A)

188994632 + 0 with itself and mate mapped

546246 + 0 singletons (0.23% : N/A)

278652 + 0 with mate mapped to a different chr

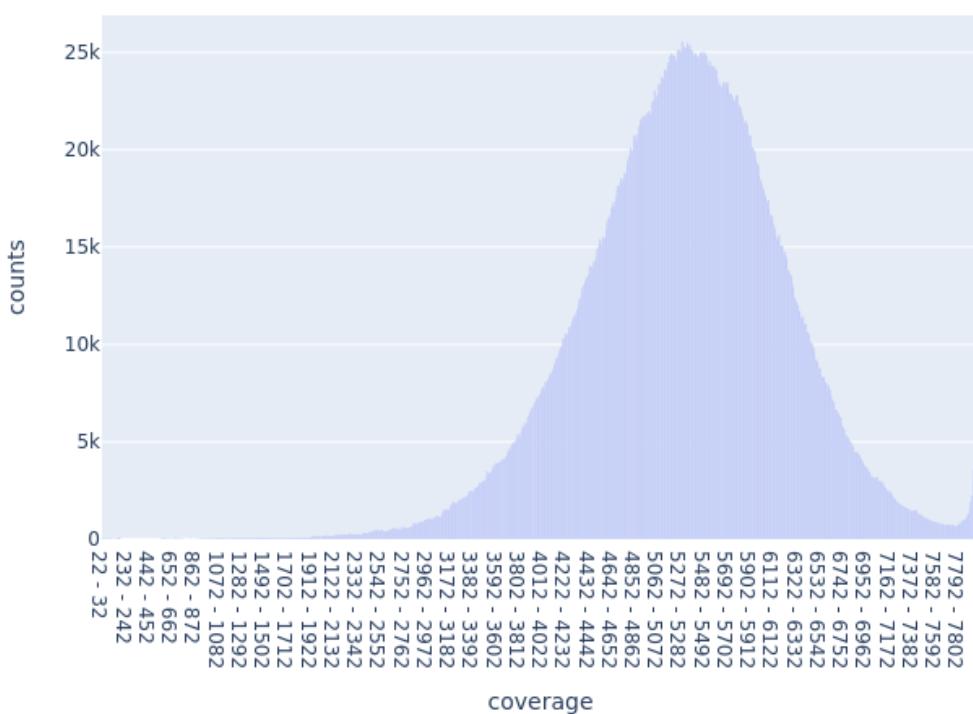
266905 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 5313.5652006049495

Agrobacterium tumefaciens in T11.4.3

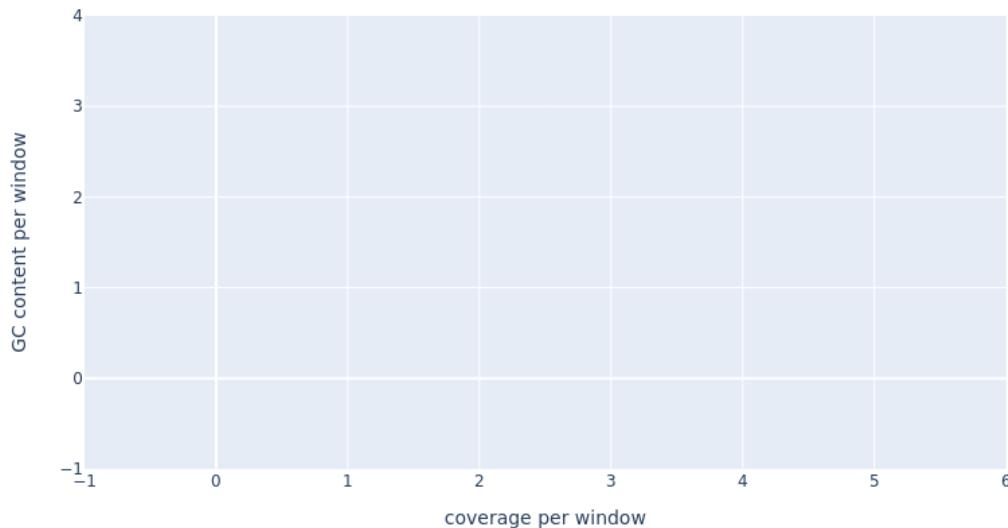


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T11.4.3



# Report of Comamonas testosterone in T11.4.3

## Mapping stats of Illumina reads

235603599 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

635 + 0 supplementary

0 + 0 duplicates

8481153 + 0 mapped (3.60% : N/A)

235602964 + 0 paired in sequencing

117801482 + 0 read1

117801482 + 0 read2

8144108 + 0 properly paired (3.46% : N/A)

8148990 + 0 with itself and mate mapped

331528 + 0 singletons (0.14% : N/A)

104 + 0 with mate mapped to a different chr

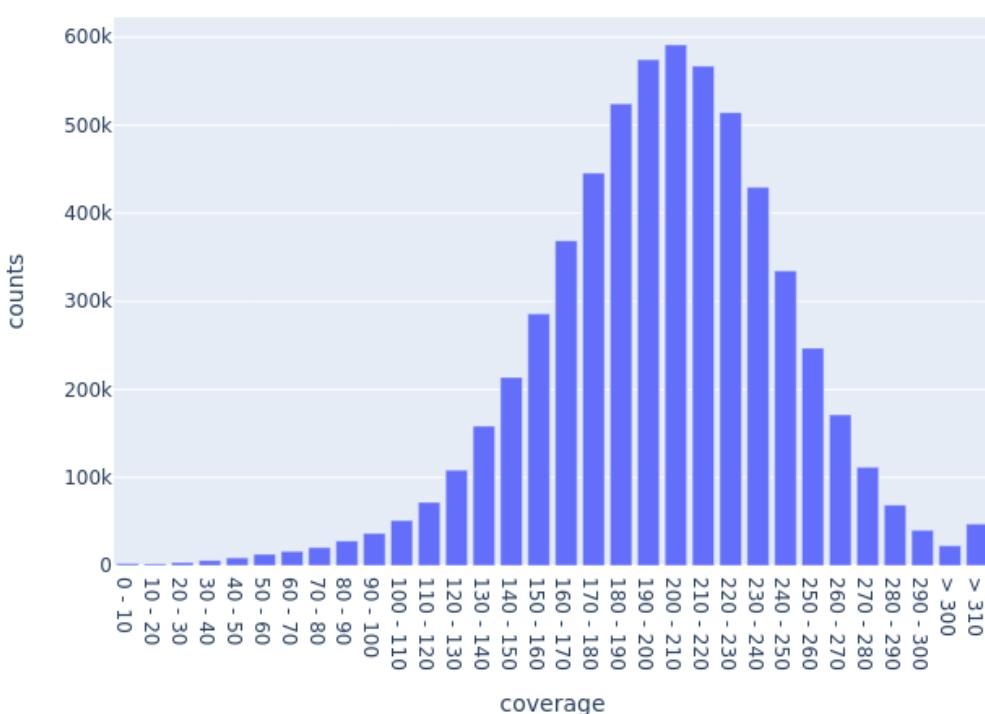
93 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 204.443173523858

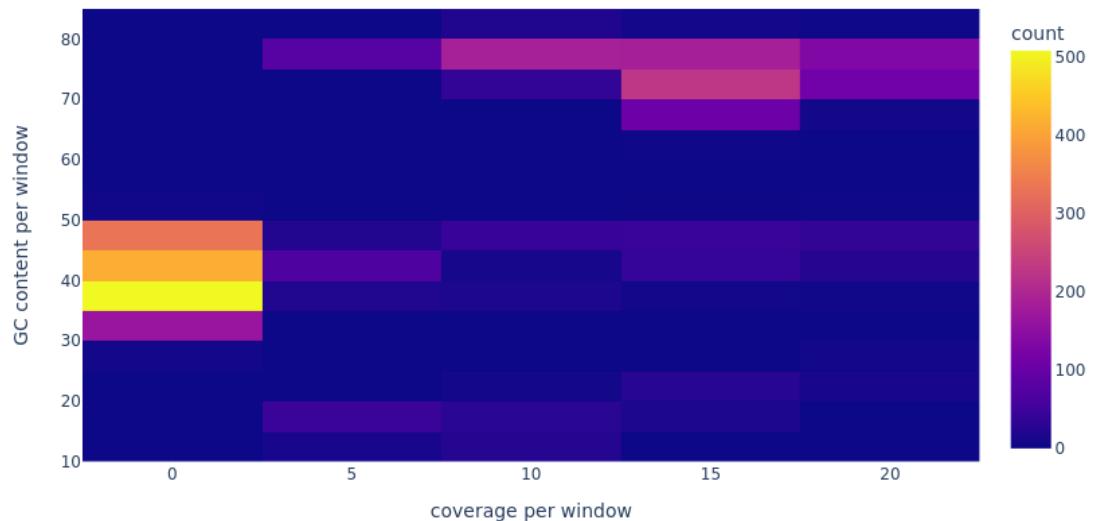
Comamonas testosterone in T11.4.3



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.4.3



# Report of *Microbacterium saperdae* in T11.4.3

## Mapping stats of Illumina reads

235603168 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

204 + 0 supplementary

0 + 0 duplicates

3630879 + 0 mapped (1.54% : N/A)

235602964 + 0 paired in sequencing

117801482 + 0 read1

117801482 + 0 read2

3503714 + 0 properly paired (1.49% : N/A)

3507520 + 0 with itself and mate mapped

123155 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

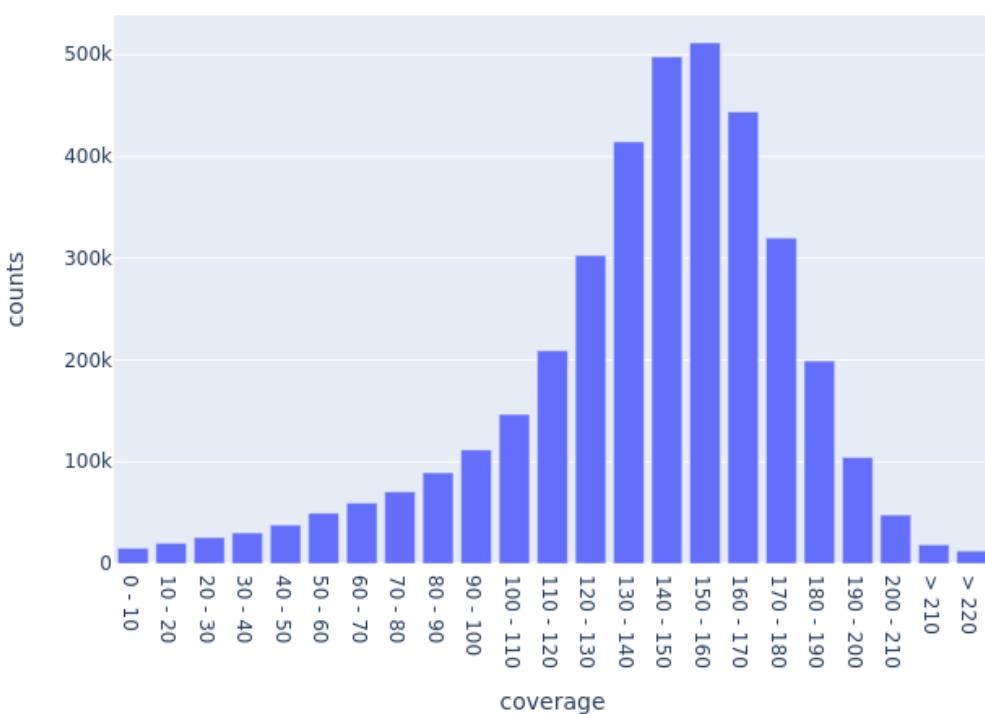
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 141.85515189979768

Microbacterium saperdae in T11.4.3

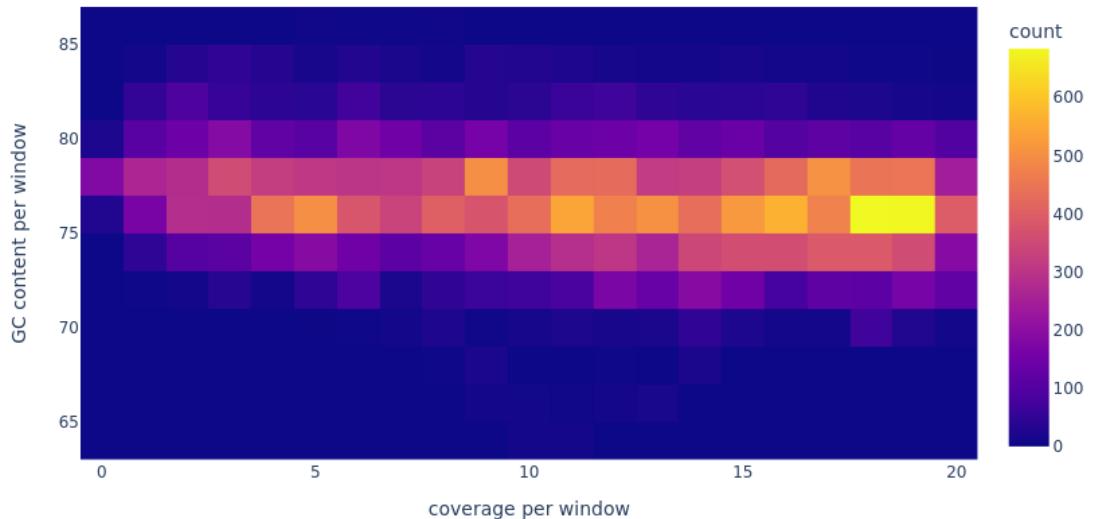


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T11.4.3



# Report of *Ochrobactrum anthropi* in T11.4.3

## Mapping stats of Illumina reads

235608534 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

5570 + 0 supplementary

0 + 0 duplicates

38220300 + 0 mapped (16.22% : N/A)

235602964 + 0 paired in sequencing

117801482 + 0 read1

117801482 + 0 read2

36349122 + 0 properly paired (15.43% : N/A)

36422088 + 0 with itself and mate mapped

1792642 + 0 singletons (0.76% : N/A)

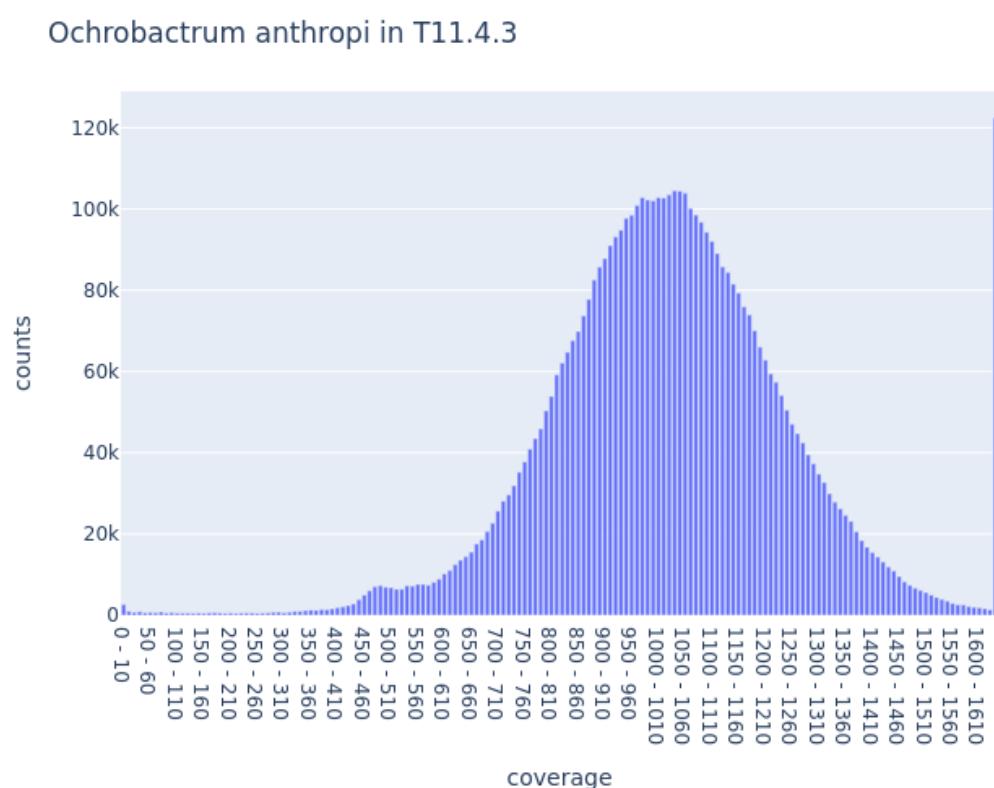
34674 + 0 with mate mapped to a different chr

26177 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 1082.696064539654

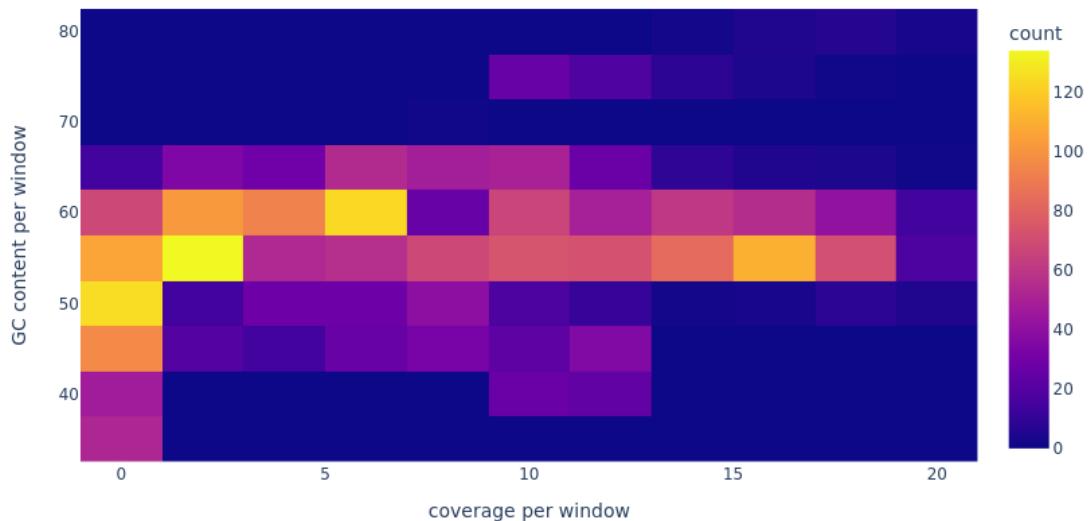


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T11.4.3



# Report of *Agrobacterium tumefaciens* in T11.4.4

## Mapping stats of Illumina reads

222659254 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

66014 + 0 supplementary

0 + 0 duplicates

198418166 + 0 mapped (89.11% : N/A)

222593240 + 0 paired in sequencing

111296620 + 0 read1

111296620 + 0 read2

197399052 + 0 properly paired (88.68% : N/A)

198044976 + 0 with itself and mate mapped

307176 + 0 singletons (0.14% : N/A)

288704 + 0 with mate mapped to a different chr

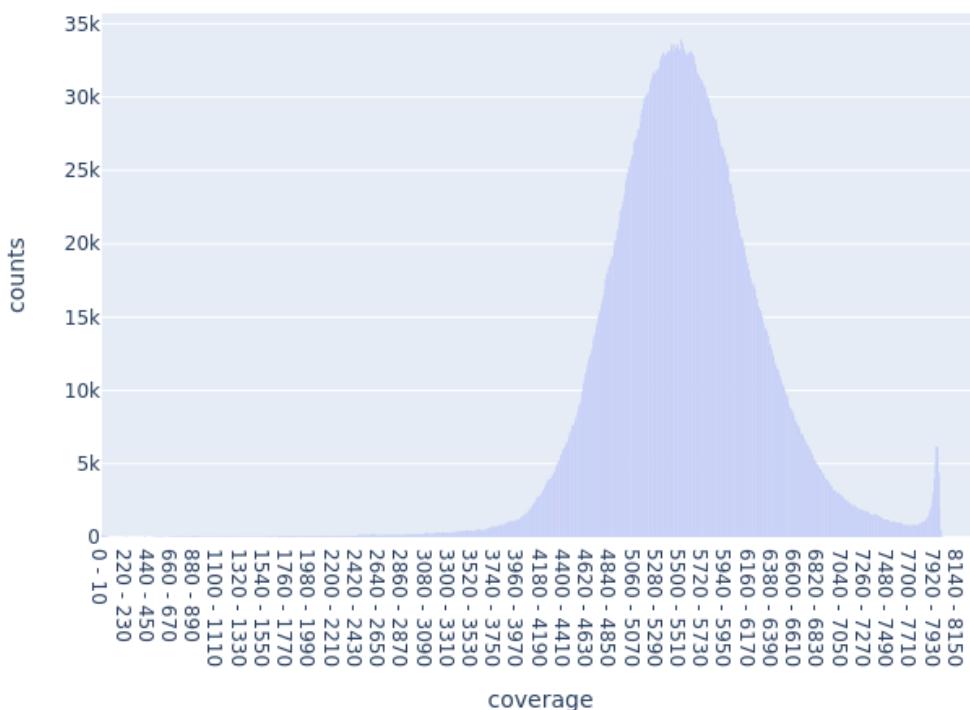
277243 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

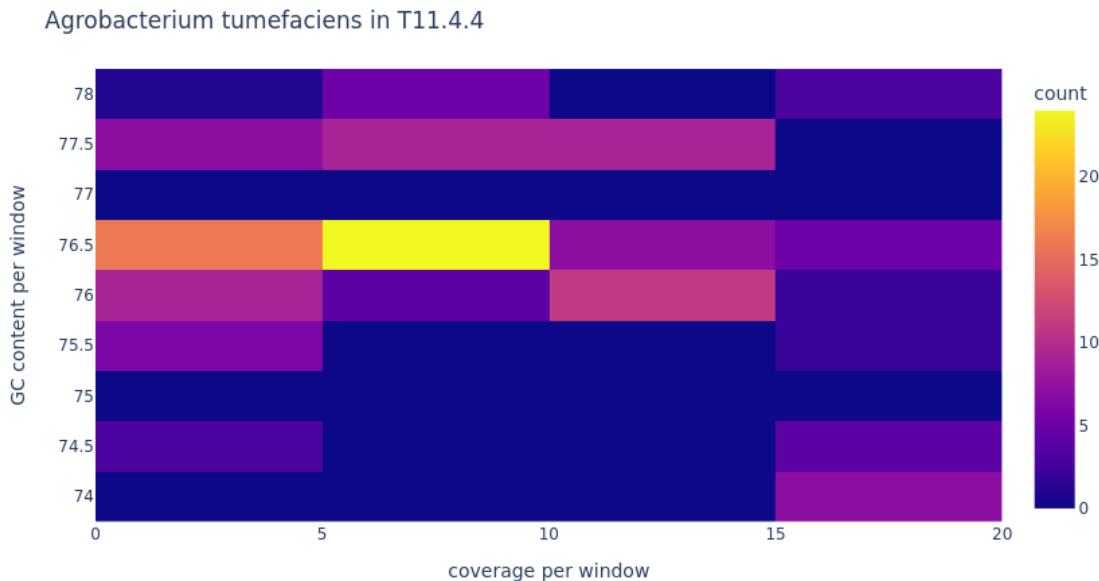
Average coverage: 5555.6619878258525

Agrobacterium tumefaciens in T11.4.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.



# Report of Comamonas testosterone in T11.4.4

## Mapping stats of Illumina reads

222594640 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1400 + 0 supplementary

0 + 0 duplicates

10359891 + 0 mapped (4.65% : N/A)

222593240 + 0 paired in sequencing

111296620 + 0 read1

111296620 + 0 read2

10010112 + 0 properly paired (4.50% : N/A)

10018368 + 0 with itself and mate mapped

340123 + 0 singletons (0.15% : N/A)

170 + 0 with mate mapped to a different chr

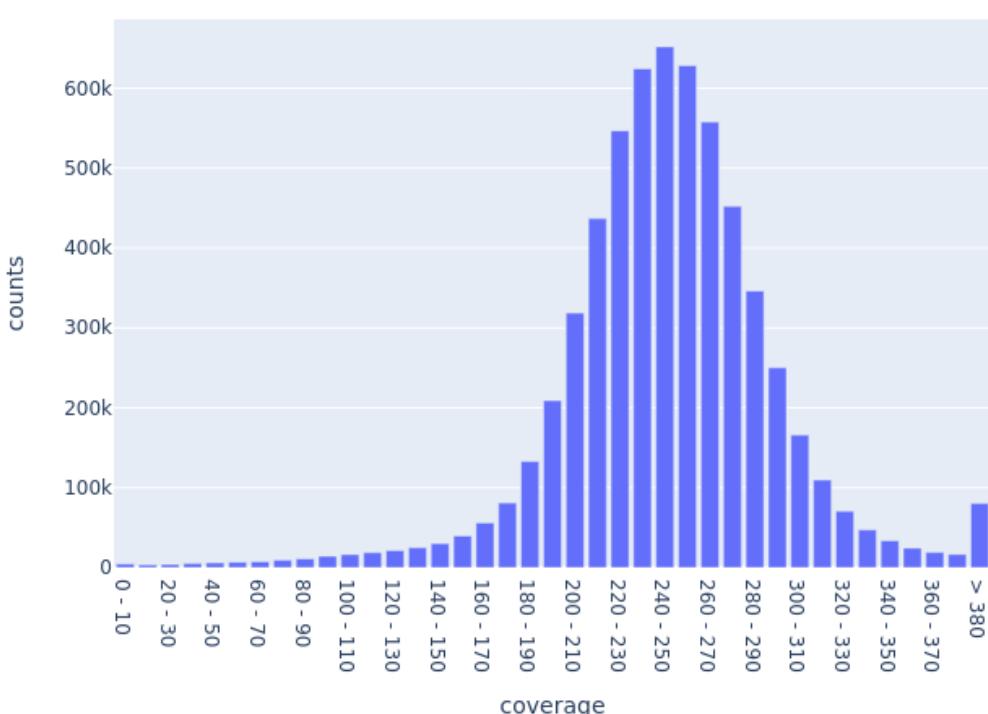
145 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 250.7987972830806

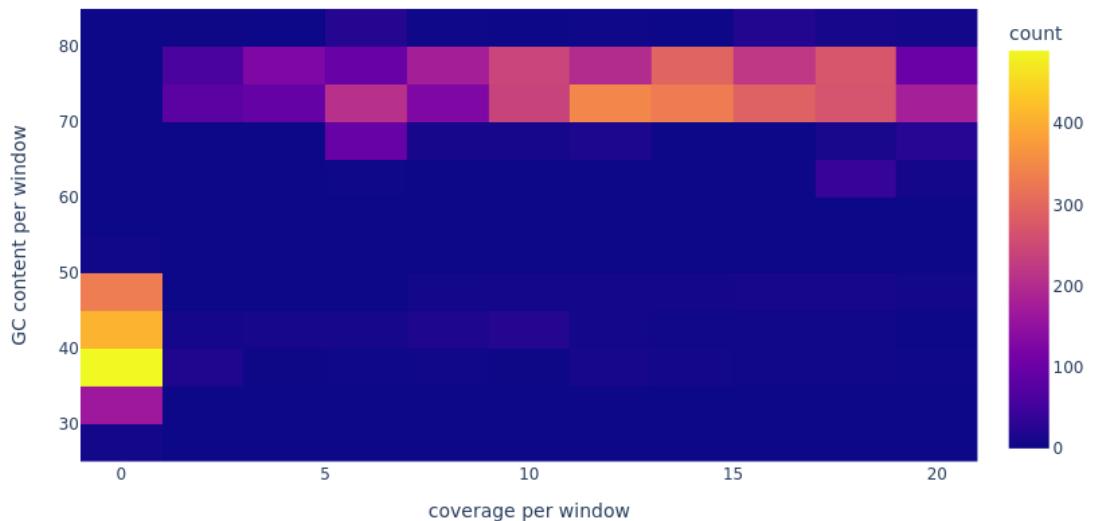
Comamonas testosterone in T11.4.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.4.4



# Report of *Microbacterium saperdae* in T11.4.4

## Mapping stats of Illumina reads

222593248 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

8 + 0 supplementary

0 + 0 duplicates

196336 + 0 mapped (0.09% : N/A)

222593240 + 0 paired in sequencing

111296620 + 0 read1

111296620 + 0 read2

81910 + 0 properly paired (0.04% : N/A)

84006 + 0 with itself and mate mapped

112322 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

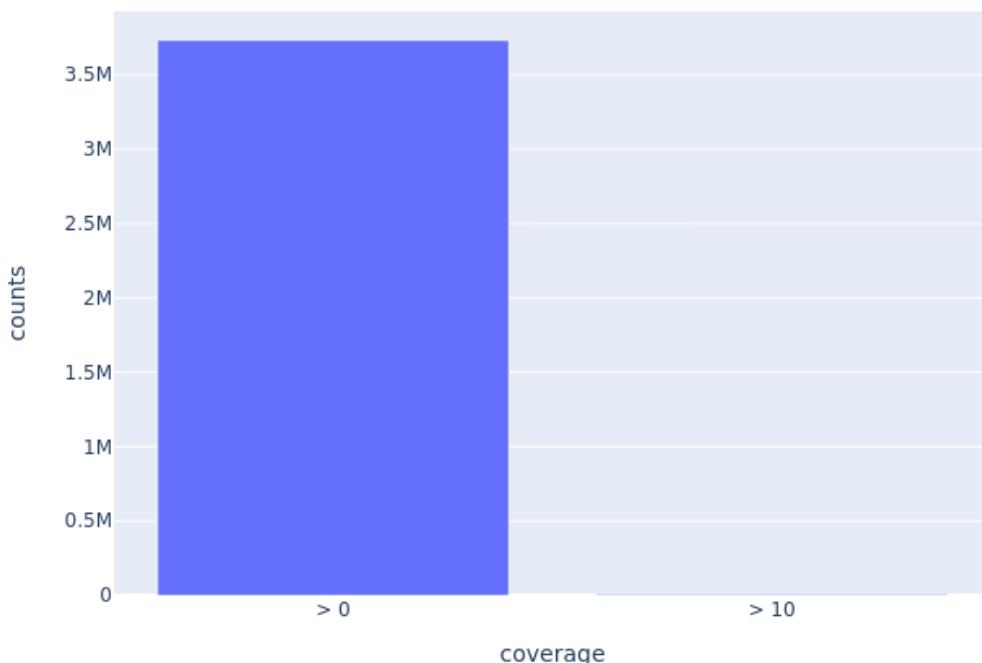
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 3.4950112350892253

Microbacterium saperdae in T11.4.4

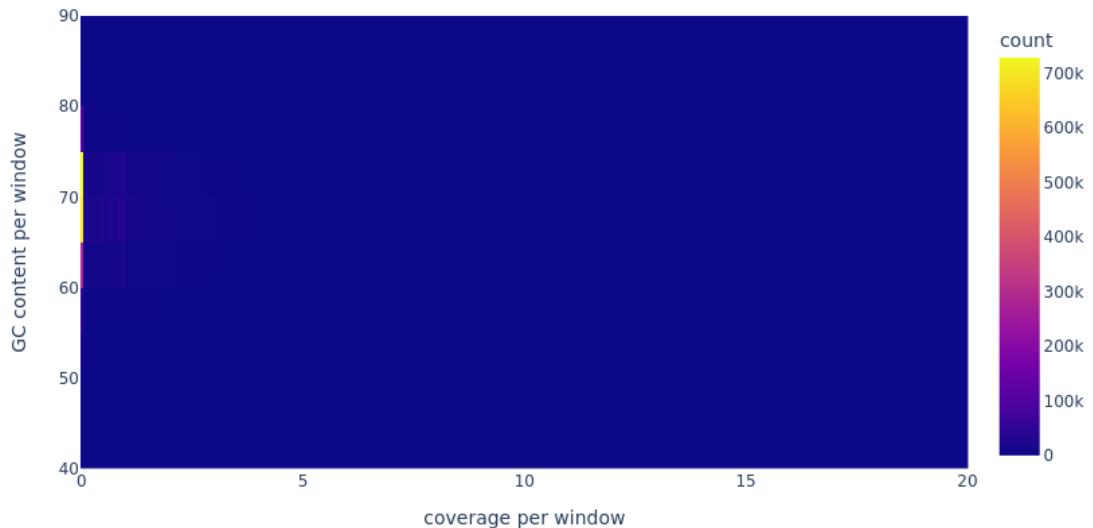


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T11.4.4



# Report of *Ochrobactrum anthropi* in T11.4.4

## Mapping stats of Illumina reads

222598393 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

5153 + 0 supplementary

0 + 0 duplicates

17477938 + 0 mapped (7.85% : N/A)

222593240 + 0 paired in sequencing

111296620 + 0 read1

111296620 + 0 read2

15619888 + 0 properly paired (7.02% : N/A)

15668216 + 0 with itself and mate mapped

1804569 + 0 singletons (0.81% : N/A)

25804 + 0 with mate mapped to a different chr

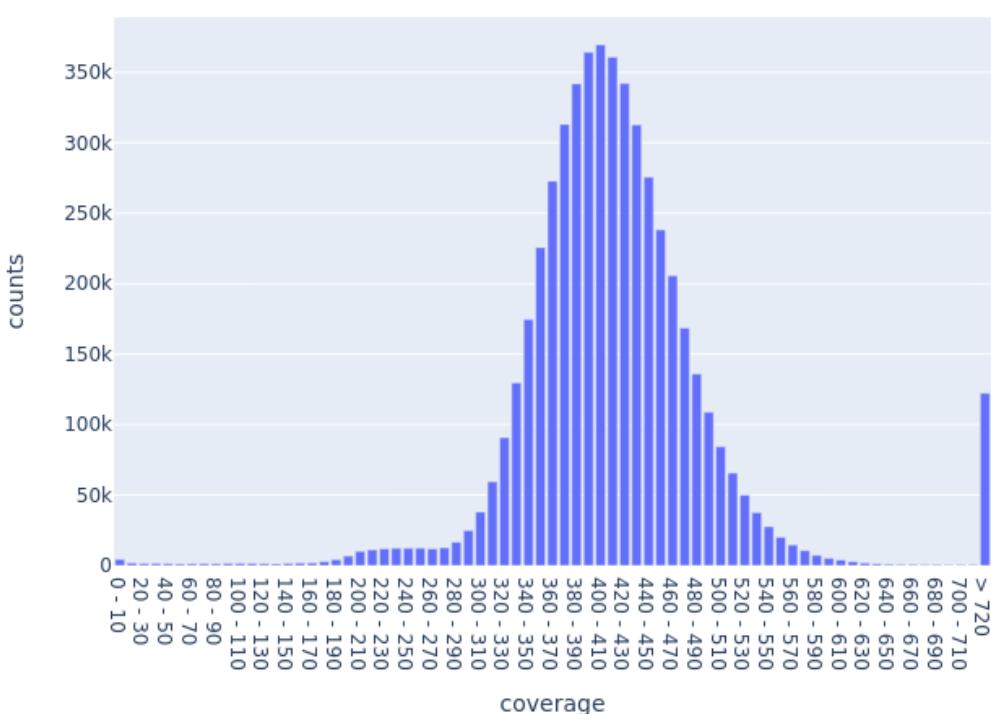
17878 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 477.8706856612829

Ochrobactrum anthropi in T11.4.4

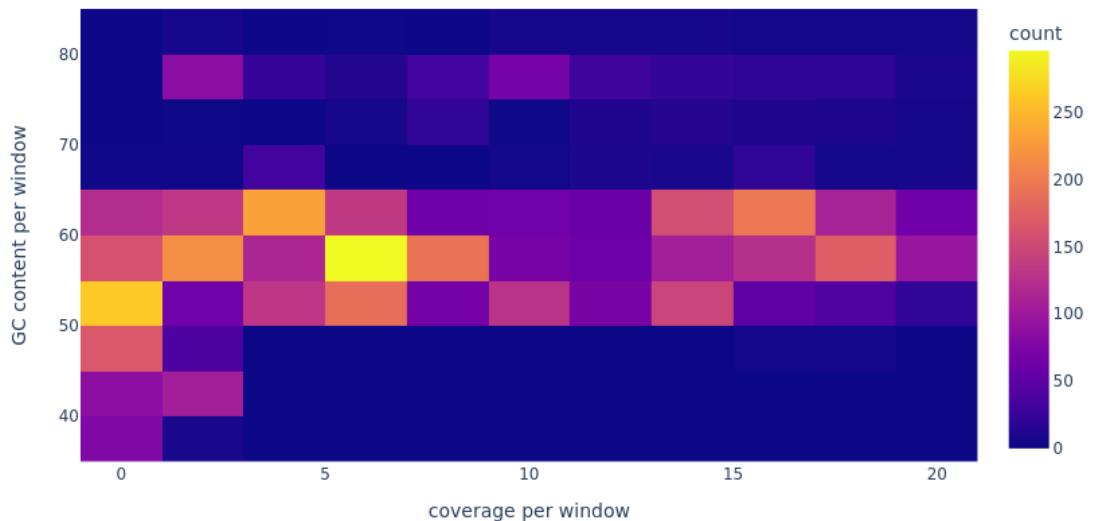


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T11.4.4



# Report of *Agrobacterium tumefaciens* in T11.4.5

## Mapping stats of Illumina reads

169157194 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

27888 + 0 supplementary

0 + 0 duplicates

158920323 + 0 mapped (93.95% : N/A)

169129306 + 0 paired in sequencing

84564653 + 0 read1

84564653 + 0 read2

158280566 + 0 properly paired (93.59% : N/A)

158737296 + 0 with itself and mate mapped

155139 + 0 singletons (0.09% : N/A)

214294 + 0 with mate mapped to a different chr

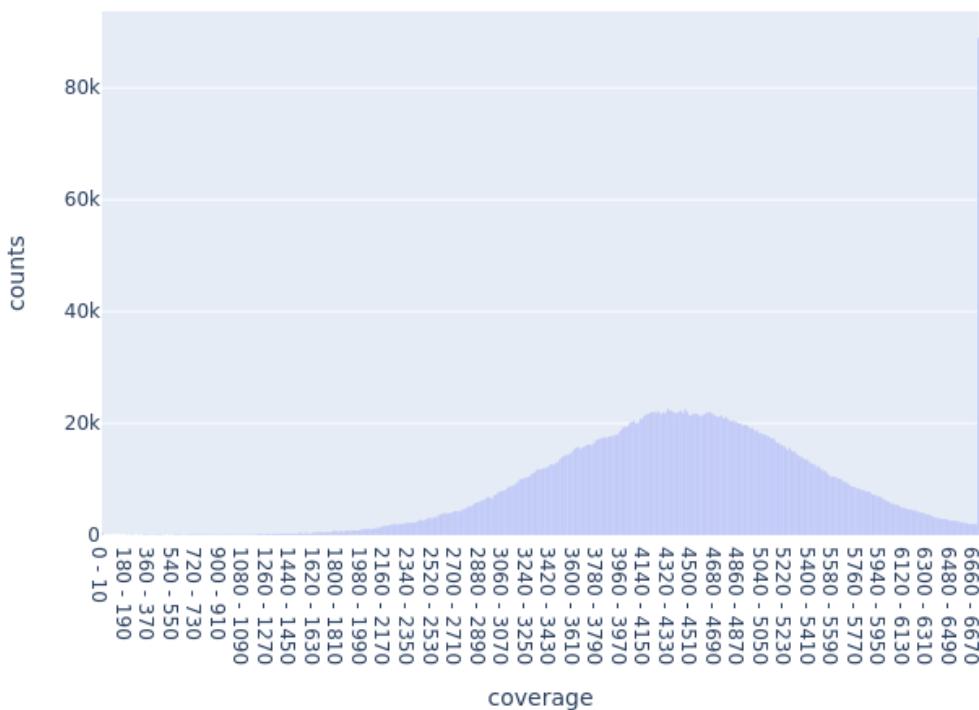
206928 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 4458.827330114142

Agrobacterium tumefaciens in T11.4.5

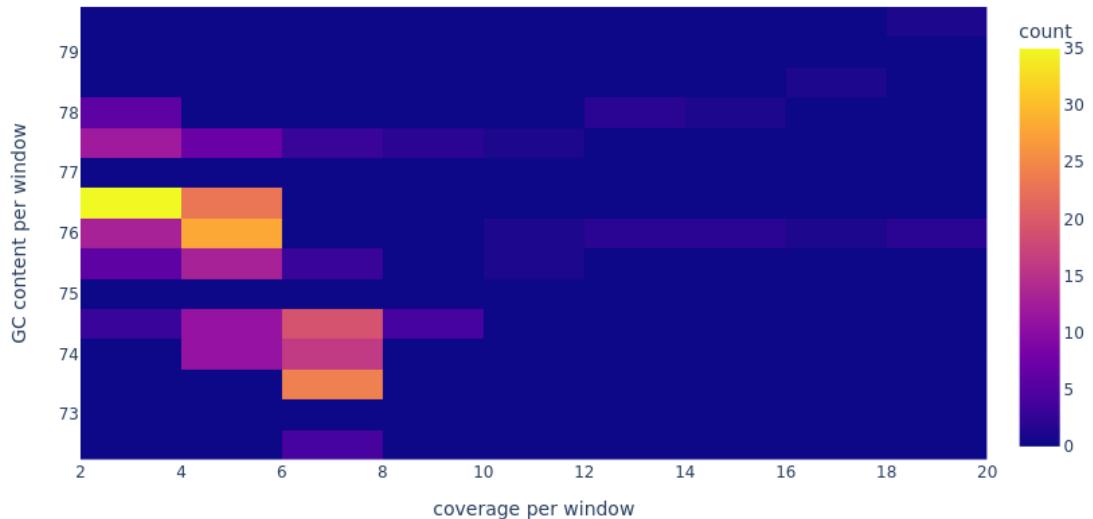


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T11.4.5



# Report of Comamonas testosterone in T11.4.5

## Mapping stats of Illumina reads

169129804 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

498 + 0 supplementary

0 + 0 duplicates

3738056 + 0 mapped (2.21% : N/A)

169129306 + 0 paired in sequencing

84564653 + 0 read1

84564653 + 0 read2

3495180 + 0 properly paired (2.07% : N/A)

3498032 + 0 with itself and mate mapped

239526 + 0 singletons (0.14% : N/A)

28 + 0 with mate mapped to a different chr

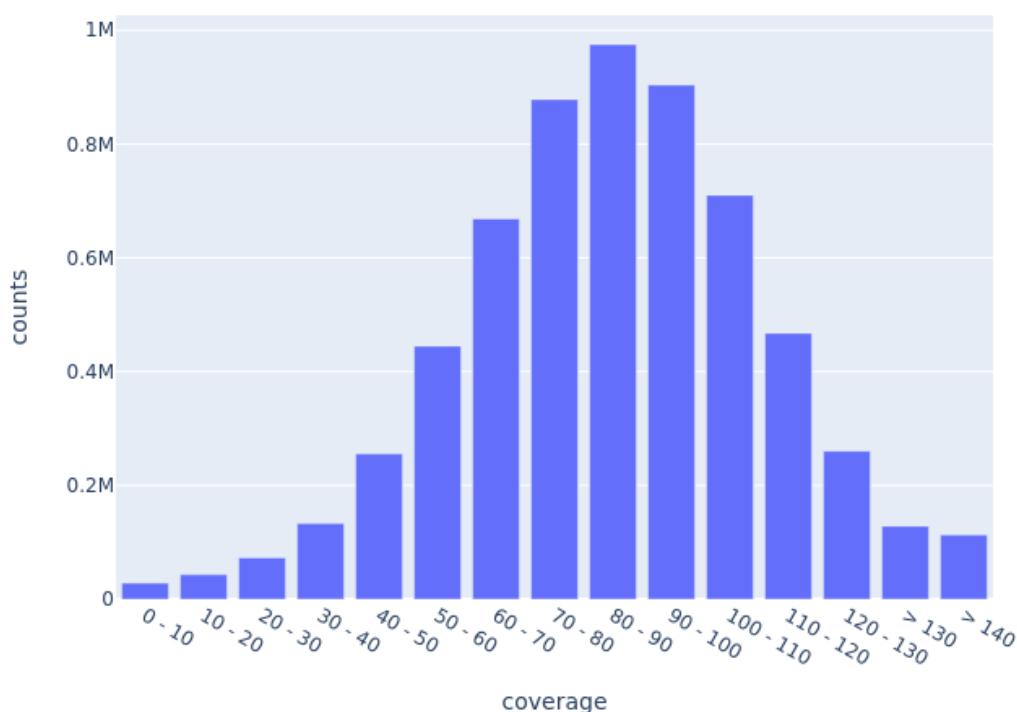
19 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 88.37143799601307

Comamonas testosterone in T11.4.5

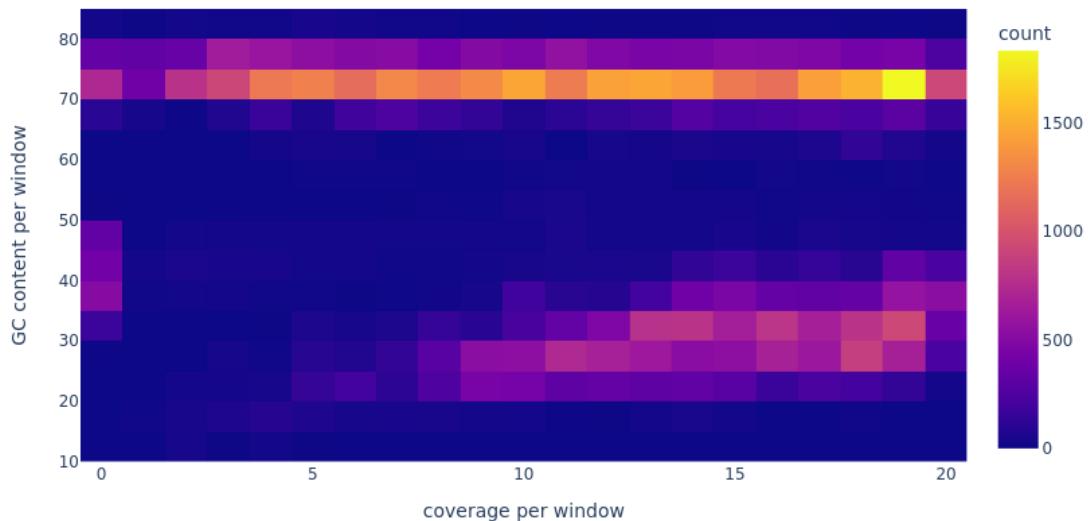


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T11.4.5



# Report of *Microbacterium saperdae* in T11.4.5

## Mapping stats of Illumina reads

169129312 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

6 + 0 supplementary

0 + 0 duplicates

137337 + 0 mapped (0.08% : N/A)

169129306 + 0 paired in sequencing

84564653 + 0 read1

84564653 + 0 read2

50922 + 0 properly paired (0.03% : N/A)

52832 + 0 with itself and mate mapped

84499 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

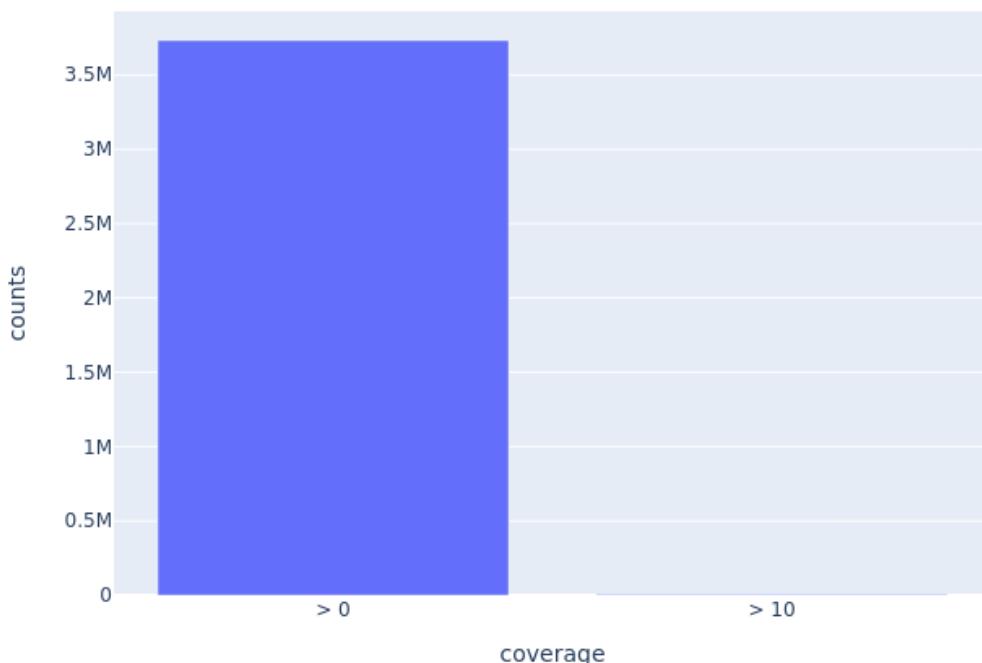
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 2.3432770606716224

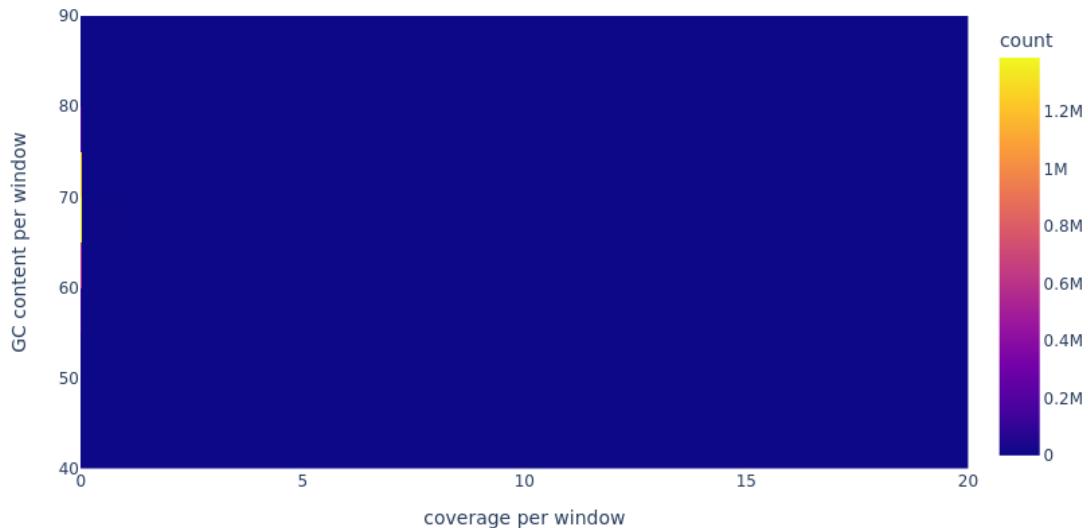
Microbacterium saperdae in T11.4.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T11.4.5



# Report of *Ochrobactrum anthropi* in T11.4.5

## Mapping stats of Illumina reads

169132525 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

3219 + 0 supplementary

0 + 0 duplicates

9525574 + 0 mapped (5.63% : N/A)

169129306 + 0 paired in sequencing

84564653 + 0 read1

84564653 + 0 read2

8067072 + 0 properly paired (4.77% : N/A)

8104832 + 0 with itself and mate mapped

1417523 + 0 singletons (0.84% : N/A)

21896 + 0 with mate mapped to a different chr

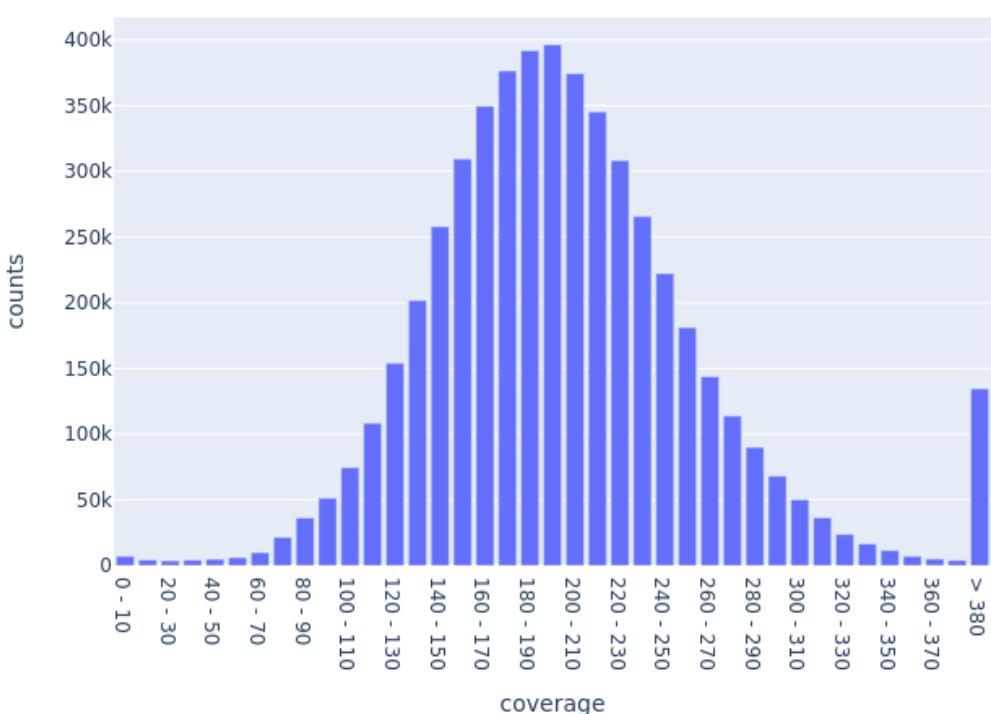
15308 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 252.9154103802373

Ochrobactrum anthropi in T11.4.5

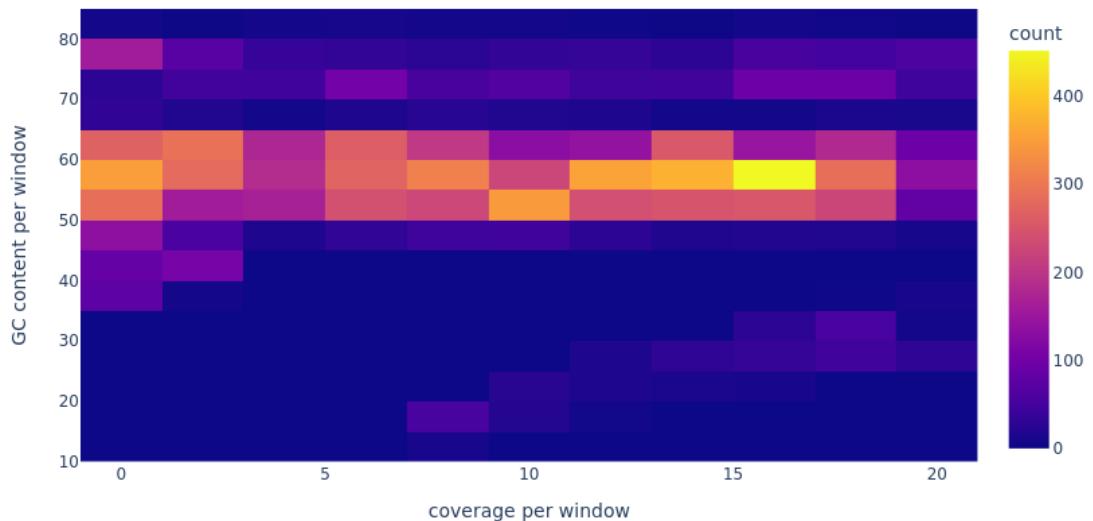


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T11.4.5



# Report of *Agrobacterium tumefaciens* in T22.1.1

## Mapping stats of Illumina reads

4128512 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1226 + 0 supplementary

0 + 0 duplicates

4107692 + 0 mapped (99.50% : N/A)

4127286 + 0 paired in sequencing

2063643 + 0 read1

2063643 + 0 read2

4074252 + 0 properly paired (98.72% : N/A)

4094474 + 0 with itself and mate mapped

11992 + 0 singletons (0.29% : N/A)

9194 + 0 with mate mapped to a different chr

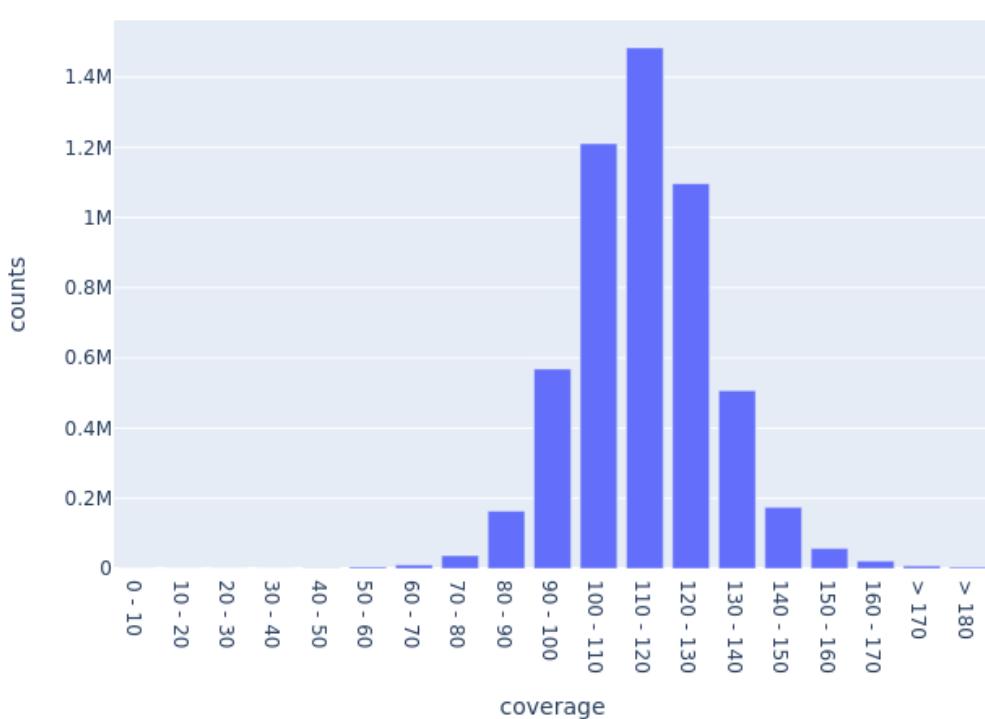
8841 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

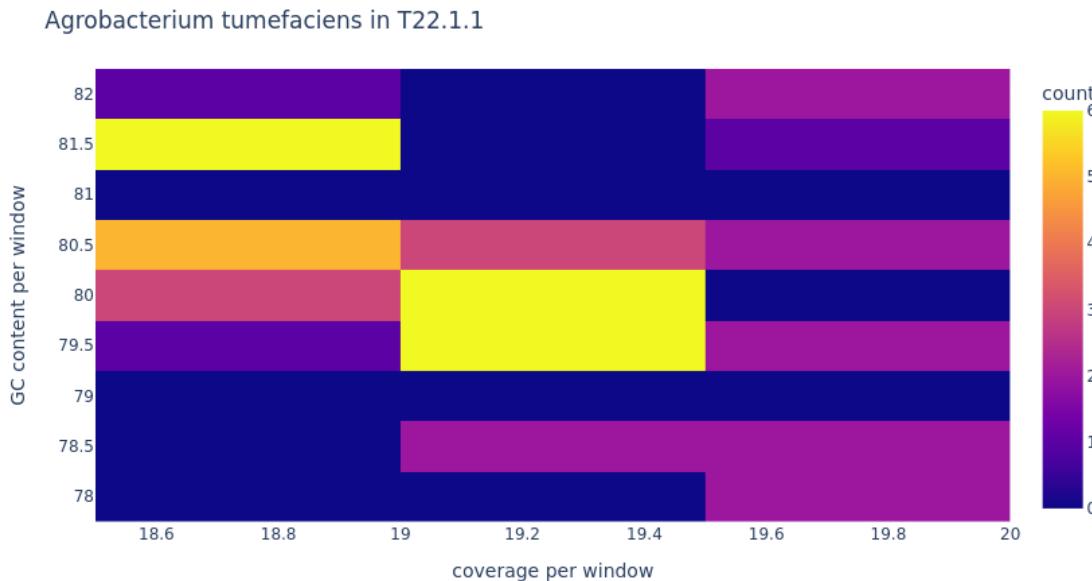
Average coverage: 114.4583169971209

Agrobacterium tumefaciens in T22.1.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.



# Report of *Agrobacterium tumefaciens* in T22.1.2

## Mapping stats of Illumina reads

4285090 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

946 + 0 supplementary

0 + 0 duplicates

4264168 + 0 mapped (99.51% : N/A)

4284144 + 0 paired in sequencing

2142072 + 0 read1

2142072 + 0 read2

4240648 + 0 properly paired (98.98% : N/A)

4254994 + 0 with itself and mate mapped

8228 + 0 singletons (0.19% : N/A)

6250 + 0 with mate mapped to a different chr

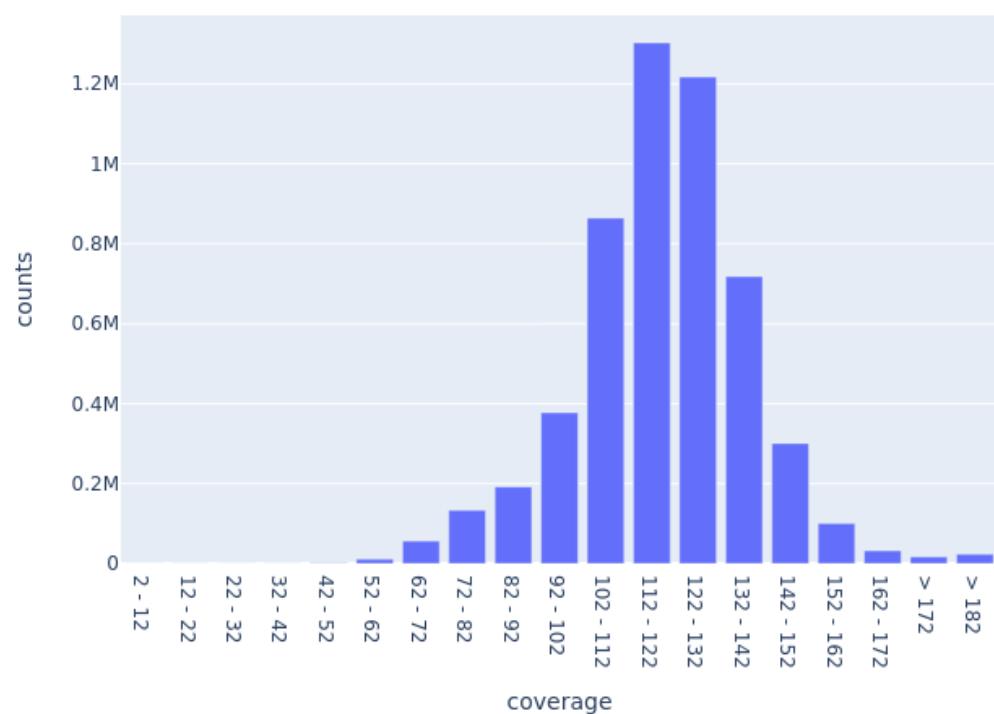
6041 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 118.97313494674349

Agrobacterium tumefaciens in T22.1.2

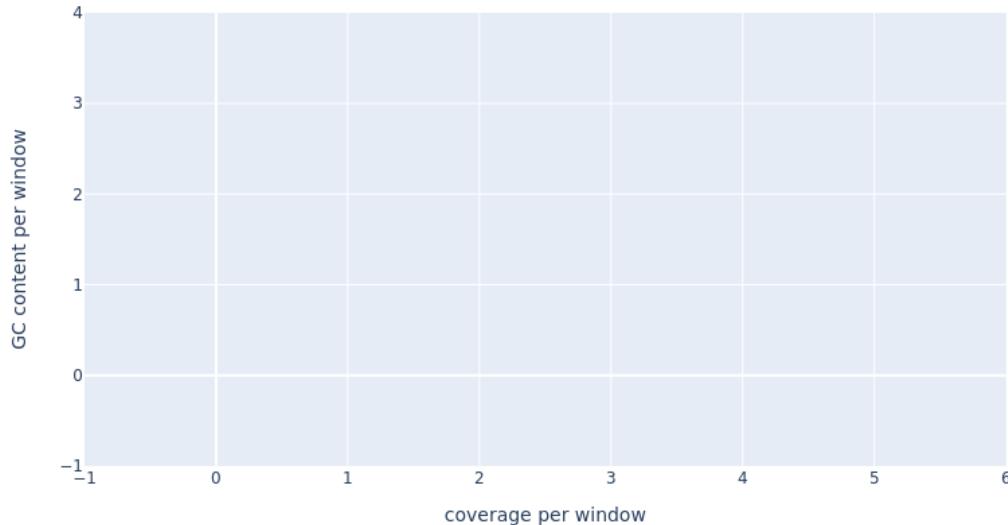


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T22.1.2



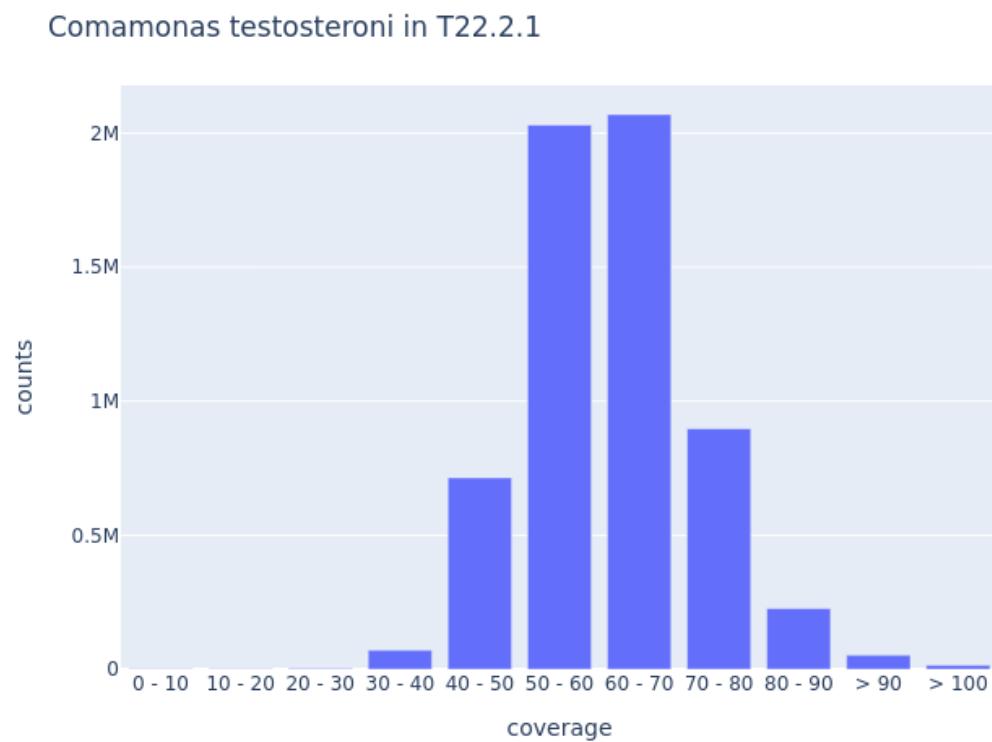
# Report of Comamonas testosterone in T22.2.1

## Mapping stats of Illumina reads

2902745 + 0 in total (QC-passed reads + QC-failed reads)  
0 + 0 secondary  
855 + 0 supplementary  
0 + 0 duplicates  
2488024 + 0 mapped (85.71% : N/A)  
2901890 + 0 paired in sequencing  
1450945 + 0 read1  
1450945 + 0 read2  
2476738 + 0 properly paired (85.35% : N/A)  
2481826 + 0 with itself and mate mapped  
5343 + 0 singletons (0.18% : N/A)  
180 + 0 with mate mapped to a different chr  
161 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.  
Average coverage: 60.99150071058878

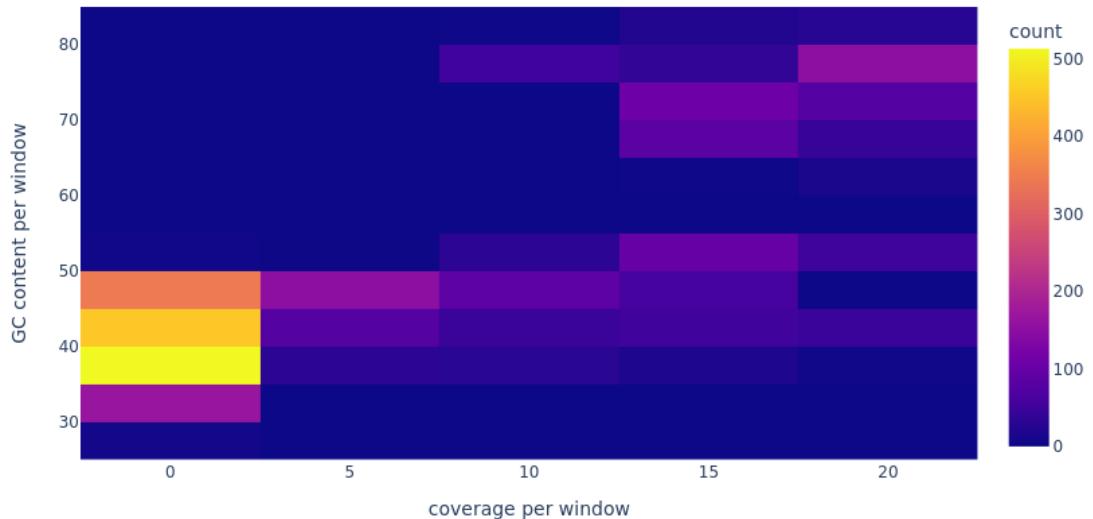


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.2.1



# Report of Comamonas testosterone in T22.2.2

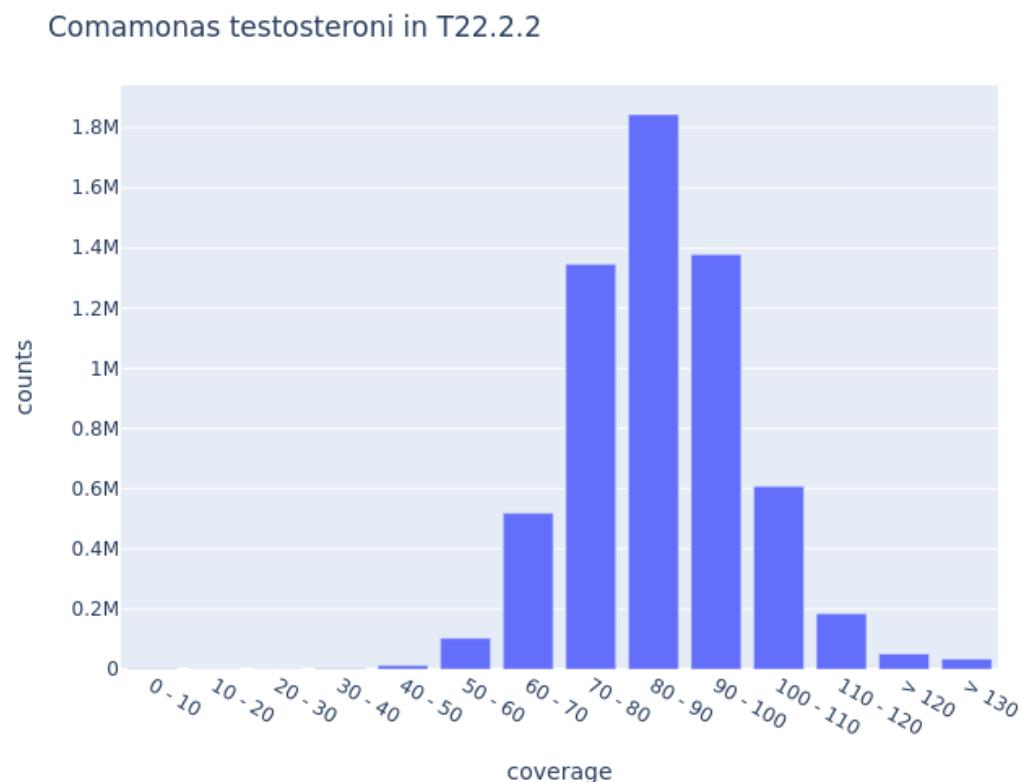
## Mapping stats of Illumina reads

3547300 + 0 in total (QC-passed reads + QC-failed reads)  
0 + 0 secondary  
1740 + 0 supplementary  
0 + 0 duplicates  
3498389 + 0 mapped (98.62% : N/A)  
3545560 + 0 paired in sequencing  
1772780 + 0 read1  
1772780 + 0 read2  
3481182 + 0 properly paired (98.18% : N/A)  
3490132 + 0 with itself and mate mapped  
6517 + 0 singletons (0.18% : N/A)  
536 + 0 with mate mapped to a different chr  
462 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

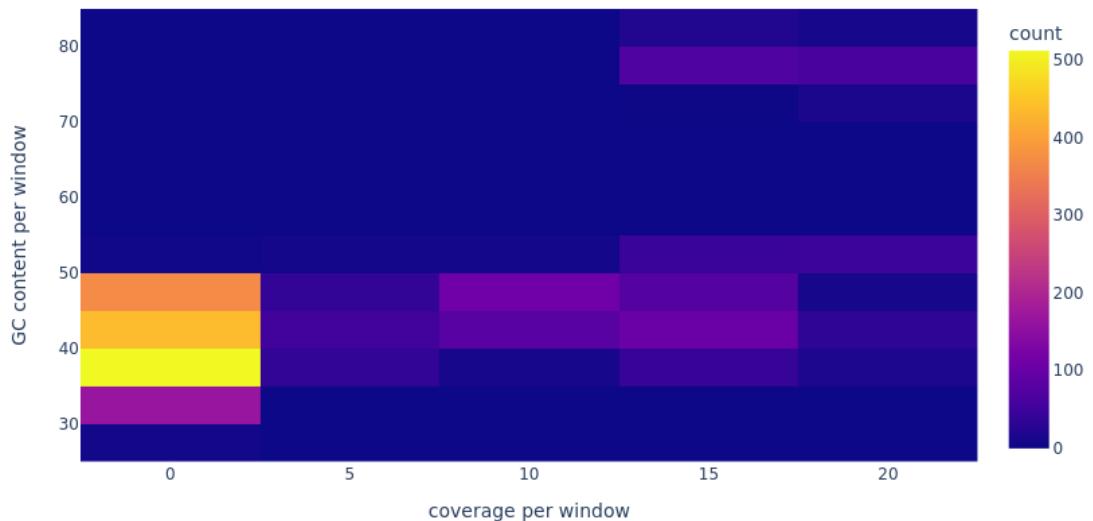
Average coverage: 85.75227676853773



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.2.2



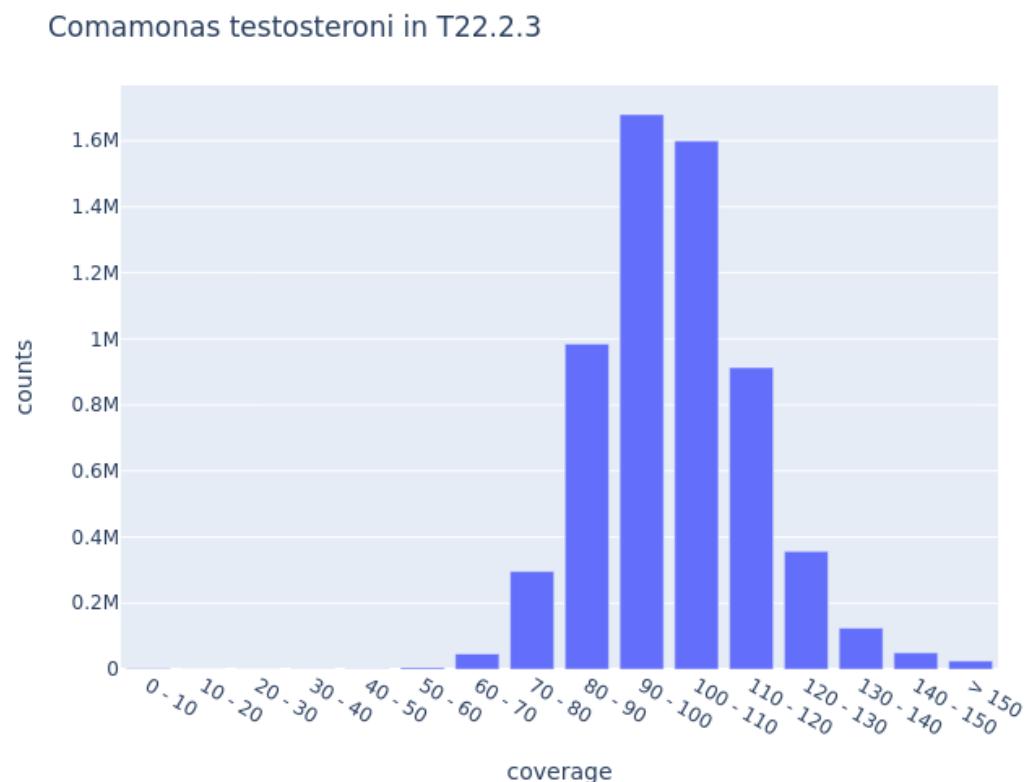
# Report of Comamonas testosterone in T22.2.3

## Mapping stats of Illumina reads

4121632 + 0 in total (QC-passed reads + QC-failed reads)  
0 + 0 secondary  
1428 + 0 supplementary  
0 + 0 duplicates  
4094519 + 0 mapped (99.34% : N/A)  
4120204 + 0 paired in sequencing  
2060102 + 0 read1  
2060102 + 0 read2  
4081428 + 0 properly paired (99.06% : N/A)  
4087772 + 0 with itself and mate mapped  
5319 + 0 singletons (0.13% : N/A)  
186 + 0 with mate mapped to a different chr  
171 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.  
Average coverage: 100.48108101533909

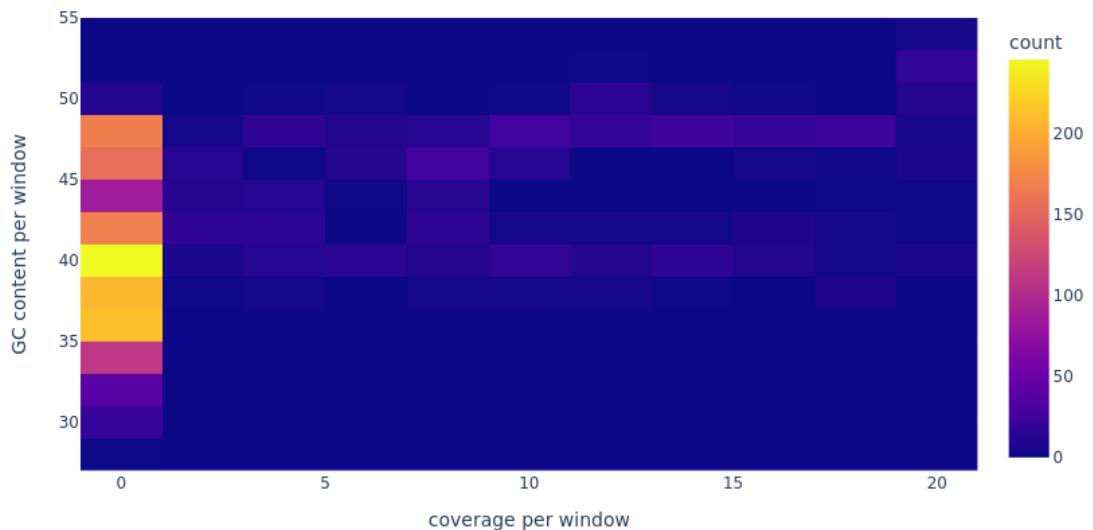


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.2.3



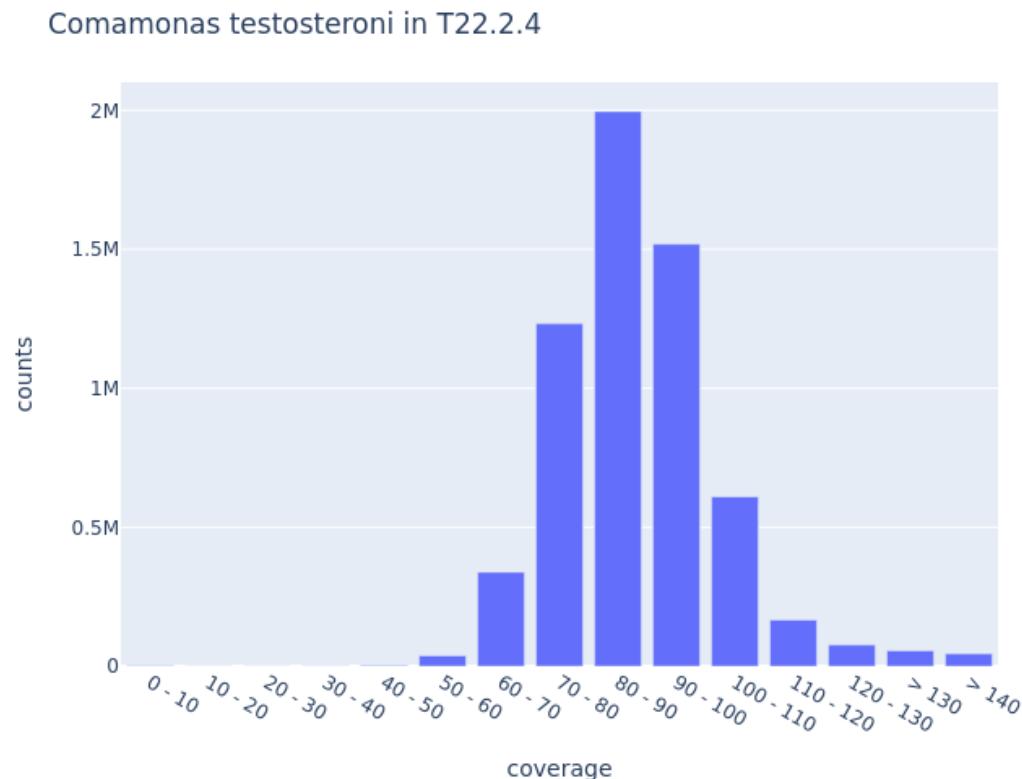
# Report of Comamonas testosterone in T22.2.4

## Mapping stats of Illumina reads

3691019 + 0 in total (QC-passed reads + QC-failed reads)  
0 + 0 secondary  
1237 + 0 supplementary  
0 + 0 duplicates  
3586631 + 0 mapped (97.17% : N/A)  
3689782 + 0 paired in sequencing  
1844891 + 0 read1  
1844891 + 0 read2  
3567194 + 0 properly paired (96.68% : N/A)  
3577460 + 0 with itself and mate mapped  
7934 + 0 singletons (0.22% : N/A)  
656 + 0 with mate mapped to a different chr  
636 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

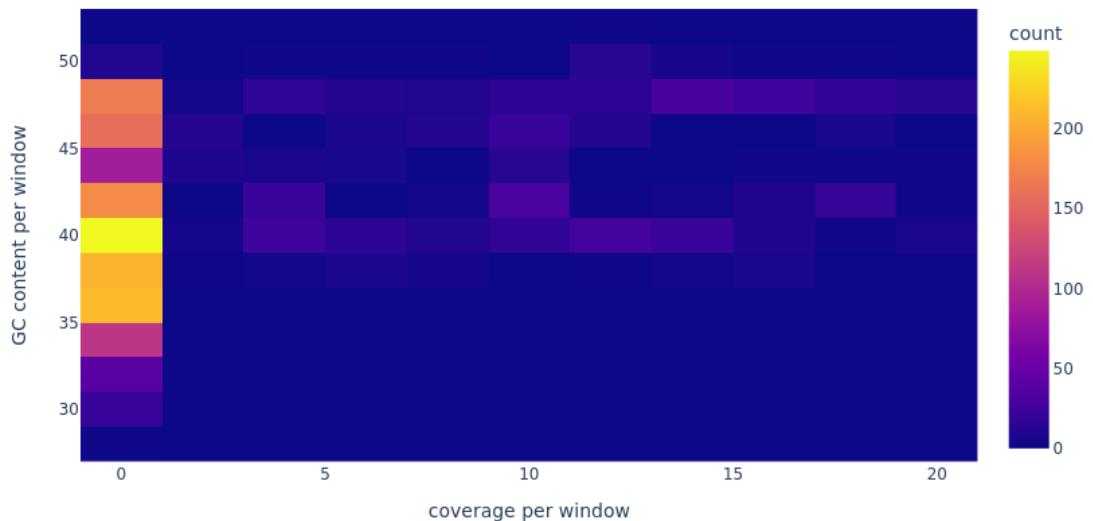
This plots shows the coverage per position in the genome.  
Average coverage: 87.89198869697887



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.2.4



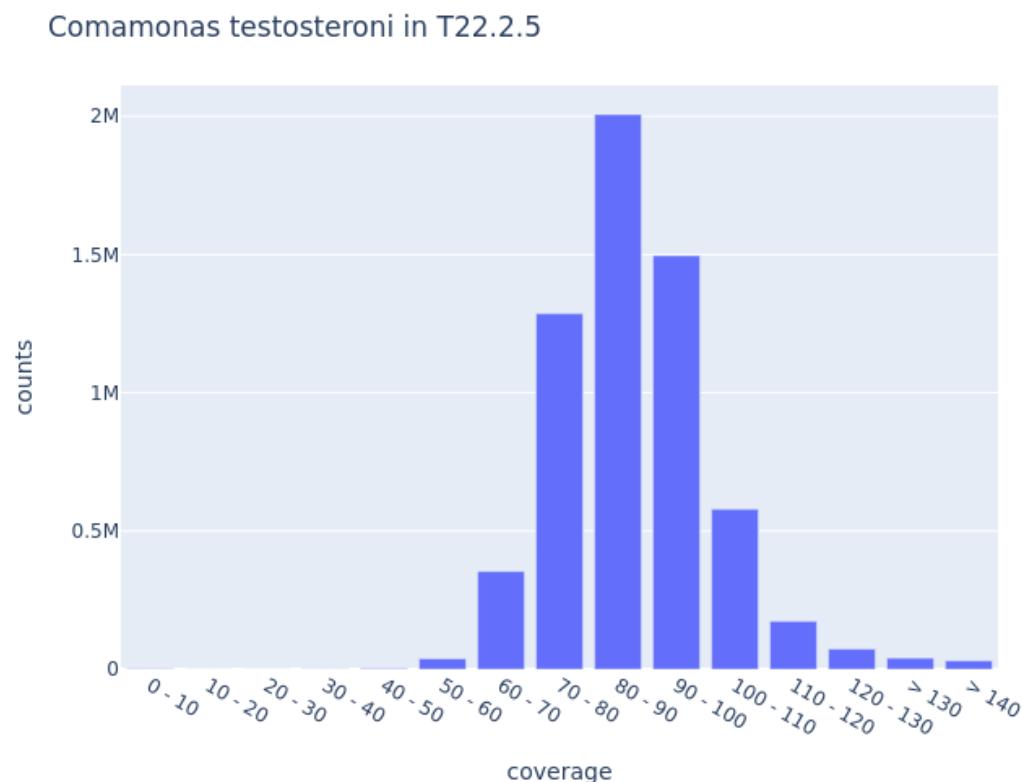
# Report of Comamonas testosterone in T22.2.5

## Mapping stats of Illumina reads

3572707 + 0 in total (QC-passed reads + QC-failed reads)  
0 + 0 secondary  
1357 + 0 supplementary  
0 + 0 duplicates  
3564187 + 0 mapped (99.76% : N/A)  
3571350 + 0 paired in sequencing  
1785675 + 0 read1  
1785675 + 0 read2  
3544542 + 0 properly paired (99.25% : N/A)  
3555146 + 0 with itself and mate mapped  
7684 + 0 singletons (0.22% : N/A)  
514 + 0 with mate mapped to a different chr  
499 + 0 with mate mapped to a different chr (mapQ>=5)

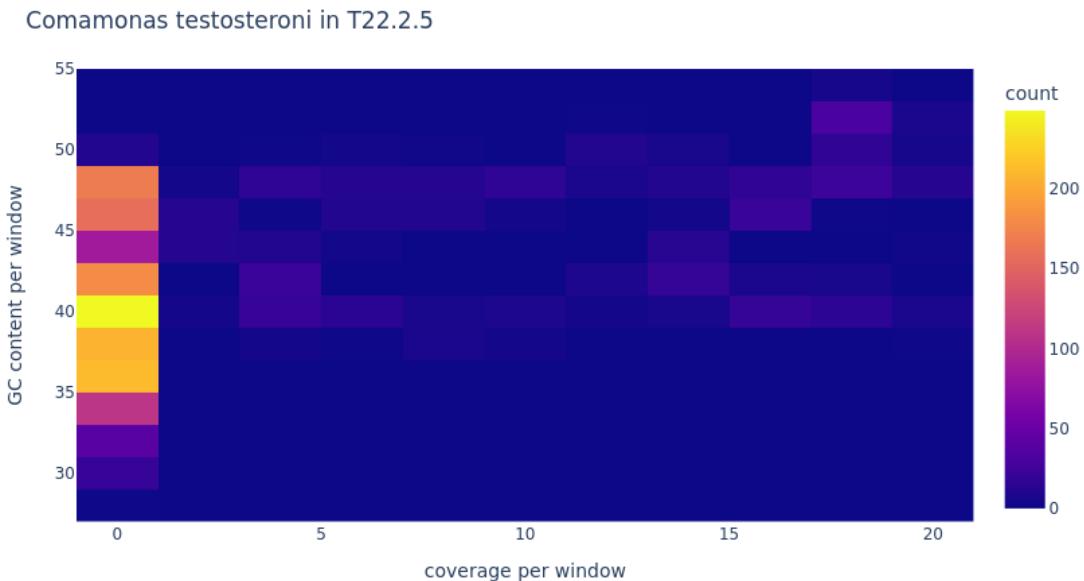
## Coverage plot

This plots shows the coverage per position in the genome.  
Average coverage: 87.34176156660543



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.



# Report of *Agrobacterium tumefaciens* in T22.3.1

## Mapping stats of Illumina reads

57924386 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

14672 + 0 supplementary

0 + 0 duplicates

52912157 + 0 mapped (91.35% : N/A)

57909714 + 0 paired in sequencing

28954857 + 0 read1

28954857 + 0 read2

52620730 + 0 properly paired (90.87% : N/A)

52775642 + 0 with itself and mate mapped

121843 + 0 singletons (0.21% : N/A)

67352 + 0 with mate mapped to a different chr

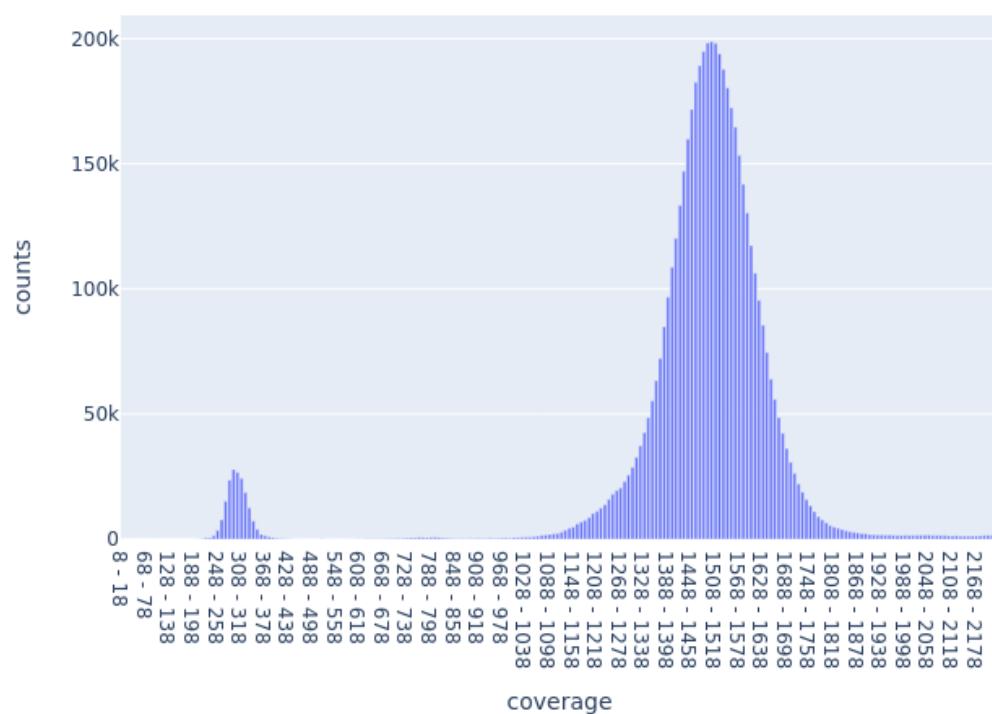
63481 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 1475.607822087008

Agrobacterium tumefaciens in T22.3.1

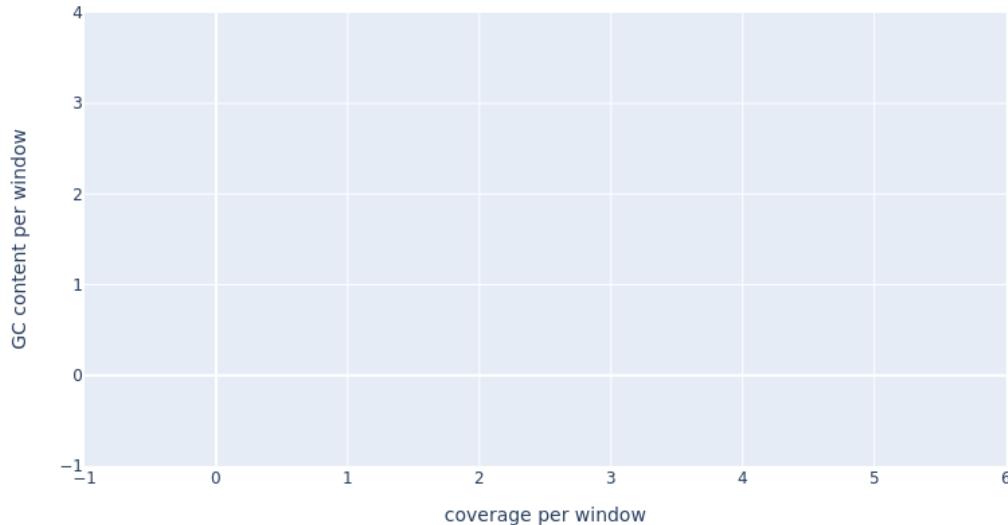


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T22.3.1



# Report of Comamonas testosterone in T22.3.1

## Mapping stats of Illumina reads

57911577 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1863 + 0 supplementary

0 + 0 duplicates

4755469 + 0 mapped (8.21% : N/A)

57909714 + 0 paired in sequencing

28954857 + 0 read1

28954857 + 0 read2

4654380 + 0 properly paired (8.04% : N/A)

4658292 + 0 with itself and mate mapped

95314 + 0 singletons (0.16% : N/A)

54 + 0 with mate mapped to a different chr

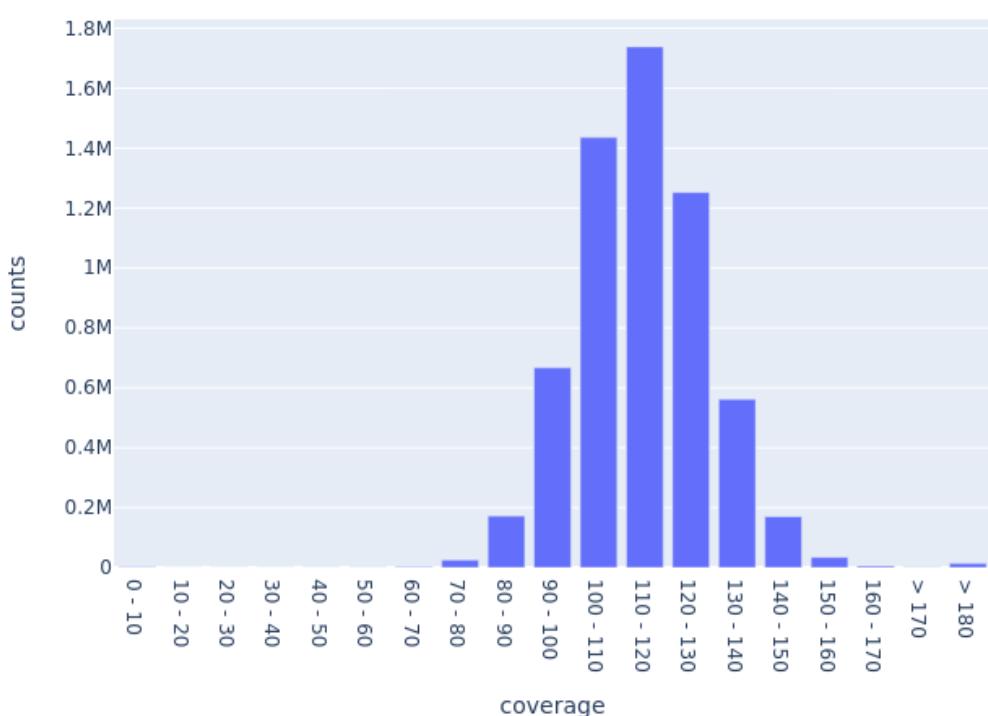
39 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 115.25771782253968

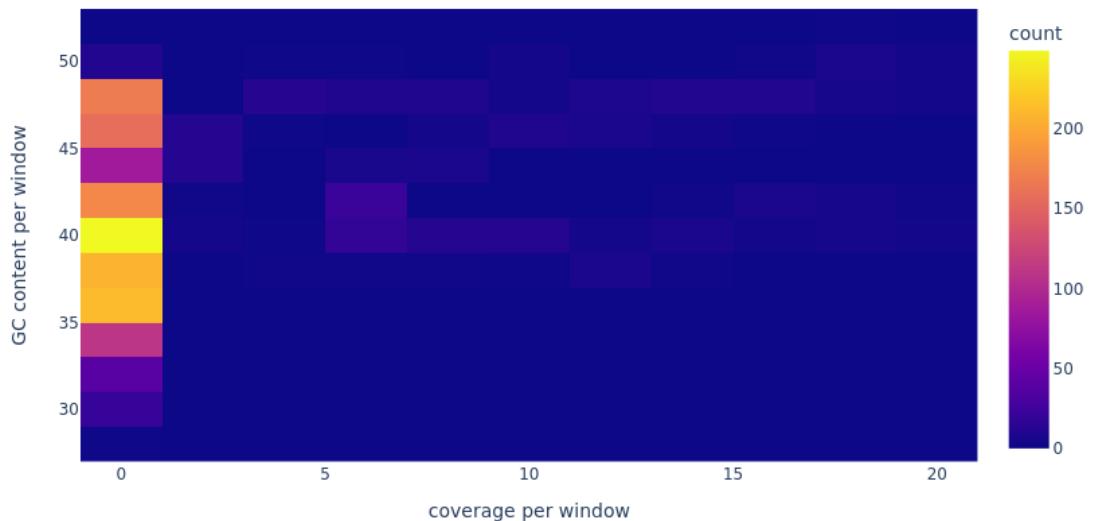
Comamonas testosterone in T22.3.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.3.1



# Report of *Microbacterium saperdae* in T22.3.1

## Mapping stats of Illumina reads

57909767 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

53 + 0 supplementary

0 + 0 duplicates

157677 + 0 mapped (0.27% : N/A)

57909714 + 0 paired in sequencing

28954857 + 0 read1

28954857 + 0 read2

126228 + 0 properly paired (0.22% : N/A)

126888 + 0 with itself and mate mapped

30736 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

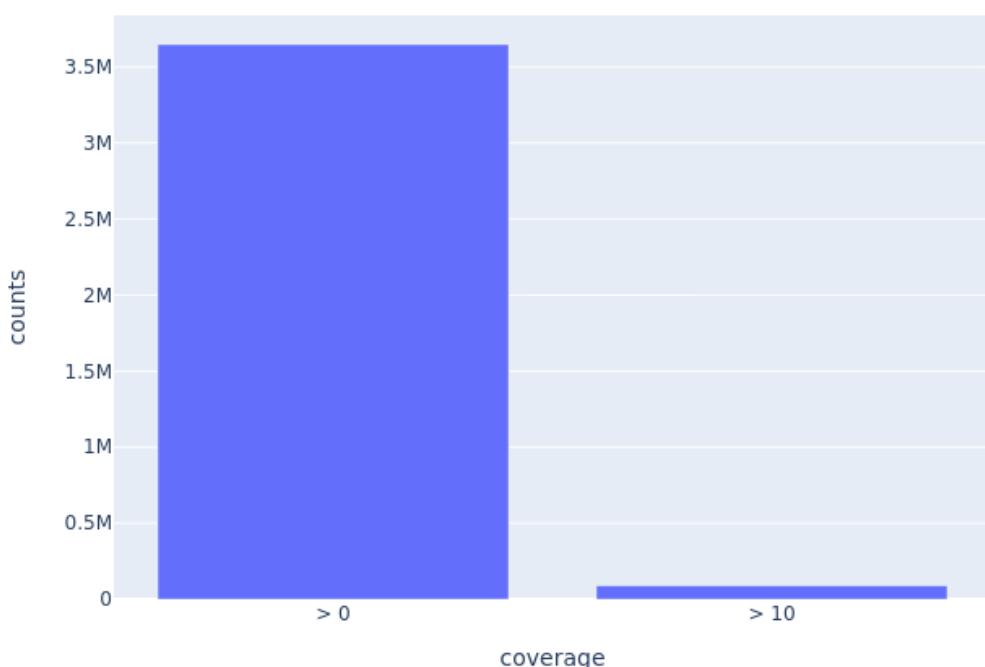
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 5.17860286755652

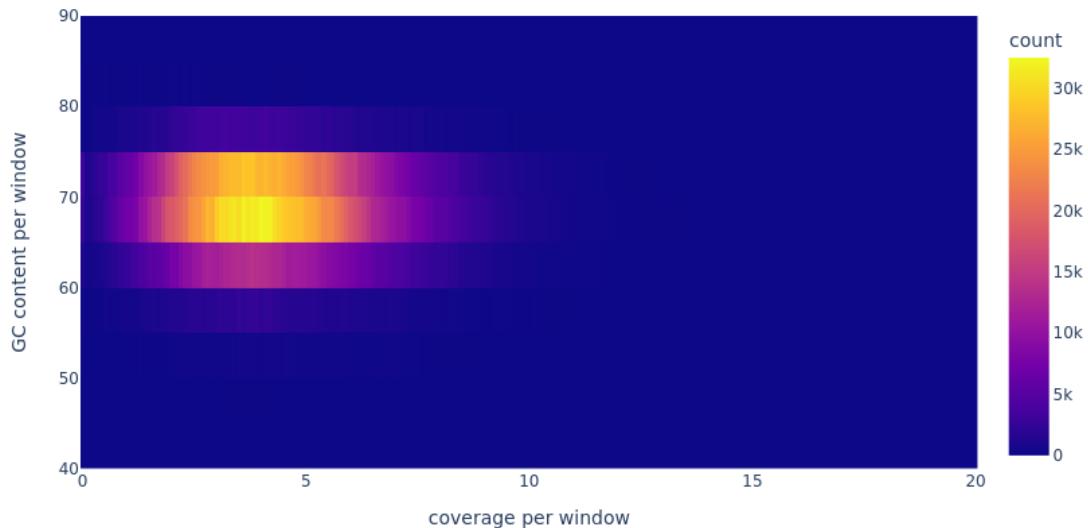
Microbacterium saperdae in T22.3.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T22.3.1



# Report of *Agrobacterium tumefaciens* in T22.3.2

## Mapping stats of Illumina reads

56876300 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

13284 + 0 supplementary

0 + 0 duplicates

53657124 + 0 mapped (94.34% : N/A)

56863016 + 0 paired in sequencing

28431508 + 0 read1

28431508 + 0 read2

53358844 + 0 properly paired (93.84% : N/A)

53519180 + 0 with itself and mate mapped

124660 + 0 singletons (0.22% : N/A)

65986 + 0 with mate mapped to a different chr

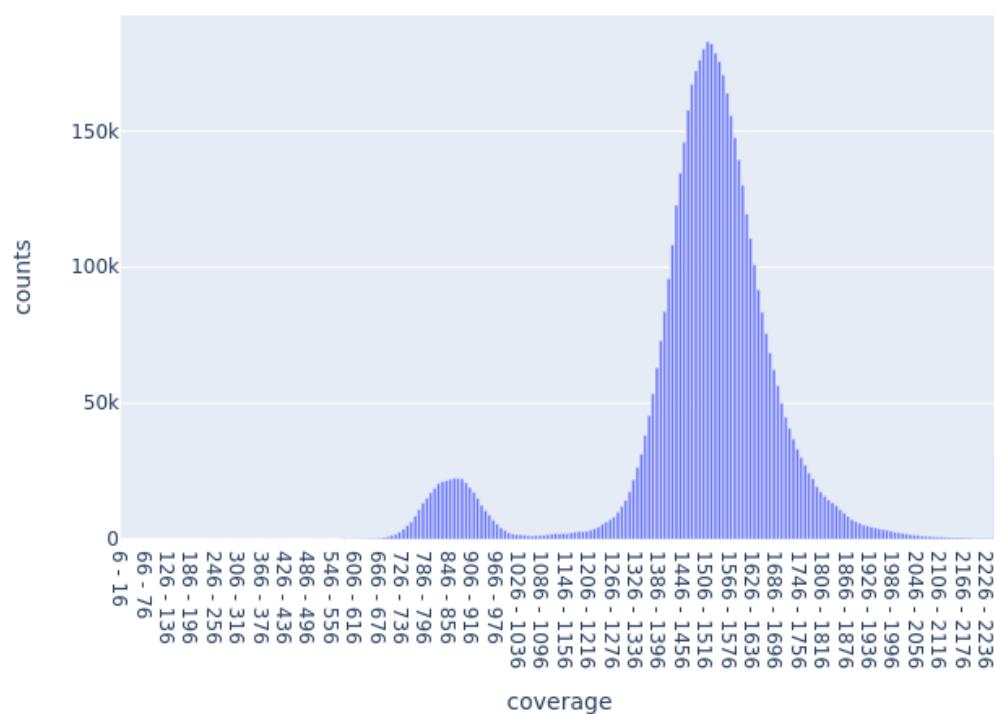
62996 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 1496.2015119246405

Agrobacterium tumefaciens in T22.3.2

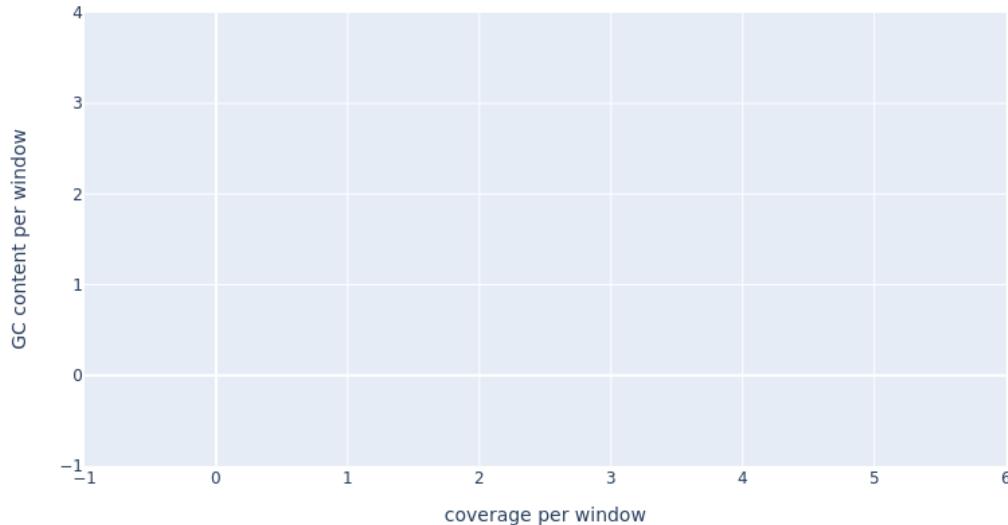


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T22.3.2



# Report of Comamonas testosterone in T22.3.2

## Mapping stats of Illumina reads

56864444 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1428 + 0 supplementary

0 + 0 duplicates

3012393 + 0 mapped (5.30% : N/A)

56863016 + 0 paired in sequencing

28431508 + 0 read1

28431508 + 0 read2

2917882 + 0 properly paired (5.13% : N/A)

2920698 + 0 with itself and mate mapped

90267 + 0 singletons (0.16% : N/A)

40 + 0 with mate mapped to a different chr

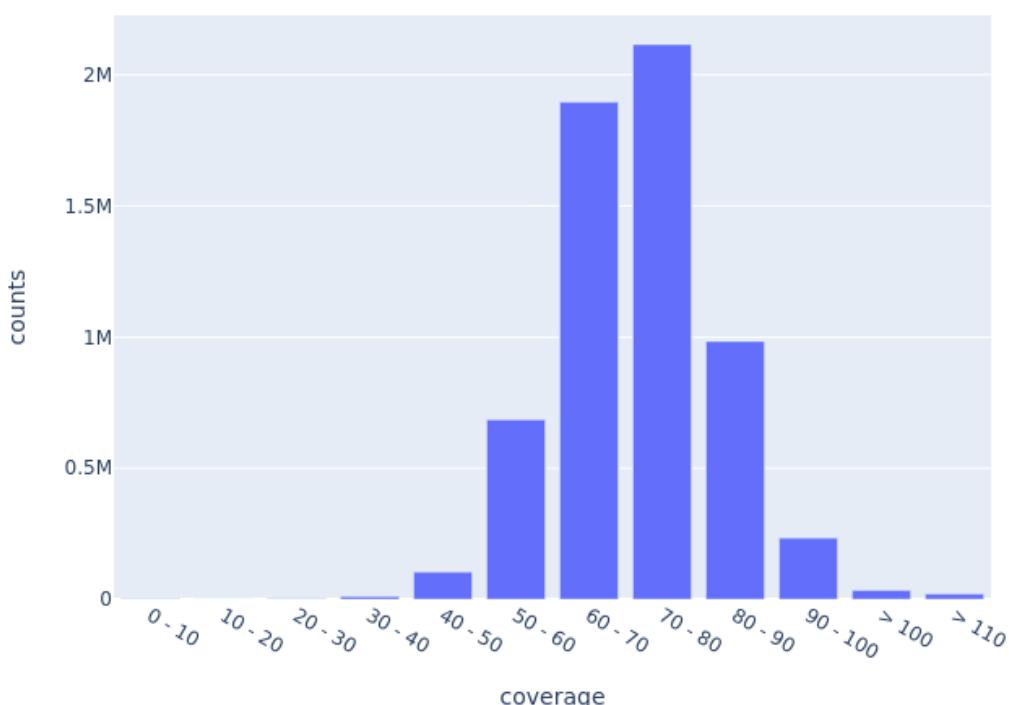
26 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 72.50631936704923

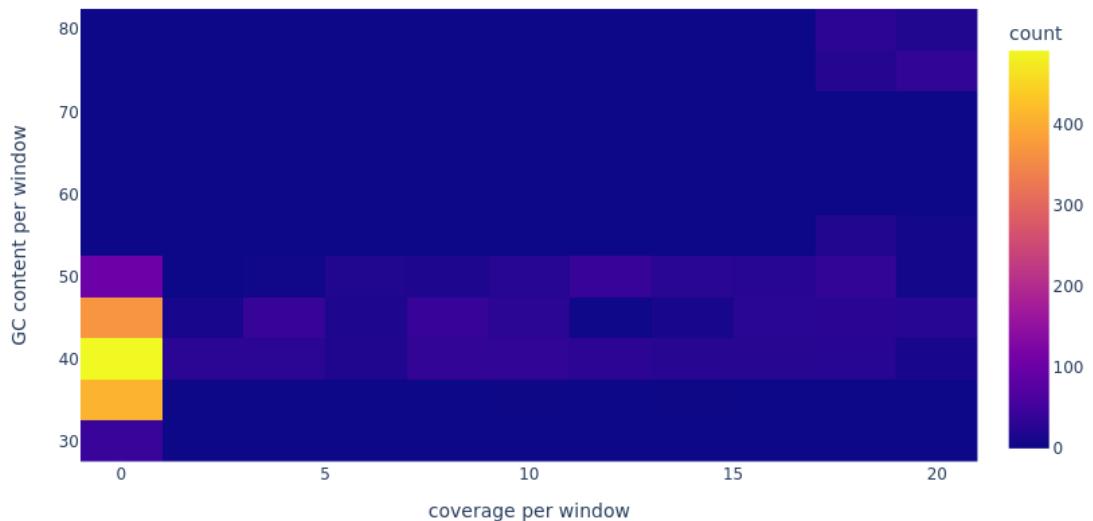
Comamonas testosterone in T22.3.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.3.2



# Report of *Microbacterium saperdae* in T22.3.2

## Mapping stats of Illumina reads

56863046 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

30 + 0 supplementary

0 + 0 duplicates

122072 + 0 mapped (0.21% : N/A)

56863016 + 0 paired in sequencing

28431508 + 0 read1

28431508 + 0 read2

91928 + 0 properly paired (0.16% : N/A)

92646 + 0 with itself and mate mapped

29396 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

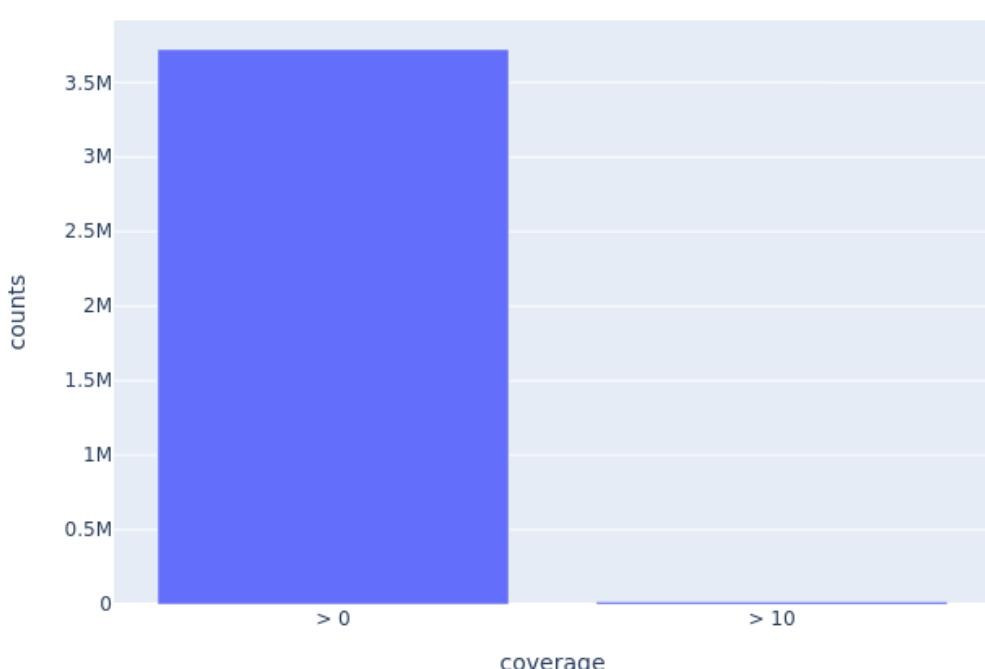
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 3.7983342956784374

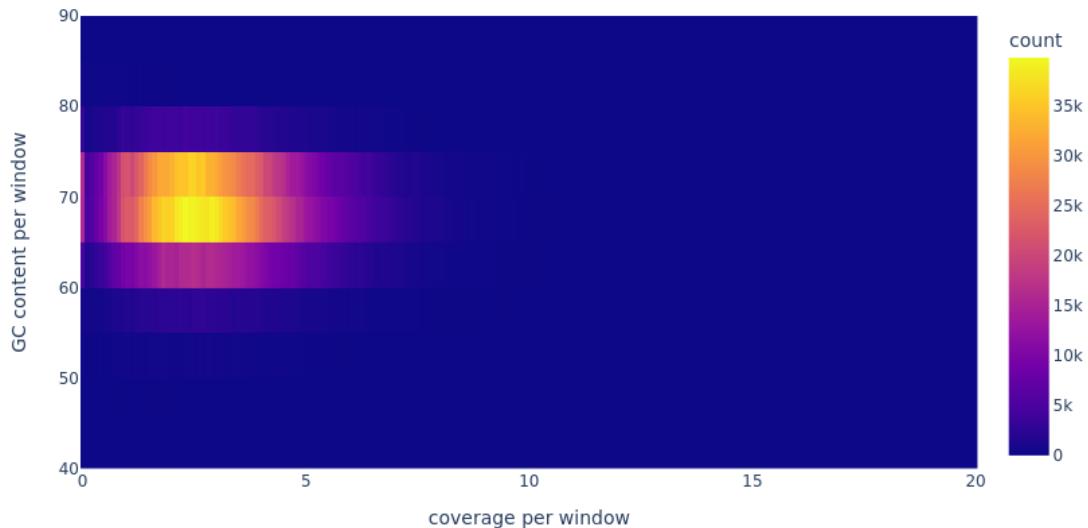
Microbacterium saperdae in T22.3.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T22.3.2



# Report of *Agrobacterium tumefaciens* in T22.3.3

## Mapping stats of Illumina reads

53405918 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

17500 + 0 supplementary

0 + 0 duplicates

47321319 + 0 mapped (88.61% : N/A)

53388418 + 0 paired in sequencing

26694209 + 0 read1

26694209 + 0 read2

47051142 + 0 properly paired (88.13% : N/A)

47194976 + 0 with itself and mate mapped

108843 + 0 singletons (0.20% : N/A)

45786 + 0 with mate mapped to a different chr

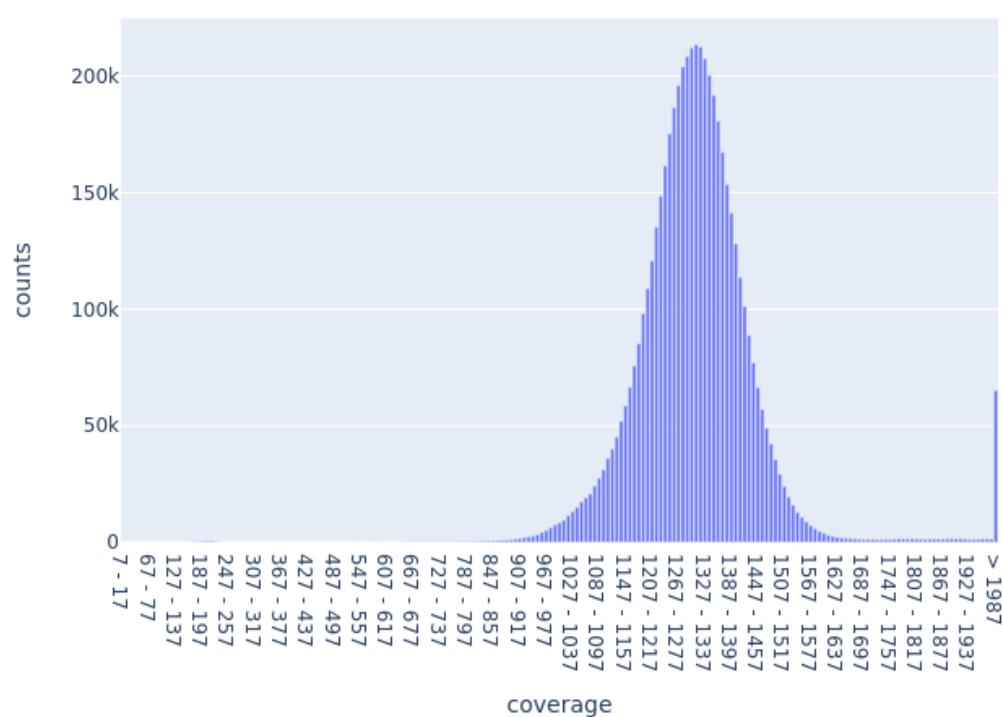
43294 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 1319.5567502725507

Agrobacterium tumefaciens in T22.3.3

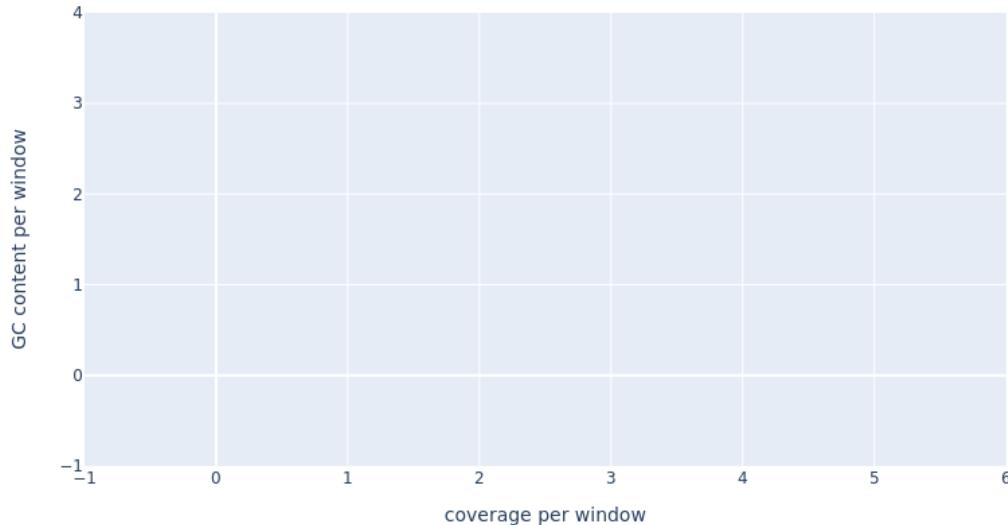


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T22.3.3



# Report of Comamonas testosterone in T22.3.3

## Mapping stats of Illumina reads

53391403 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

2985 + 0 supplementary

0 + 0 duplicates

5861773 + 0 mapped (10.98% : N/A)

53388418 + 0 paired in sequencing

26694209 + 0 read1

26694209 + 0 read2

5766074 + 0 properly paired (10.80% : N/A)

5774844 + 0 with itself and mate mapped

83944 + 0 singletons (0.16% : N/A)

68 + 0 with mate mapped to a different chr

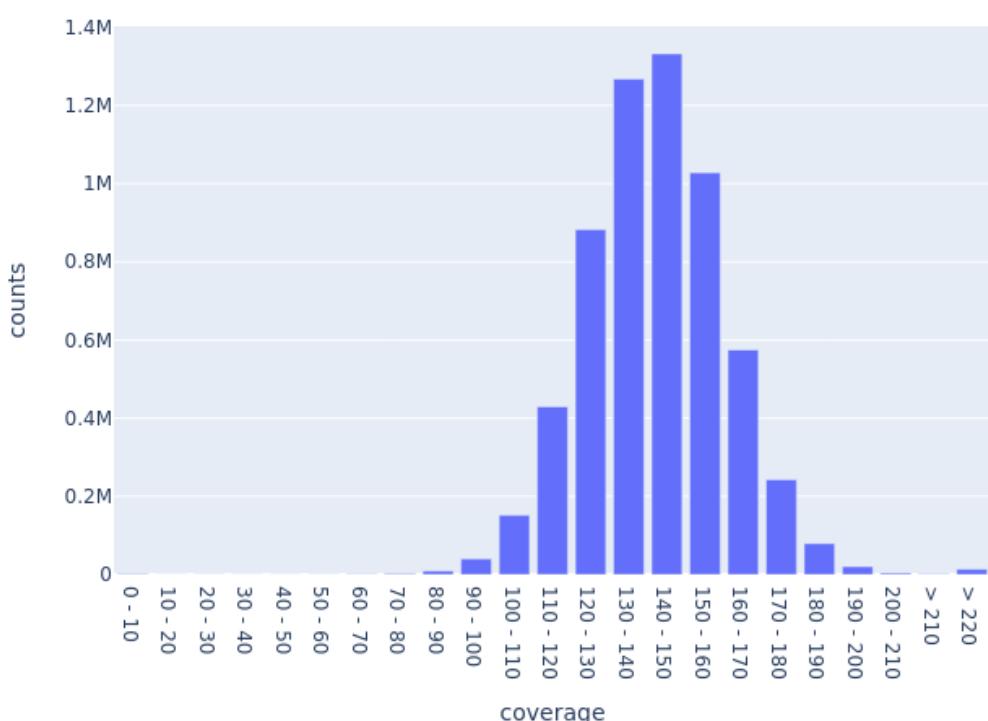
46 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 142.55134277202106

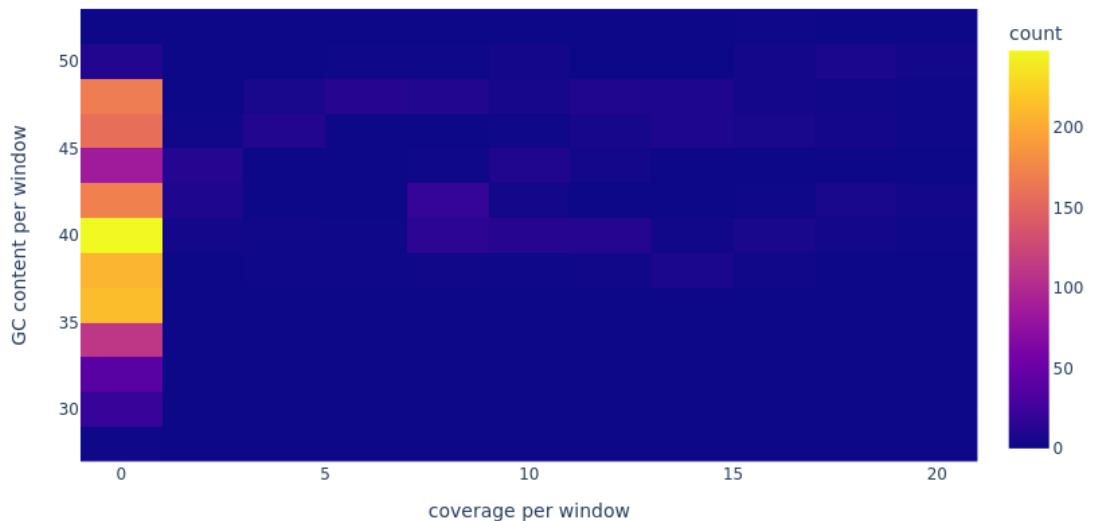
Comamonas testosterone in T22.3.3



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.3.3



# Report of *Microbacterium saperdae* in T22.3.3

## Mapping stats of Illumina reads

53388478 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

60 + 0 supplementary

0 + 0 duplicates

111374 + 0 mapped (0.21% : N/A)

53388418 + 0 paired in sequencing

26694209 + 0 read1

26694209 + 0 read2

83932 + 0 properly paired (0.16% : N/A)

84642 + 0 with itself and mate mapped

26672 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

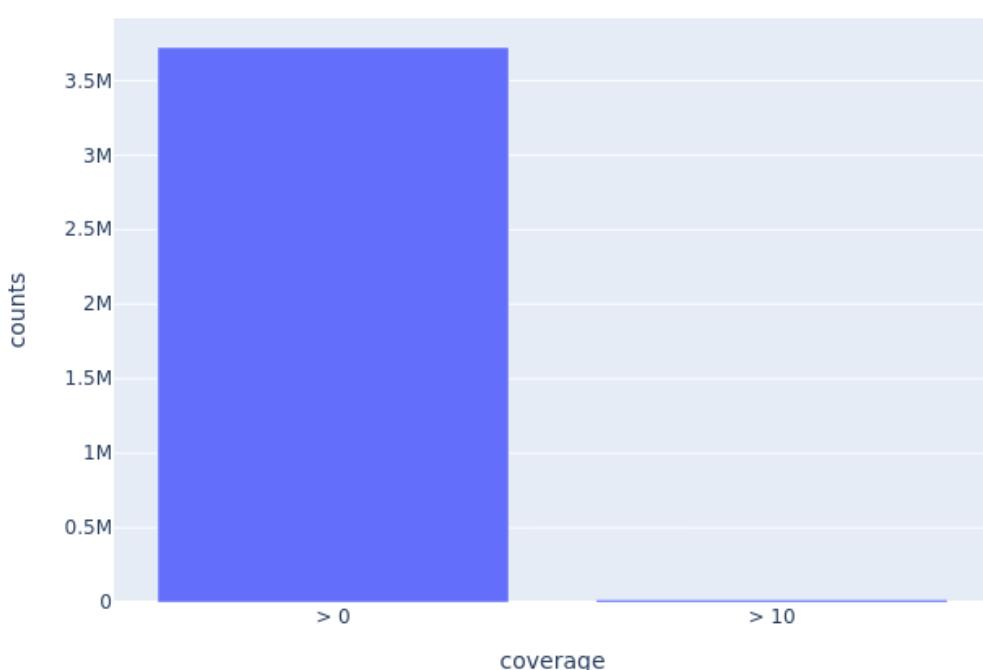
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 3.4414255586373192

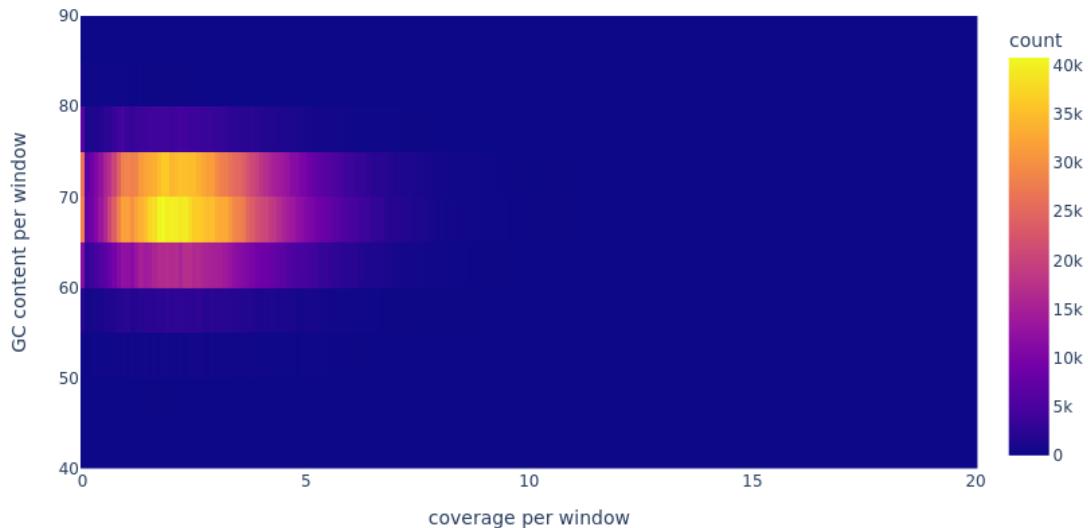
Microbacterium saperdae in T22.3.3



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T22.3.3



# Report of *Agrobacterium tumefaciens* in T22.3.4

## Mapping stats of Illumina reads

63894587 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

16003 + 0 supplementary

0 + 0 duplicates

58841812 + 0 mapped (92.09% : N/A)

63878584 + 0 paired in sequencing

31939292 + 0 read1

31939292 + 0 read2

58463192 + 0 properly paired (91.52% : N/A)

58660878 + 0 with itself and mate mapped

164931 + 0 singletons (0.26% : N/A)

85614 + 0 with mate mapped to a different chr

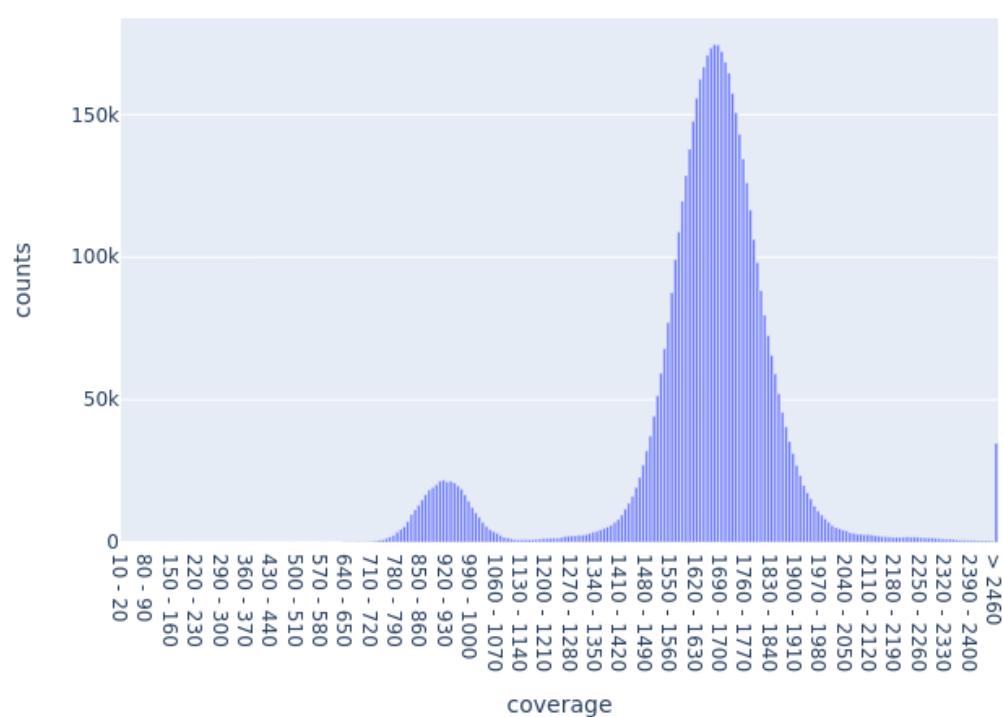
80438 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 1640.2846859156327

Agrobacterium tumefaciens in T22.3.4

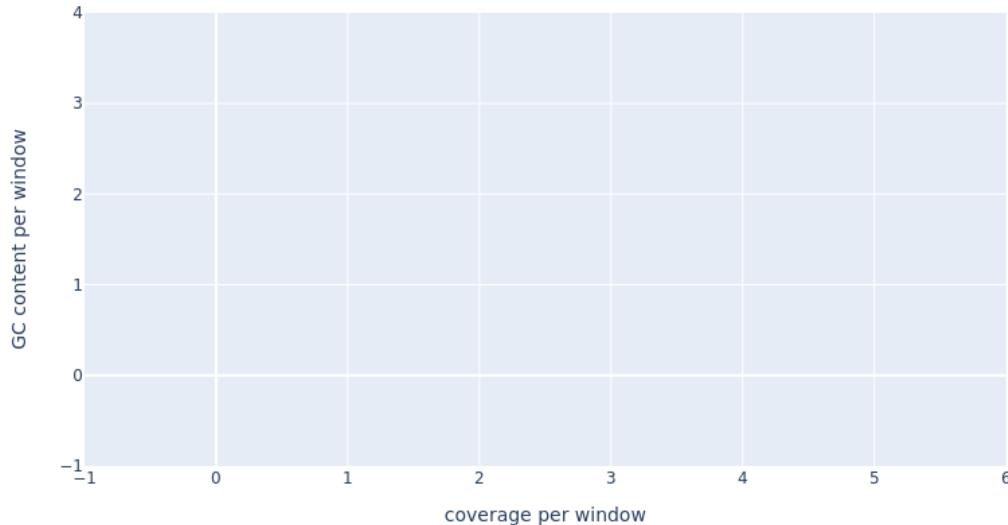


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T22.3.4



# Report of Comamonas testosterone in T22.3.4

## Mapping stats of Illumina reads

63880334 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1750 + 0 supplementary

0 + 0 duplicates

4768738 + 0 mapped (7.47% : N/A)

63878584 + 0 paired in sequencing

31939292 + 0 read1

31939292 + 0 read2

4653978 + 0 properly paired (7.29% : N/A)

4658624 + 0 with itself and mate mapped

108364 + 0 singletons (0.17% : N/A)

66 + 0 with mate mapped to a different chr

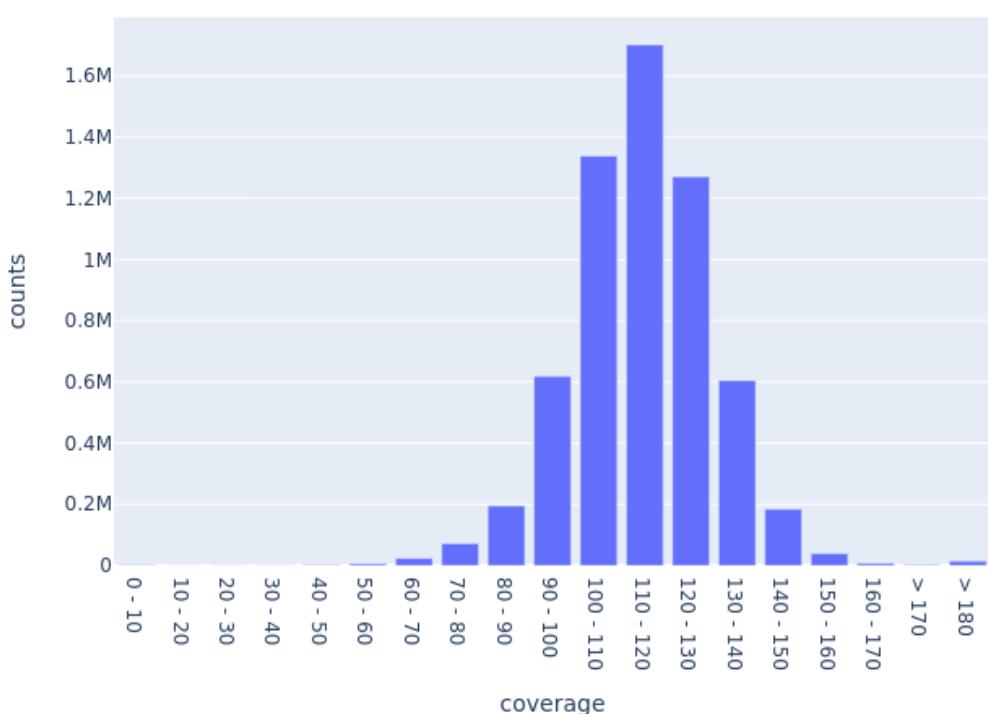
42 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 115.39658299409095

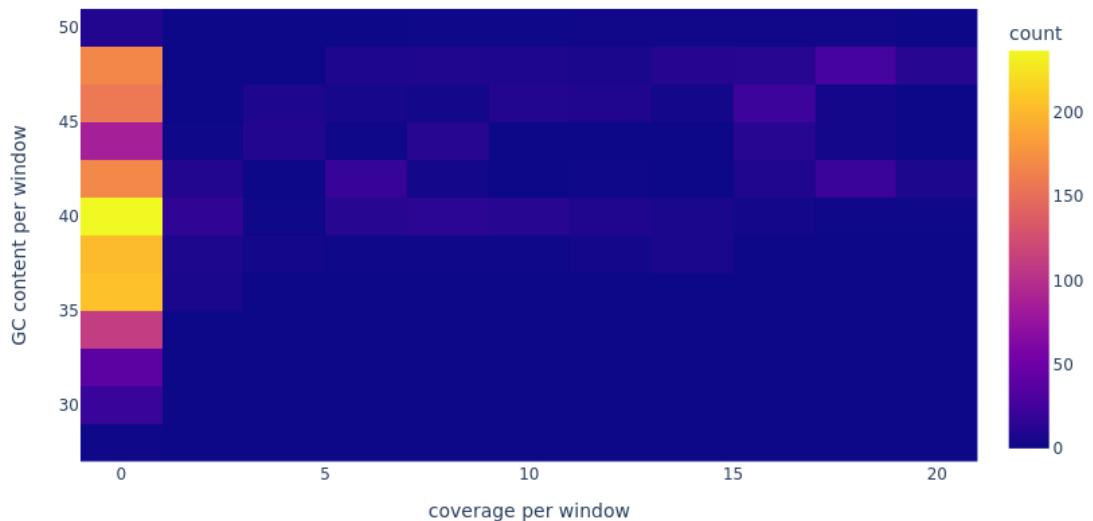
Comamonas testosterone in T22.3.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.3.4



# Report of *Microbacterium saperdae* in T22.3.4

## Mapping stats of Illumina reads

63878630 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

46 + 0 supplementary

0 + 0 duplicates

158961 + 0 mapped (0.25% : N/A)

63878584 + 0 paired in sequencing

31939292 + 0 read1

31939292 + 0 read2

124700 + 0 properly paired (0.20% : N/A)

125420 + 0 with itself and mate mapped

33495 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

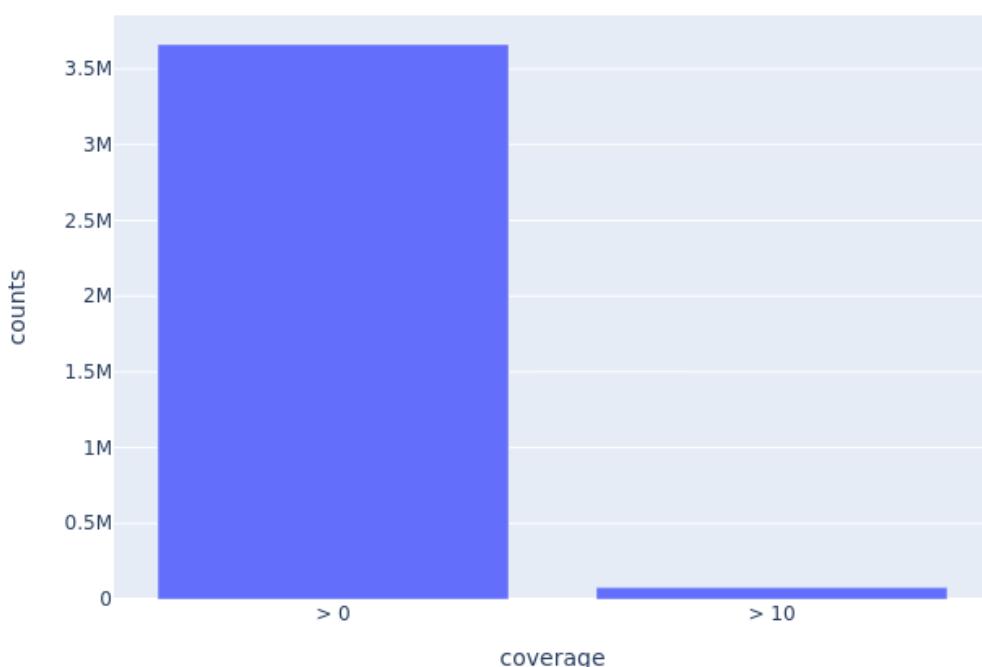
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 5.124748555010732

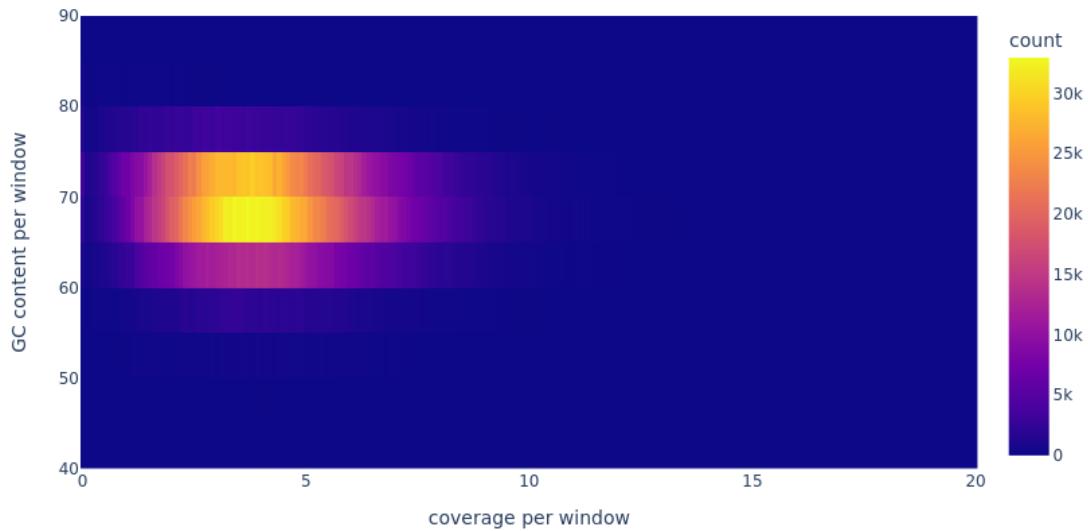
Microbacterium saperdae in T22.3.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T22.3.4



# Report of *Agrobacterium tumefaciens* in T22.3.5

## Mapping stats of Illumina reads

54355246 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

15956 + 0 supplementary

0 + 0 duplicates

52264376 + 0 mapped (96.15% : N/A)

54339290 + 0 paired in sequencing

27169645 + 0 read1

27169645 + 0 read2

51962992 + 0 properly paired (95.63% : N/A)

52132478 + 0 with itself and mate mapped

115942 + 0 singletons (0.21% : N/A)

78878 + 0 with mate mapped to a different chr

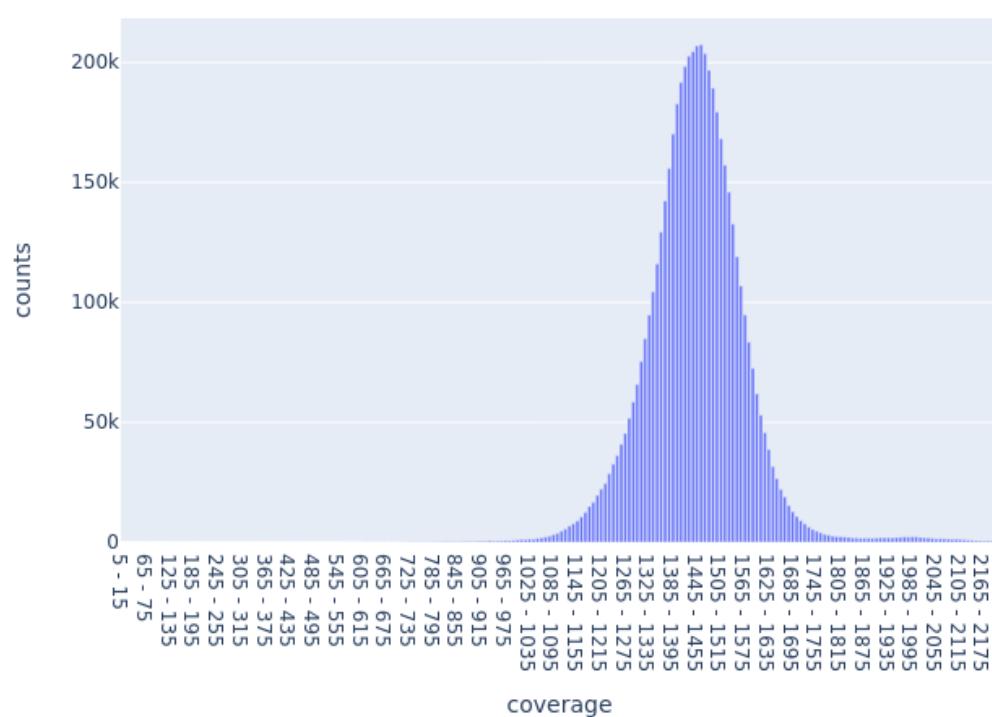
74398 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 1457.5432804460725

Agrobacterium tumefaciens in T22.3.5

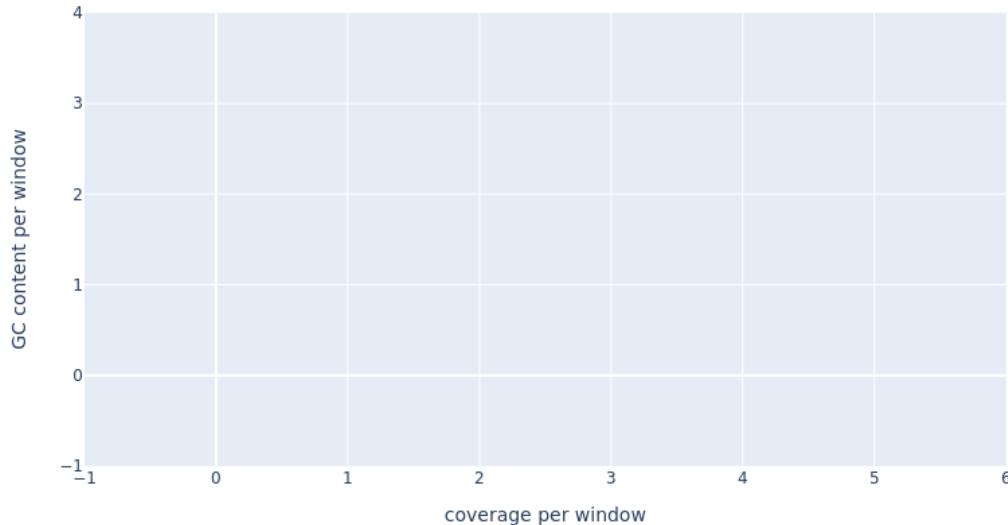


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T22.3.5



# Report of Comamonas testosterone in T22.3.5

## Mapping stats of Illumina reads

54339876 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

586 + 0 supplementary

0 + 0 duplicates

1701063 + 0 mapped (3.13% : N/A)

54339290 + 0 paired in sequencing

27169645 + 0 read1

27169645 + 0 read2

1616862 + 0 properly paired (2.98% : N/A)

1618084 + 0 with itself and mate mapped

82393 + 0 singletons (0.15% : N/A)

10 + 0 with mate mapped to a different chr

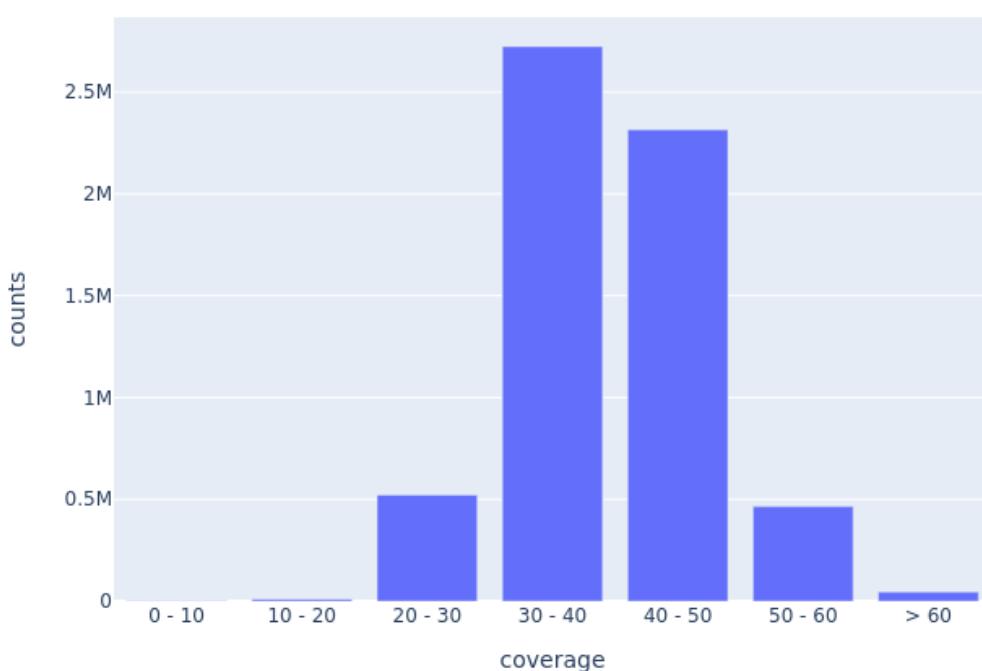
6 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 40.43905659580392

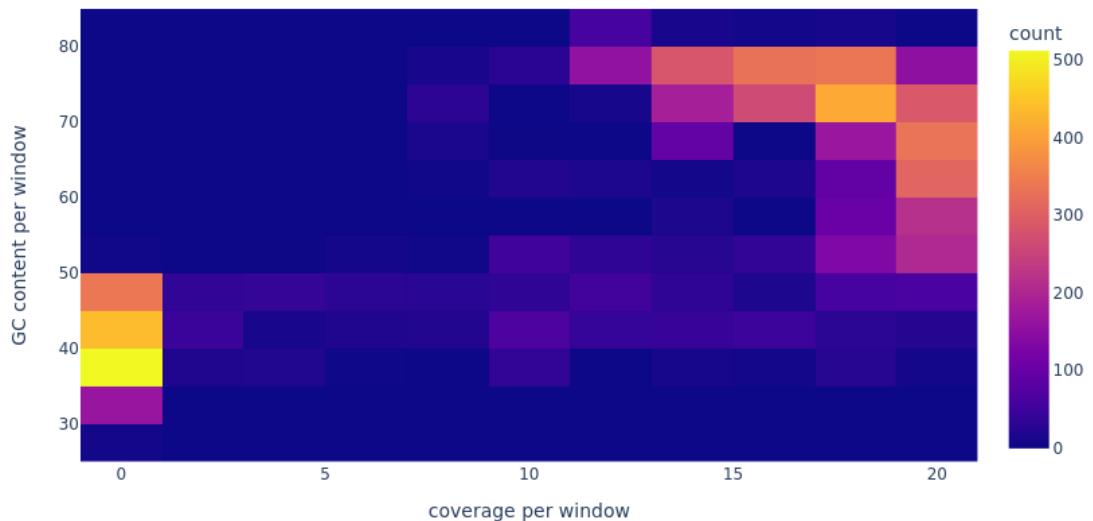
Comamonas testosterone in T22.3.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.3.5



# Report of *Microbacterium saperdae* in T22.3.5

## Mapping stats of Illumina reads

54339352 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

62 + 0 supplementary

0 + 0 duplicates

295599 + 0 mapped (0.54% : N/A)

54339290 + 0 paired in sequencing

27169645 + 0 read1

27169645 + 0 read2

267378 + 0 properly paired (0.49% : N/A)

268156 + 0 with itself and mate mapped

27381 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

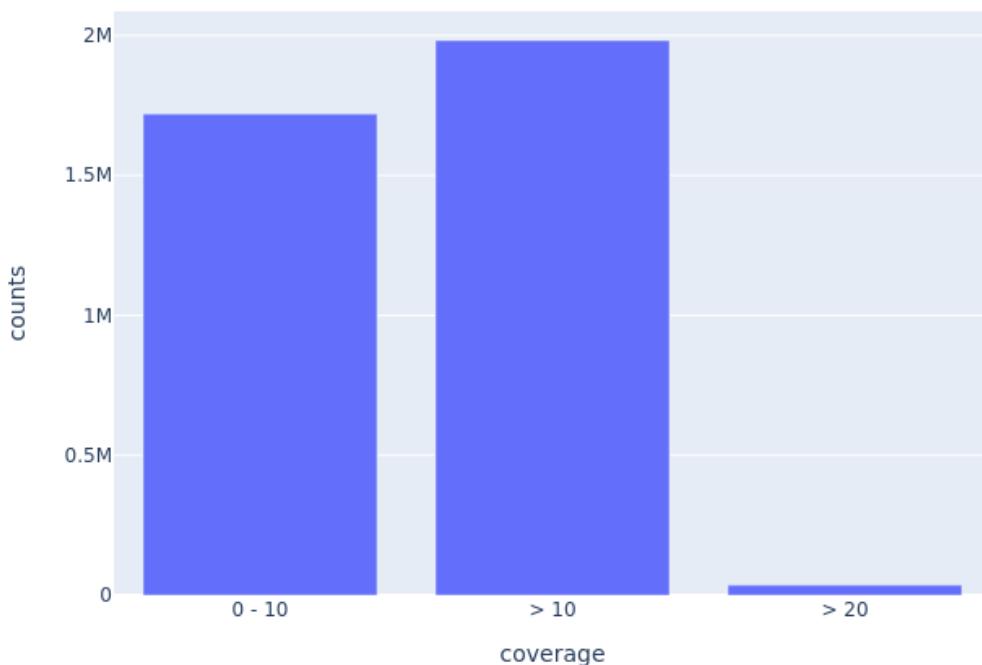
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 10.821579344774092

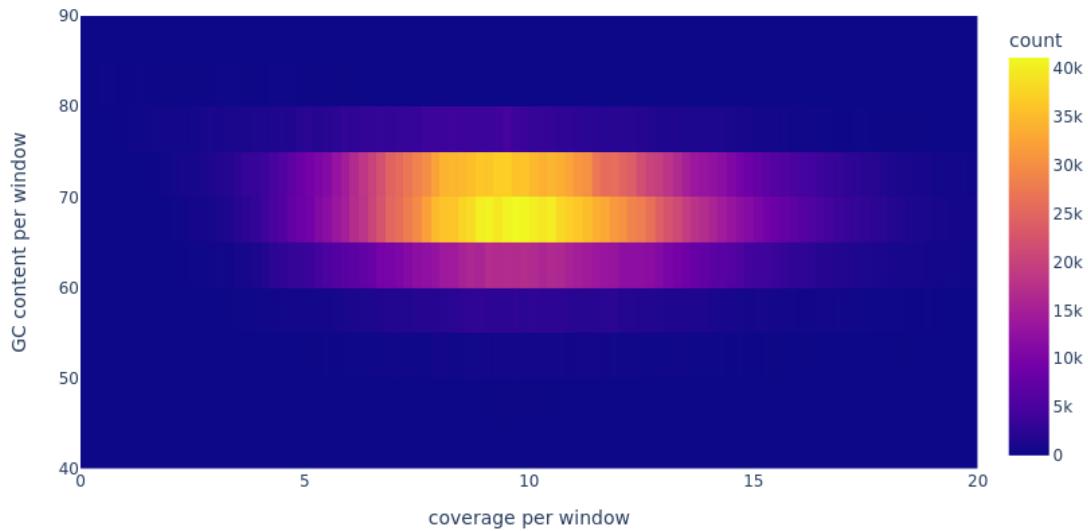
Microbacterium saperdae in T22.3.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T22.3.5



# Report of *Agrobacterium tumefaciens* in T22.4.1

## Mapping stats of Illumina reads

56713084 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

12732 + 0 supplementary

0 + 0 duplicates

51089467 + 0 mapped (90.08% : N/A)

56700352 + 0 paired in sequencing

28350176 + 0 read1

28350176 + 0 read2

50801294 + 0 properly paired (89.60% : N/A)

50939618 + 0 with itself and mate mapped

137117 + 0 singletons (0.24% : N/A)

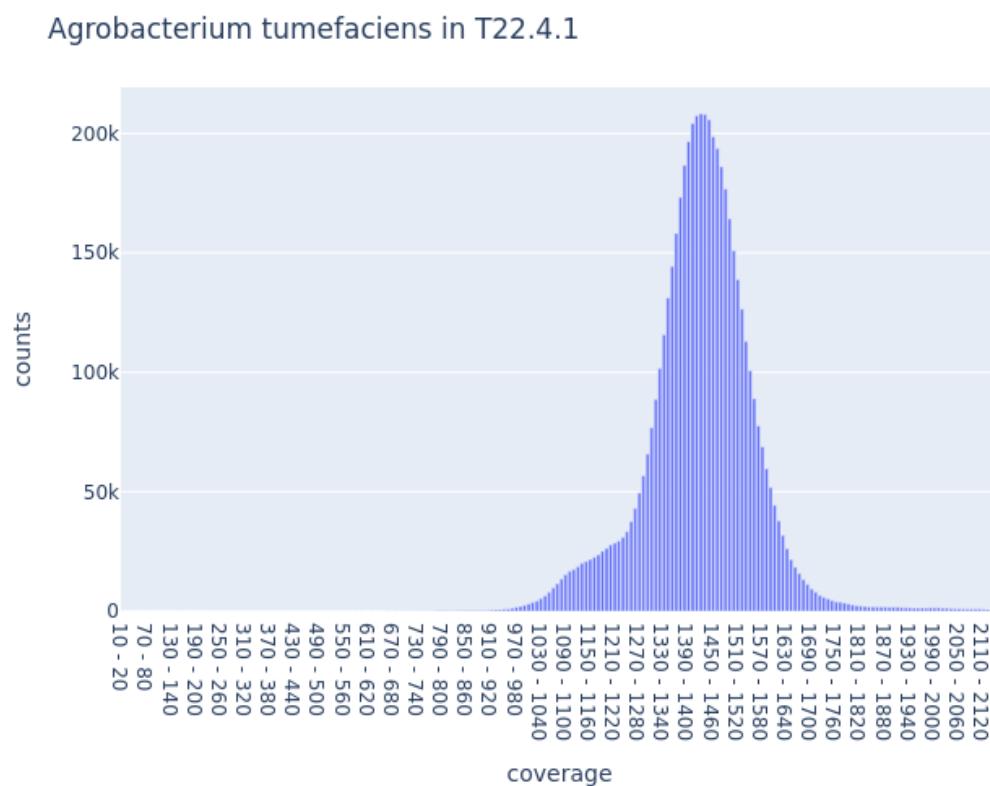
47868 + 0 with mate mapped to a different chr

45281 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 1424.7511950441867

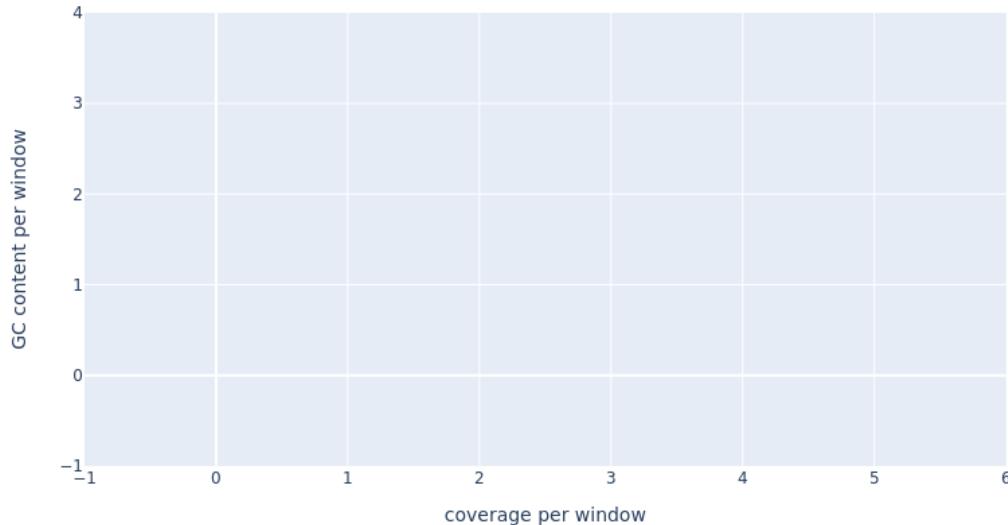


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T22.4.1



# Report of Comamonas testosterone in T22.4.1

## Mapping stats of Illumina reads

56701183 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

831 + 0 supplementary

0 + 0 duplicates

2787662 + 0 mapped (4.92% : N/A)

56700352 + 0 paired in sequencing

28350176 + 0 read1

28350176 + 0 read2

2697720 + 0 properly paired (4.76% : N/A)

2700906 + 0 with itself and mate mapped

85925 + 0 singletons (0.15% : N/A)

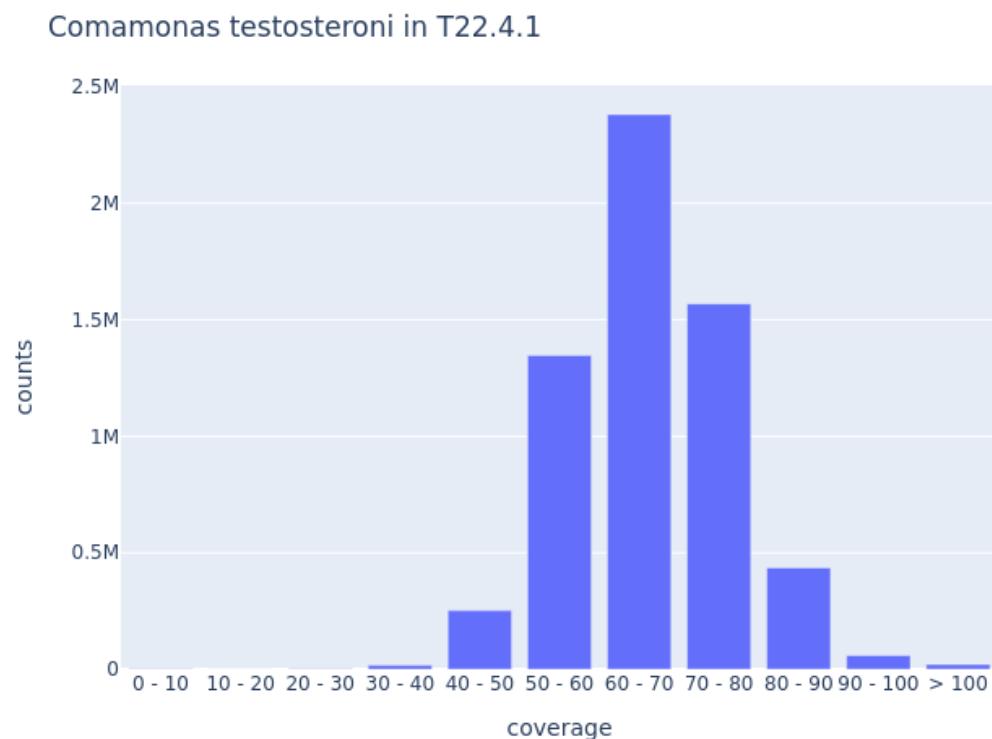
32 + 0 with mate mapped to a different chr

21 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

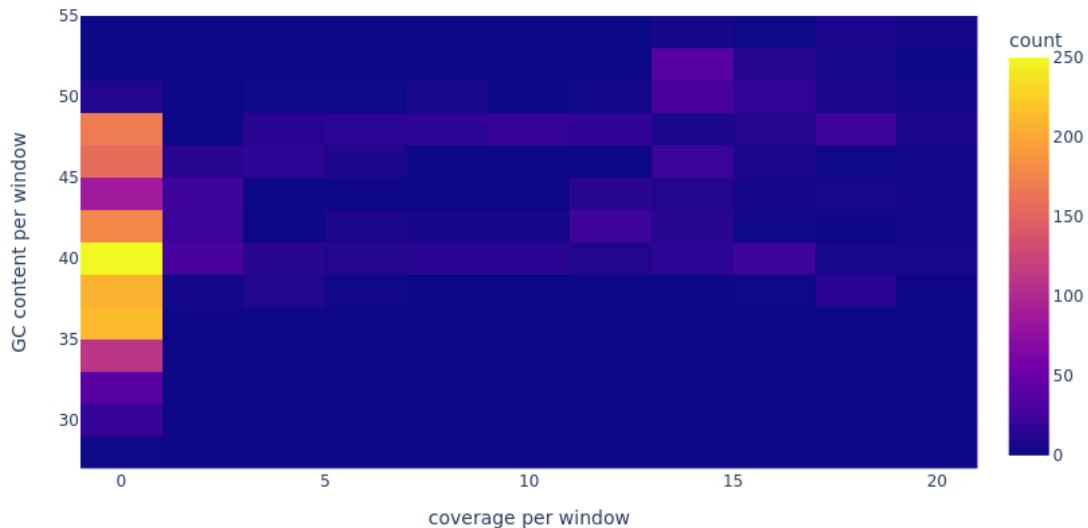
Average coverage: 67.06585687869172



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.4.1



# Report of *Microbacterium saperdae* in T22.4.1

## Mapping stats of Illumina reads

56700358 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

6 + 0 supplementary

0 + 0 duplicates

46706 + 0 mapped (0.08% : N/A)

56700352 + 0 paired in sequencing

28350176 + 0 read1

28350176 + 0 read2

17904 + 0 properly paired (0.03% : N/A)

18538 + 0 with itself and mate mapped

28162 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

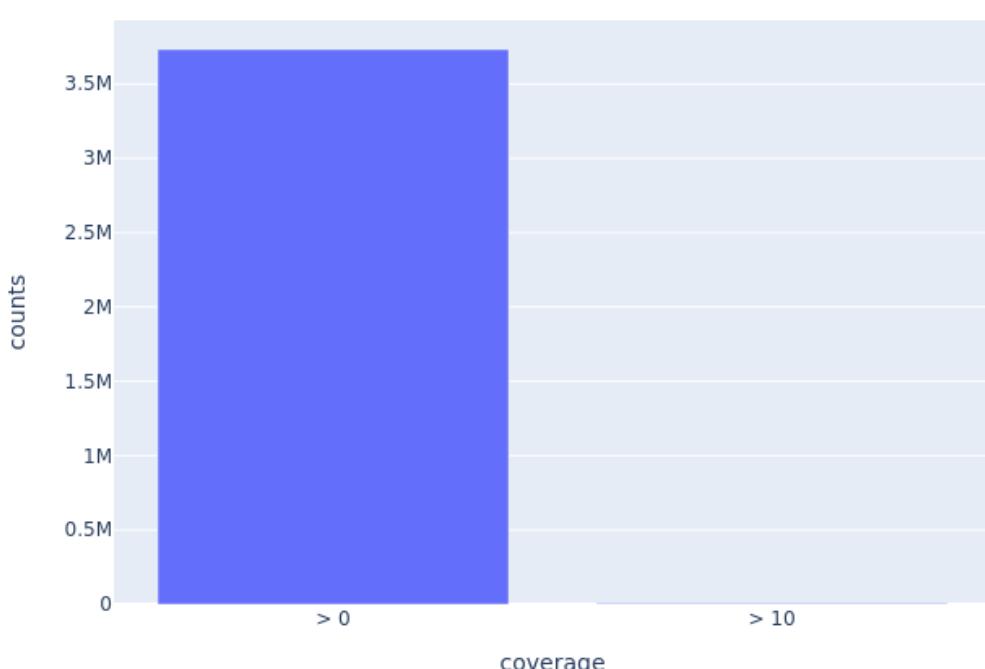
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 0.8279153036417315

Microbacterium saperdae in T22.4.1

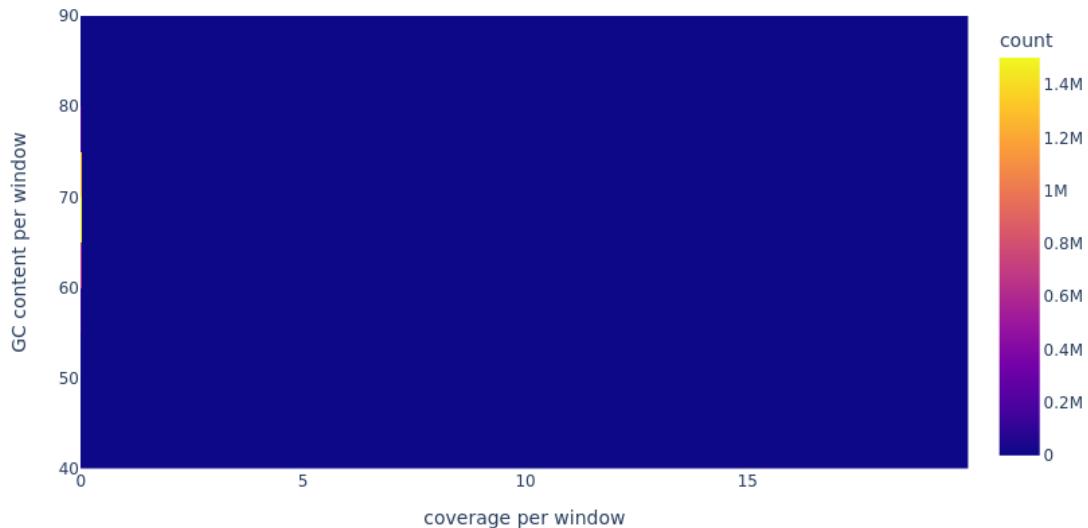


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T22.4.1



# Report of *Ochrobactrum anthropi* in T22.4.1

## Mapping stats of Illumina reads

56701754 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1402 + 0 supplementary

0 + 0 duplicates

3638500 + 0 mapped (6.42% : N/A)

56700352 + 0 paired in sequencing

28350176 + 0 read1

28350176 + 0 read2

3161210 + 0 properly paired (5.58% : N/A)

3173998 + 0 with itself and mate mapped

463100 + 0 singletons (0.82% : N/A)

6174 + 0 with mate mapped to a different chr

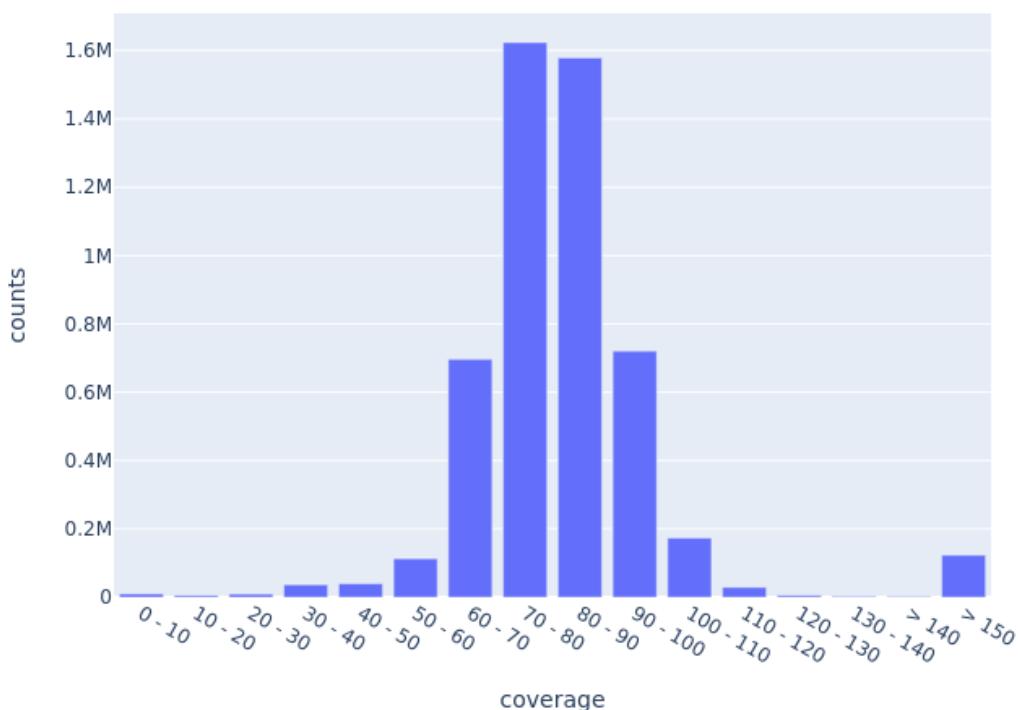
4194 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 97.48209771285038

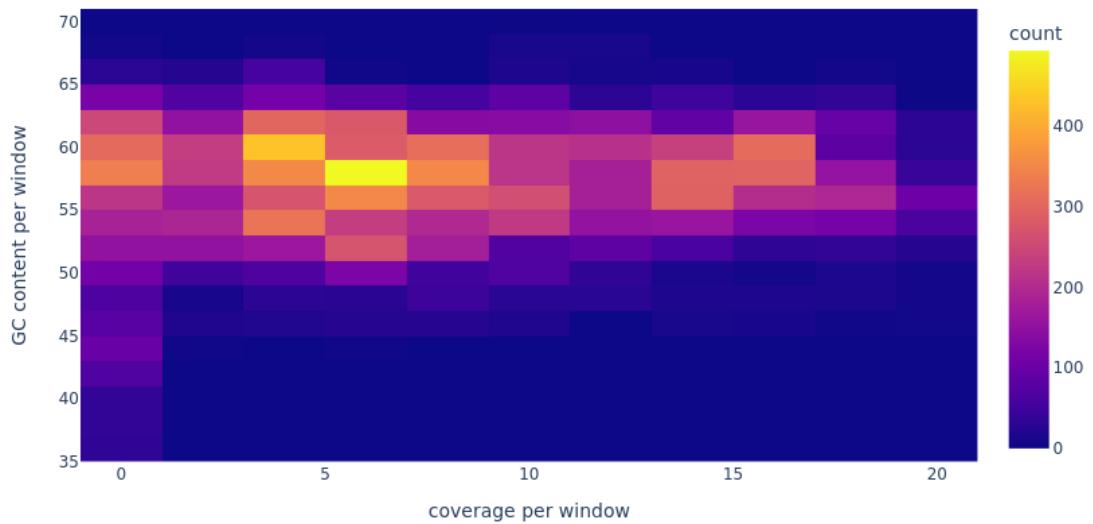
Ochrobactrum anthropi in T22.4.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T22.4.1



# Report of *Agrobacterium tumefaciens* in T22.4.2

## Mapping stats of Illumina reads

50426400 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

11916 + 0 supplementary

0 + 0 duplicates

46609213 + 0 mapped (92.43% : N/A)

50414484 + 0 paired in sequencing

25207242 + 0 read1

25207242 + 0 read2

46270280 + 0 properly paired (91.78% : N/A)

46457424 + 0 with itself and mate mapped

139873 + 0 singletons (0.28% : N/A)

85402 + 0 with mate mapped to a different chr

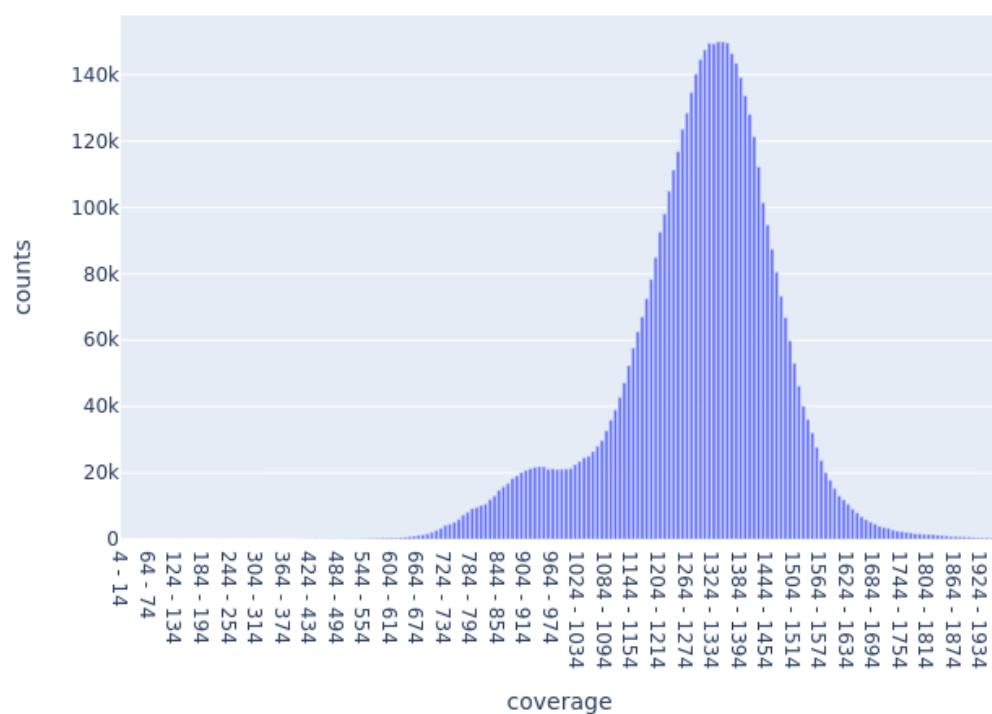
82468 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 1299.1144206080642

Agrobacterium tumefaciens in T22.4.2

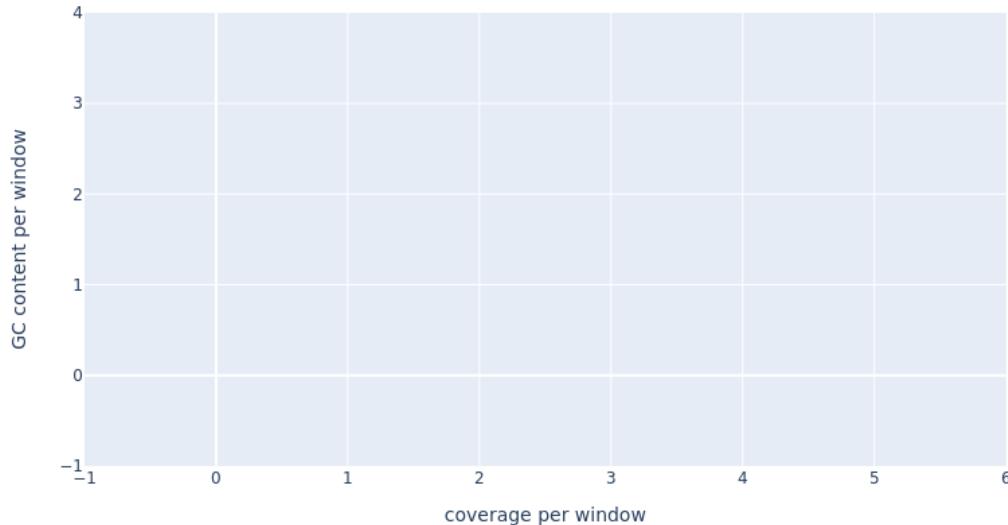


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T22.4.2



# Report of Comamonas testosterone in T22.4.2

## Mapping stats of Illumina reads

50415123 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

639 + 0 supplementary

0 + 0 duplicates

3146885 + 0 mapped (6.24% : N/A)

50414484 + 0 paired in sequencing

25207242 + 0 read1

25207242 + 0 read2

3060198 + 0 properly paired (6.07% : N/A)

3062972 + 0 with itself and mate mapped

83274 + 0 singletons (0.17% : N/A)

20 + 0 with mate mapped to a different chr

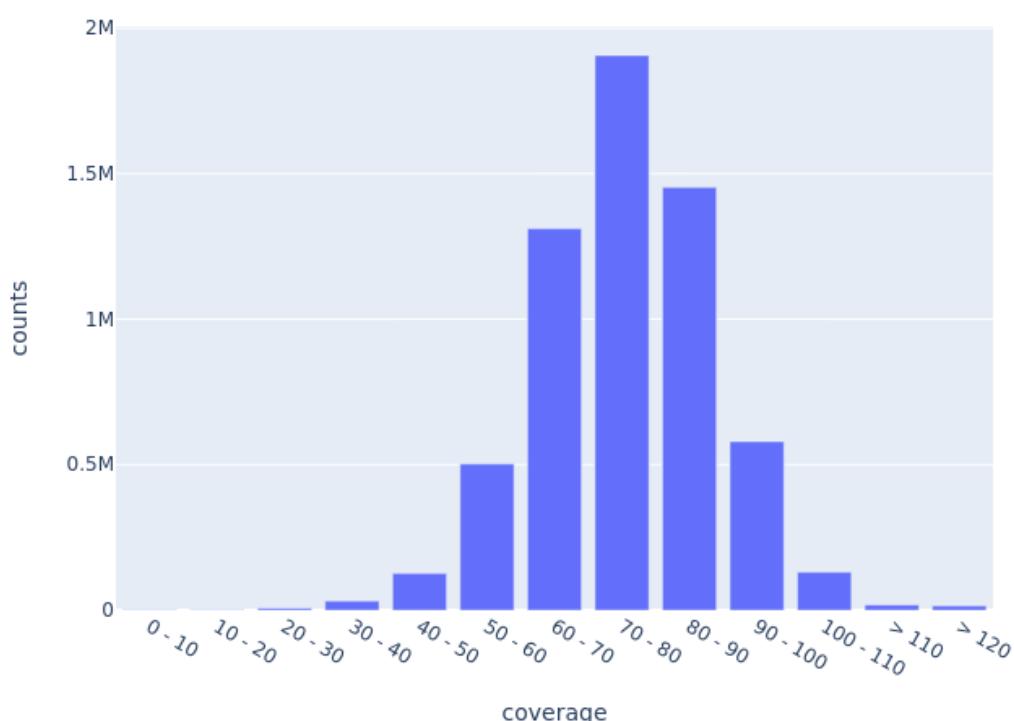
16 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 75.9913603514304

Comamonas testosterone in T22.4.2

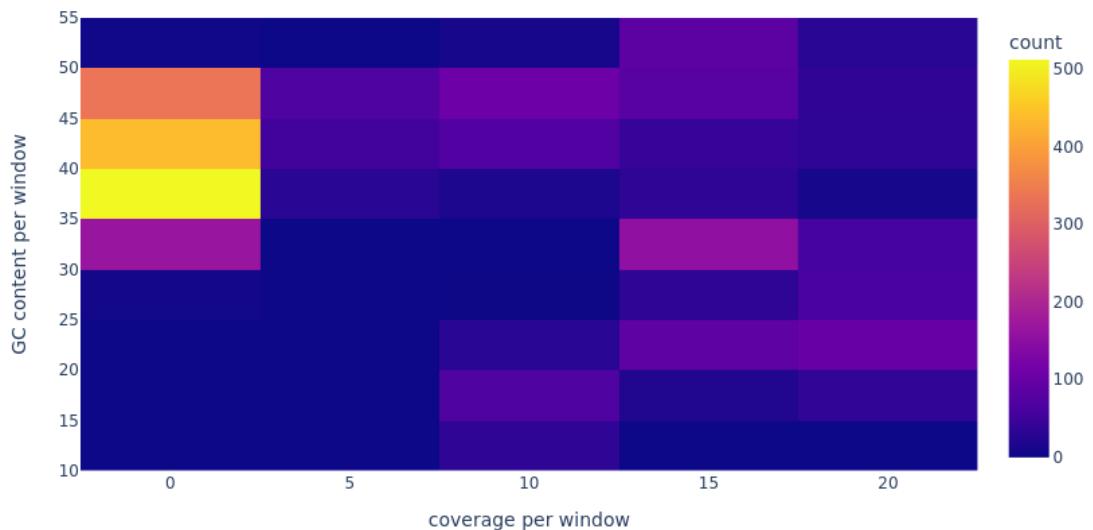


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.4.2



# Report of *Microbacterium saperdae* in T22.4.2

## Mapping stats of Illumina reads

50414524 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

40 + 0 supplementary

0 + 0 duplicates

225627 + 0 mapped (0.45% : N/A)

50414484 + 0 paired in sequencing

25207242 + 0 read1

25207242 + 0 read2

198526 + 0 properly paired (0.39% : N/A)

199192 + 0 with itself and mate mapped

26395 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

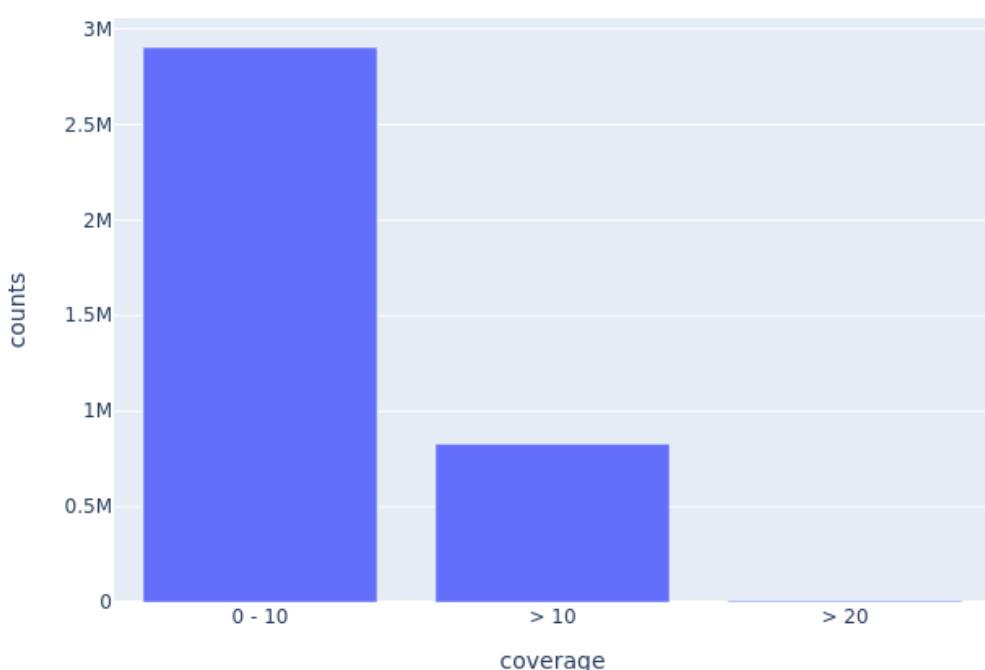
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 8.057645987930641

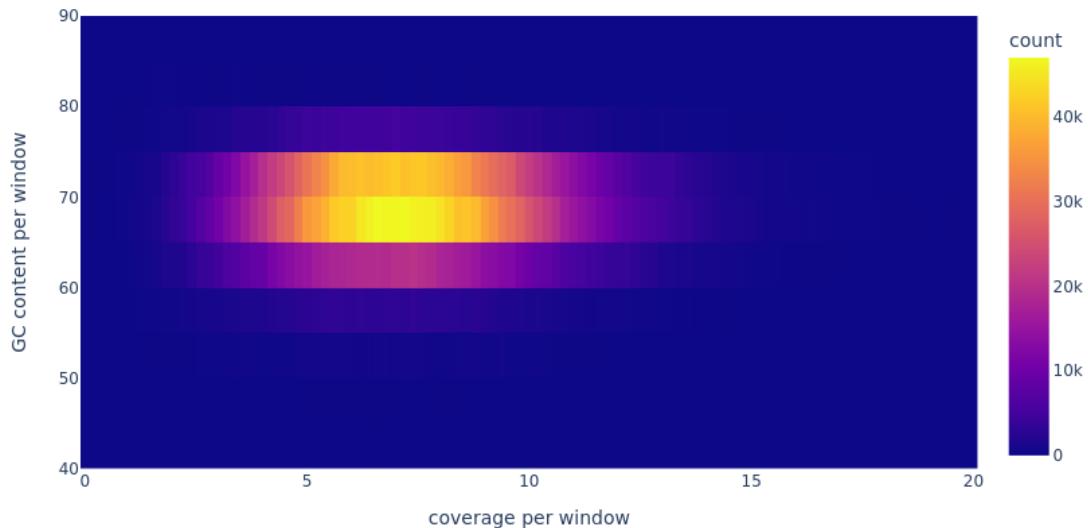
Microbacterium saperdae in T22.4.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T22.4.2



# Report of *Ochrobactrum anthropi* in T22.4.2

## Mapping stats of Illumina reads

50415358 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

874 + 0 supplementary

0 + 0 duplicates

1189362 + 0 mapped (2.36% : N/A)

50414484 + 0 paired in sequencing

25207242 + 0 read1

25207242 + 0 read2

758766 + 0 properly paired (1.51% : N/A)

767456 + 0 with itself and mate mapped

421032 + 0 singletons (0.84% : N/A)

5306 + 0 with mate mapped to a different chr

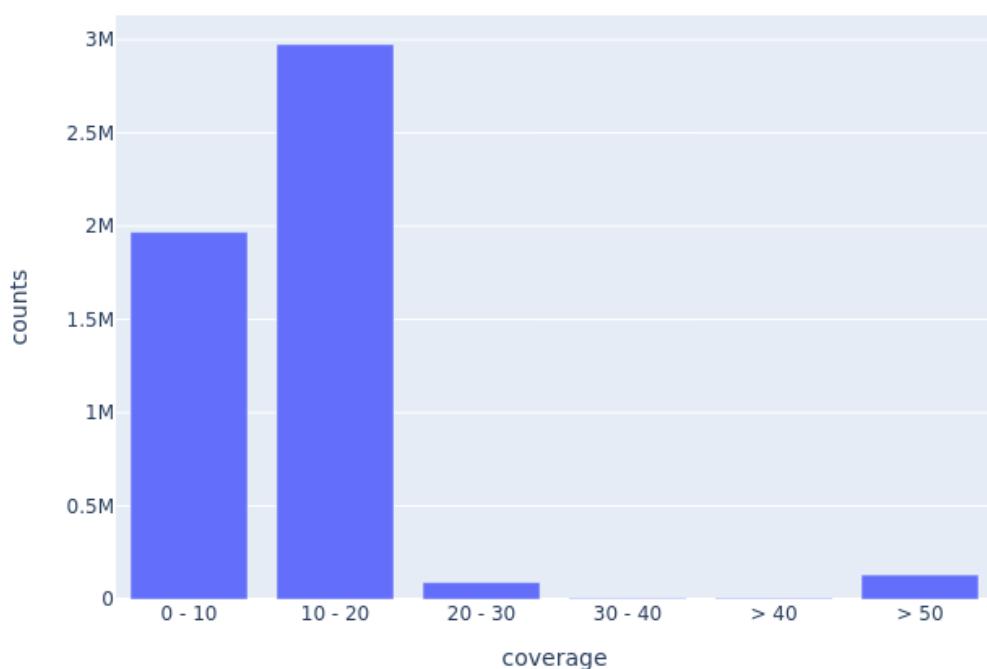
3596 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 27.40228337751848

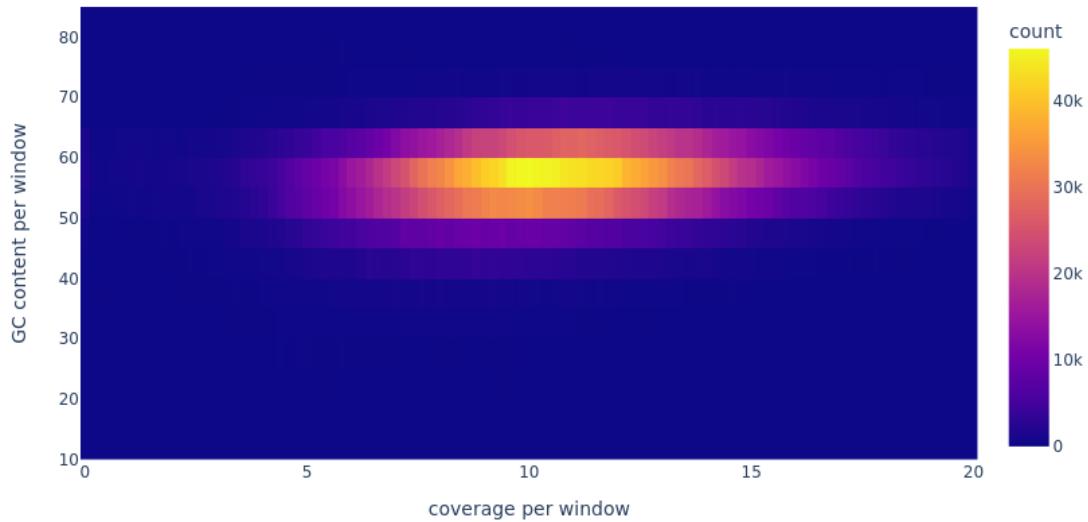
Ochrobactrum anthropi in T22.4.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T22.4.2



# Report of *Agrobacterium tumefaciens* in T22.4.3

## Mapping stats of Illumina reads

46935680 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

11288 + 0 supplementary

0 + 0 duplicates

39064352 + 0 mapped (83.23% : N/A)

46924392 + 0 paired in sequencing

23462196 + 0 read1

23462196 + 0 read2

38768316 + 0 properly paired (82.62% : N/A)

38900022 + 0 with itself and mate mapped

153042 + 0 singletons (0.33% : N/A)

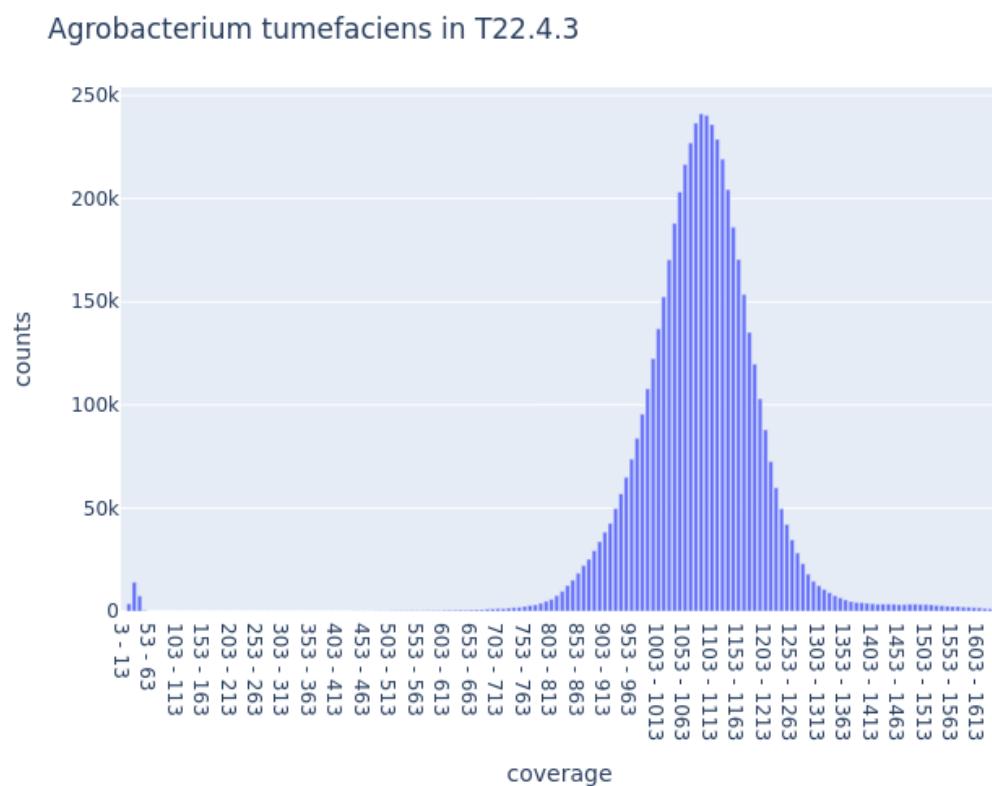
57132 + 0 with mate mapped to a different chr

52996 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

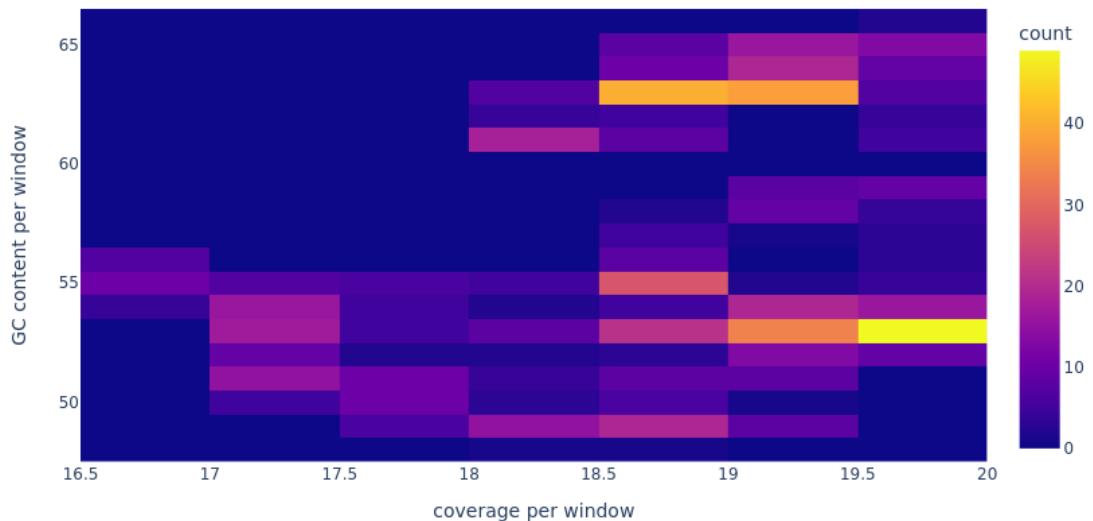
Average coverage: 1088.330007196347



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T22.4.3



# Report of Comamonas testosterone in T22.4.3

## Mapping stats of Illumina reads

46925390 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

998 + 0 supplementary

0 + 0 duplicates

4298925 + 0 mapped (9.16% : N/A)

46924392 + 0 paired in sequencing

23462196 + 0 read1

23462196 + 0 read2

4212976 + 0 properly paired (8.98% : N/A)

4217216 + 0 with itself and mate mapped

80711 + 0 singletons (0.17% : N/A)

50 + 0 with mate mapped to a different chr

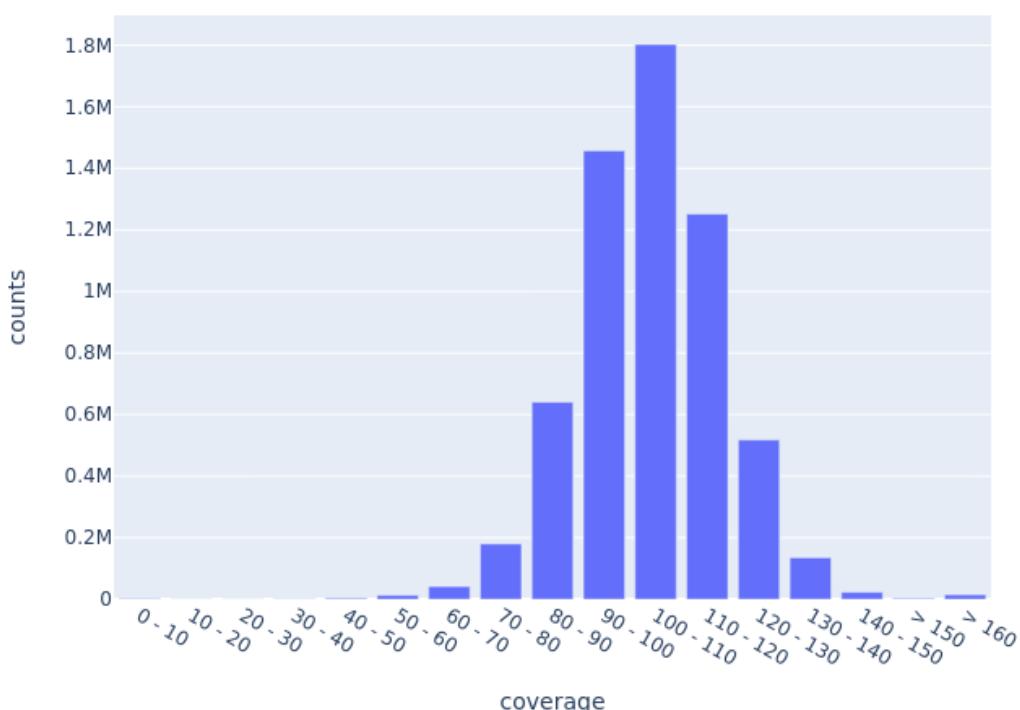
41 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 104.32931742881087

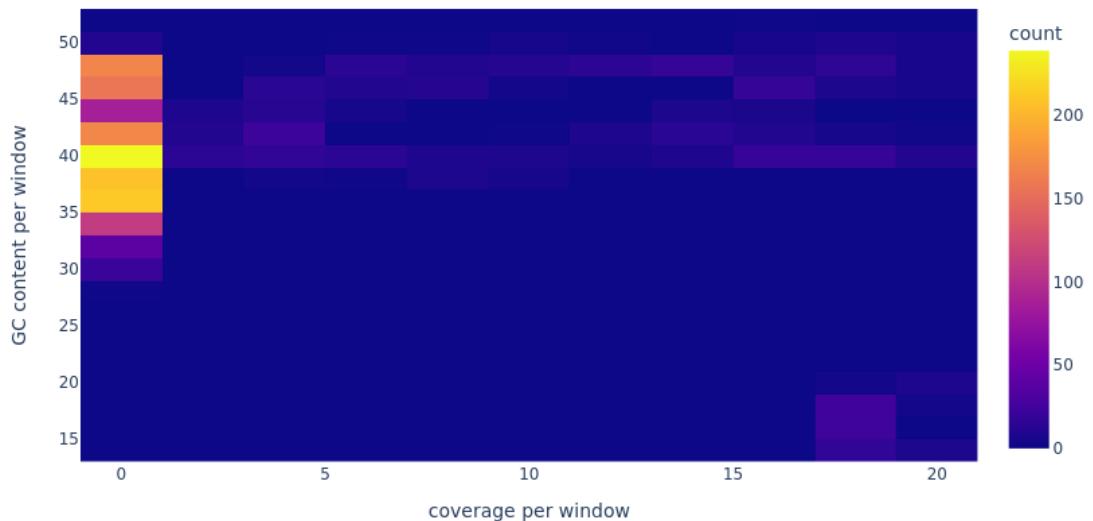
Comamonas testosterone in T22.4.3



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.4.3



# Report of *Microbacterium saperdae* in T22.4.3

## Mapping stats of Illumina reads

46924459 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

67 + 0 supplementary

0 + 0 duplicates

291136 + 0 mapped (0.62% : N/A)

46924392 + 0 paired in sequencing

23462196 + 0 read1

23462196 + 0 read2

265136 + 0 properly paired (0.57% : N/A)

265778 + 0 with itself and mate mapped

25291 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

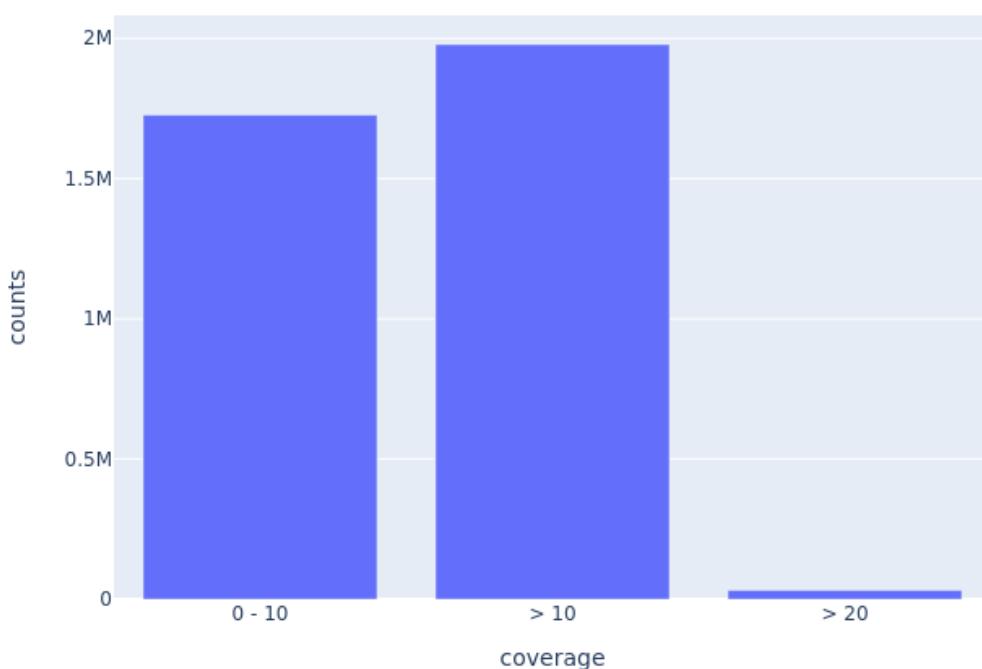
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 10.732704678495574

Microbacterium saperdae in T22.4.3

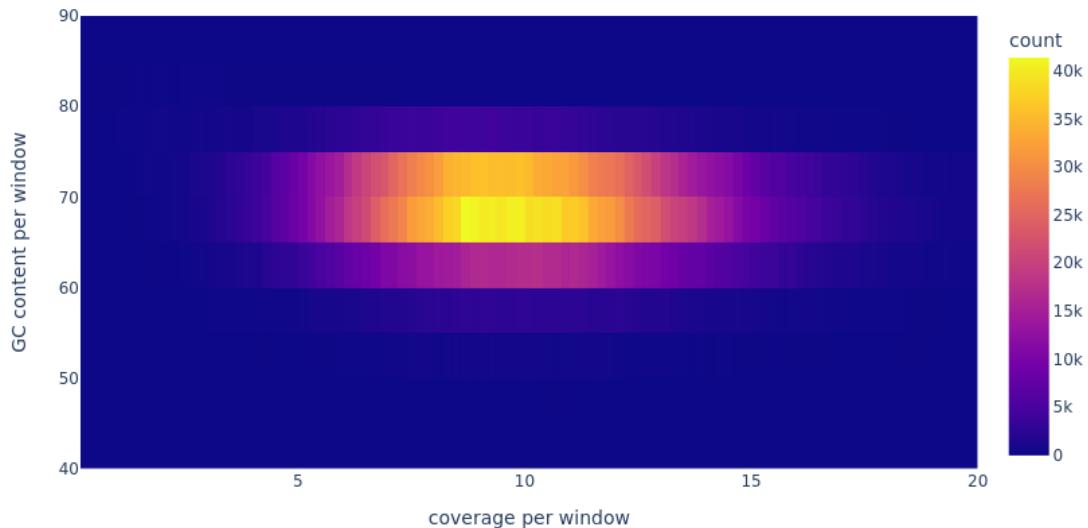


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T22.4.3



# Report of *Ochrobactrum anthropi* in T22.4.3

## Mapping stats of Illumina reads

46925575 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1183 + 0 supplementary

0 + 0 duplicates

3943584 + 0 mapped (8.40% : N/A)

46924392 + 0 paired in sequencing

23462196 + 0 read1

23462196 + 0 read2

3564664 + 0 properly paired (7.60% : N/A)

3574328 + 0 with itself and mate mapped

368073 + 0 singletons (0.78% : N/A)

4518 + 0 with mate mapped to a different chr

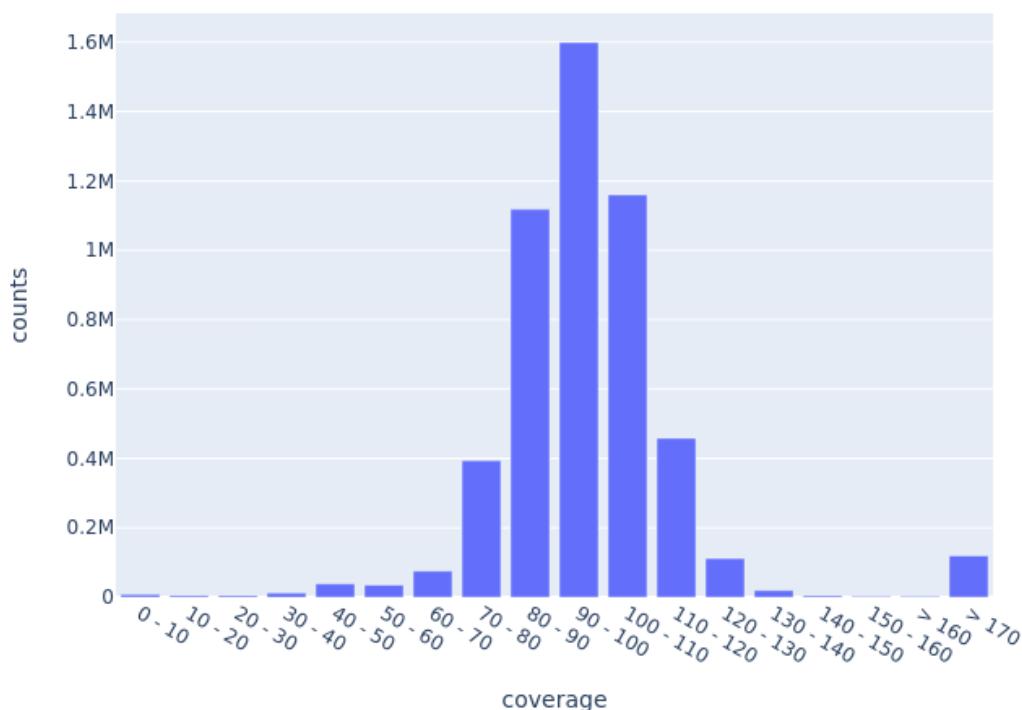
3091 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 108.03725189983238

Ochrobactrum anthropi in T22.4.3

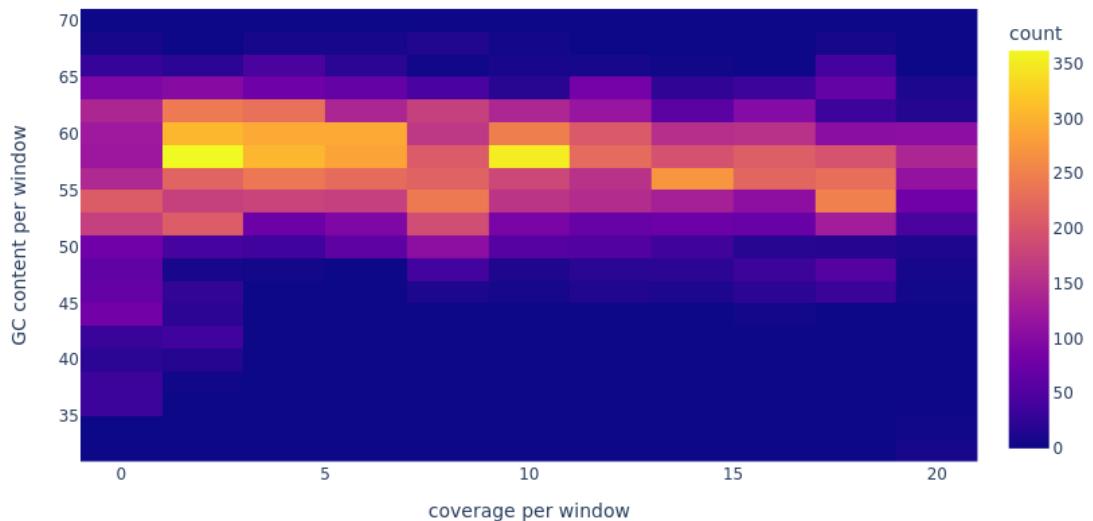


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T22.4.3



# Report of *Agrobacterium tumefaciens* in T22.4.4

## Mapping stats of Illumina reads

64652461 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

15259 + 0 supplementary

0 + 0 duplicates

53386064 + 0 mapped (82.57% : N/A)

64637202 + 0 paired in sequencing

32318601 + 0 read1

32318601 + 0 read2

53097228 + 0 properly paired (82.15% : N/A)

53223788 + 0 with itself and mate mapped

147017 + 0 singletons (0.23% : N/A)

41768 + 0 with mate mapped to a different chr

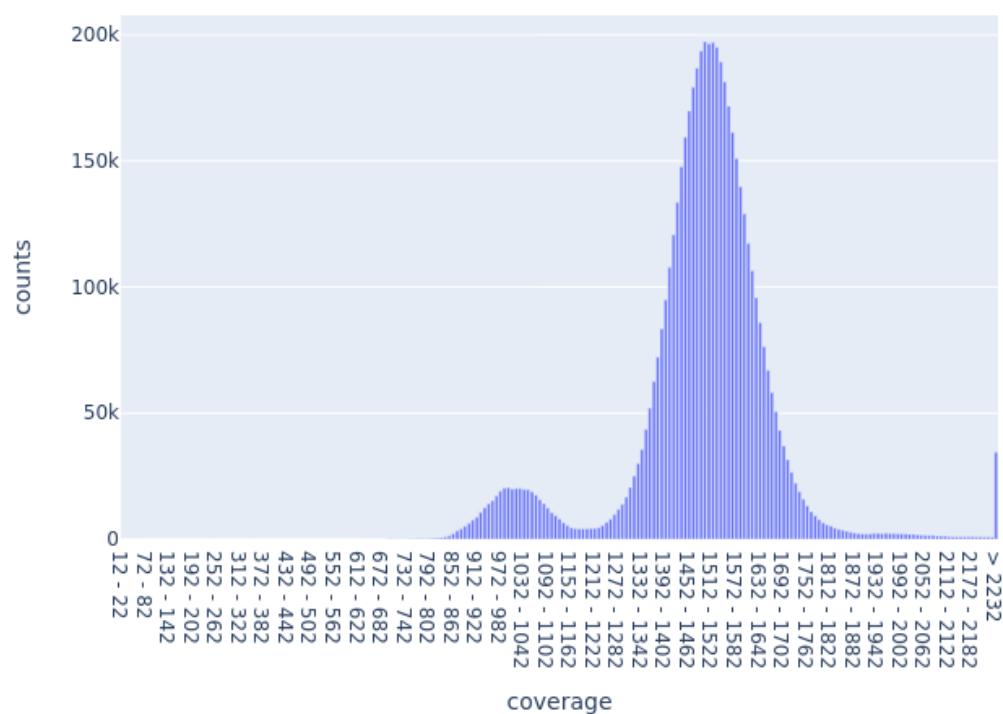
39772 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 1488.619125156795

Agrobacterium tumefaciens in T22.4.4

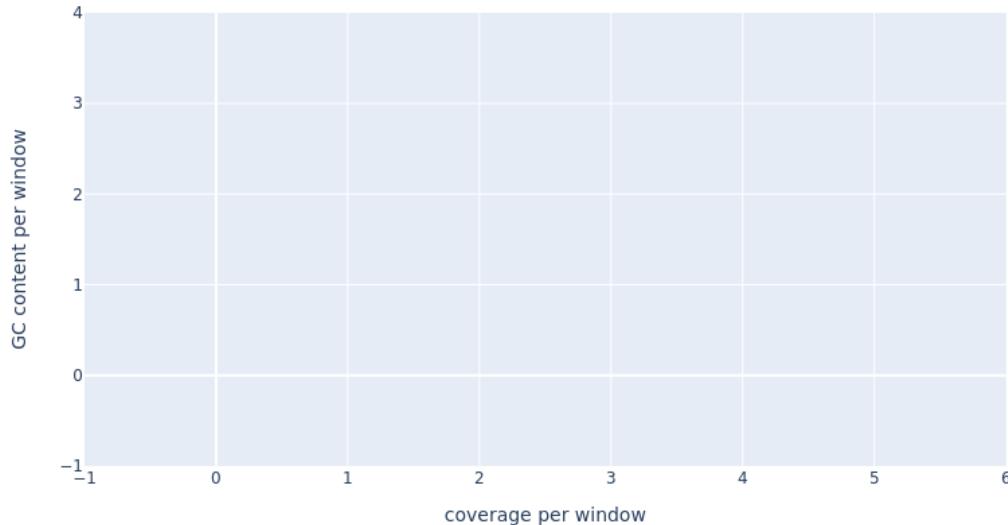


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T22.4.4



# Report of Comamonas testosterone in T22.4.4

## Mapping stats of Illumina reads

64640760 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

3558 + 0 supplementary

0 + 0 duplicates

9628367 + 0 mapped (14.90% : N/A)

64637202 + 0 paired in sequencing

32318601 + 0 read1

32318601 + 0 read2

9505588 + 0 properly paired (14.71% : N/A)

9516770 + 0 with itself and mate mapped

108039 + 0 singletons (0.17% : N/A)

142 + 0 with mate mapped to a different chr

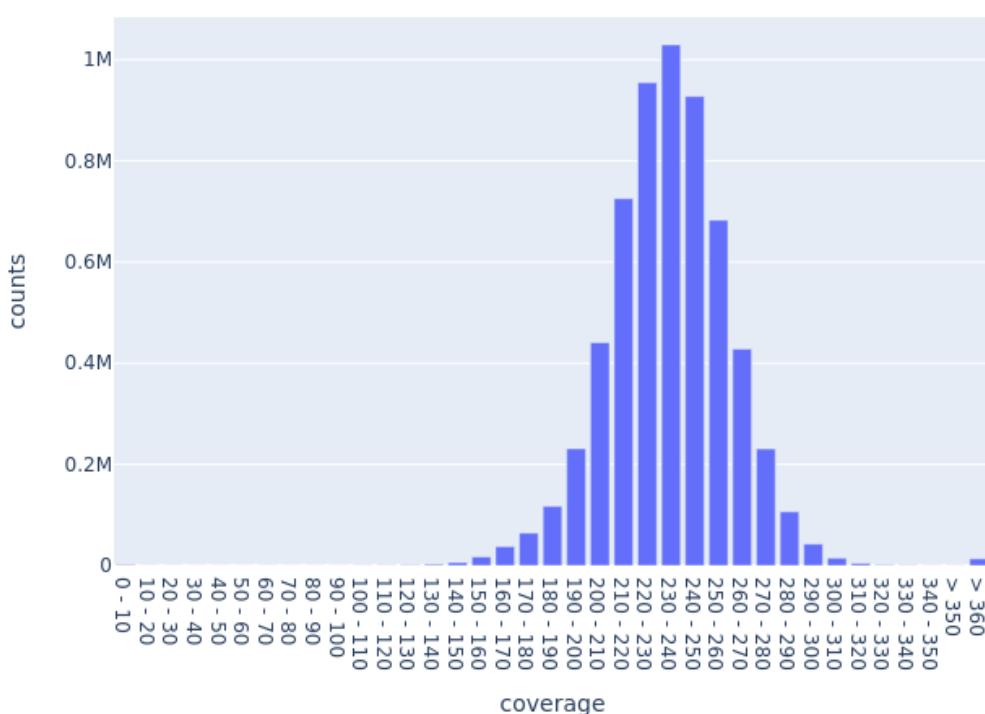
99 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 234.70166858112833

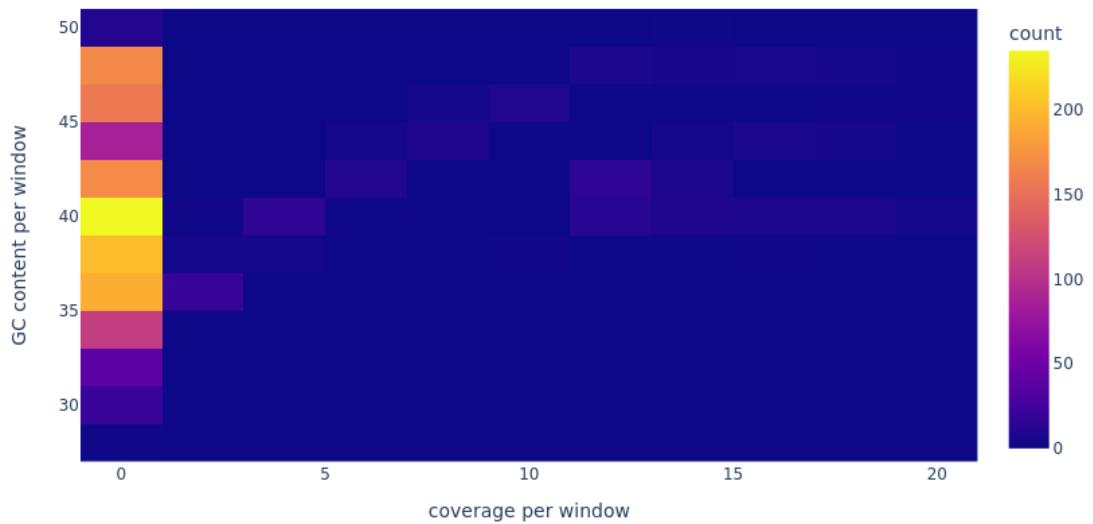
Comamonas testosterone in T22.4.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.4.4



# Report of *Microbacterium saperdae* in T22.4.4

## Mapping stats of Illumina reads

64637225 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

23 + 0 supplementary

0 + 0 duplicates

57448 + 0 mapped (0.09% : N/A)

64637202 + 0 paired in sequencing

32318601 + 0 read1

32318601 + 0 read2

24042 + 0 properly paired (0.04% : N/A)

24720 + 0 with itself and mate mapped

32705 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

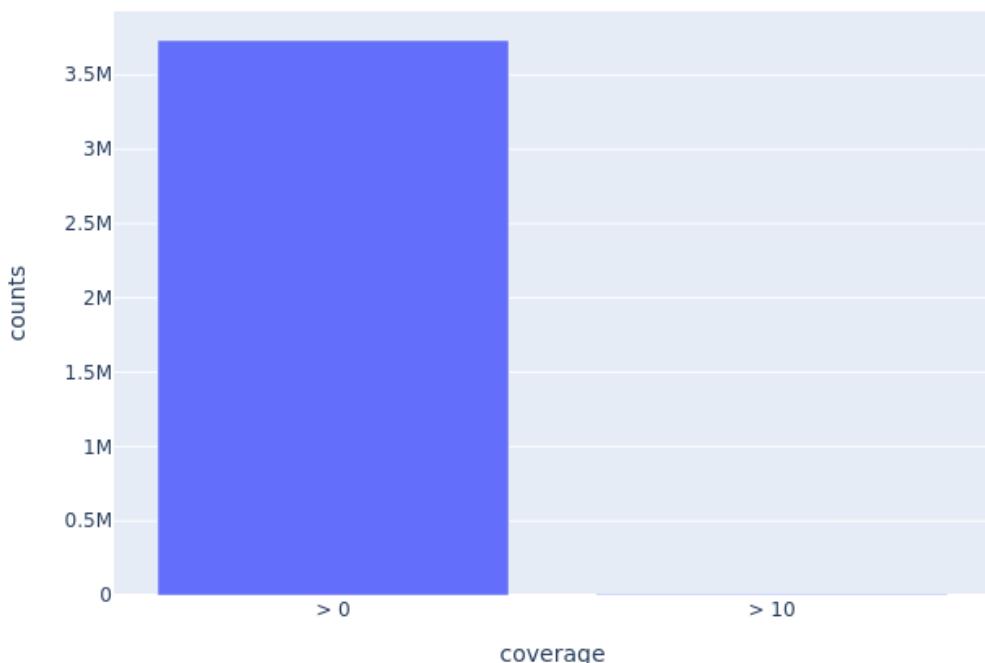
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 1.0310734901661531

*Microbacterium saperdae* in T22.4.4

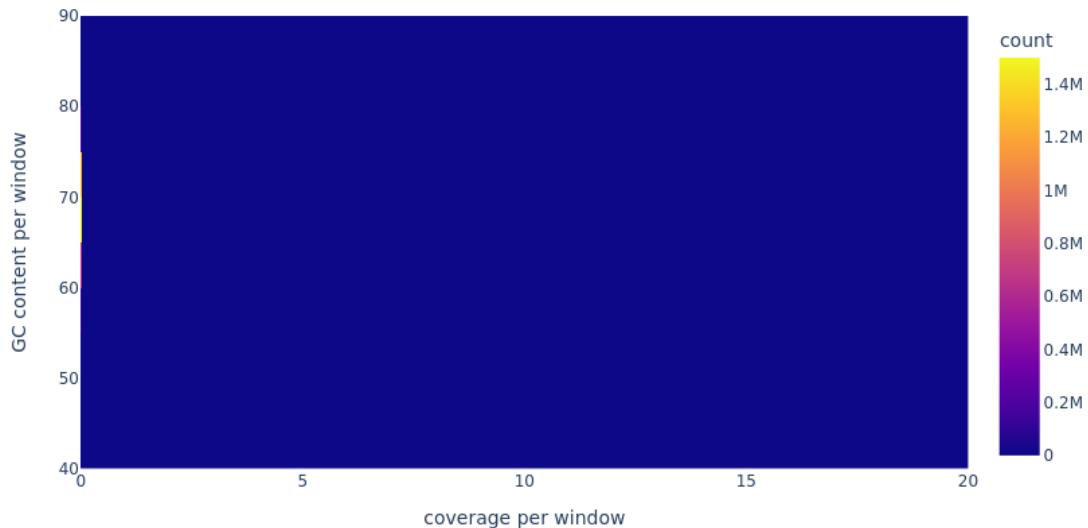


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T22.4.4



# Report of *Ochrobactrum anthropi* in T22.4.4

## Mapping stats of Illumina reads

64638431 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1229 + 0 supplementary

0 + 0 duplicates

2481783 + 0 mapped (3.84% : N/A)

64637202 + 0 paired in sequencing

32318601 + 0 read1

32318601 + 0 read2

1983202 + 0 properly paired (3.07% : N/A)

1994996 + 0 with itself and mate mapped

485558 + 0 singletons (0.75% : N/A)

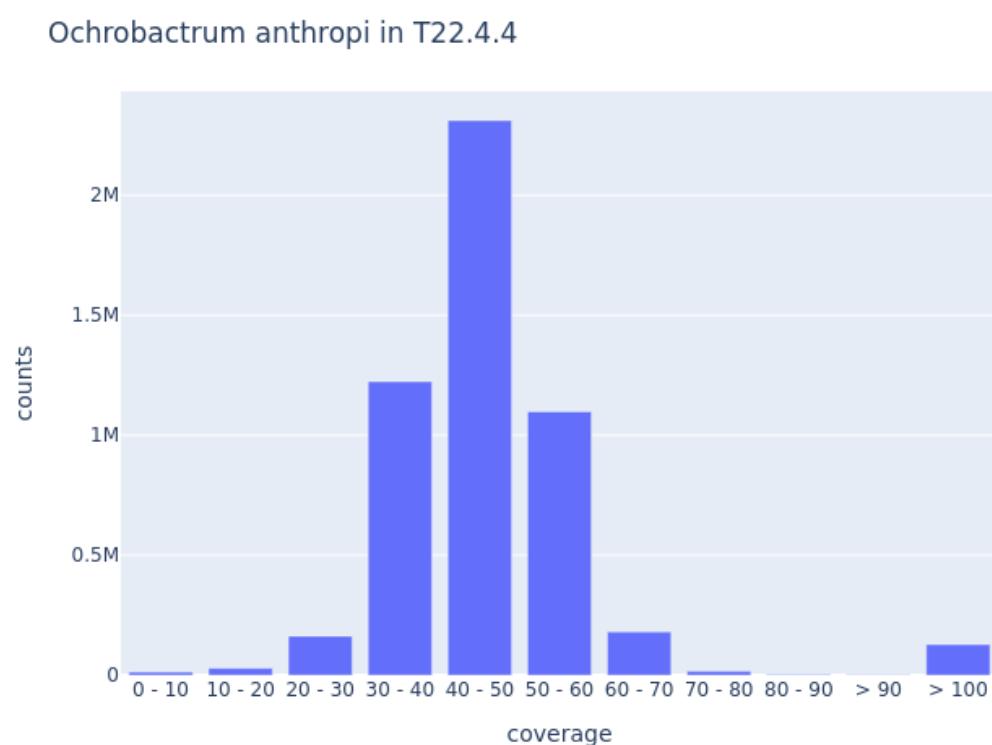
6418 + 0 with mate mapped to a different chr

4370 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

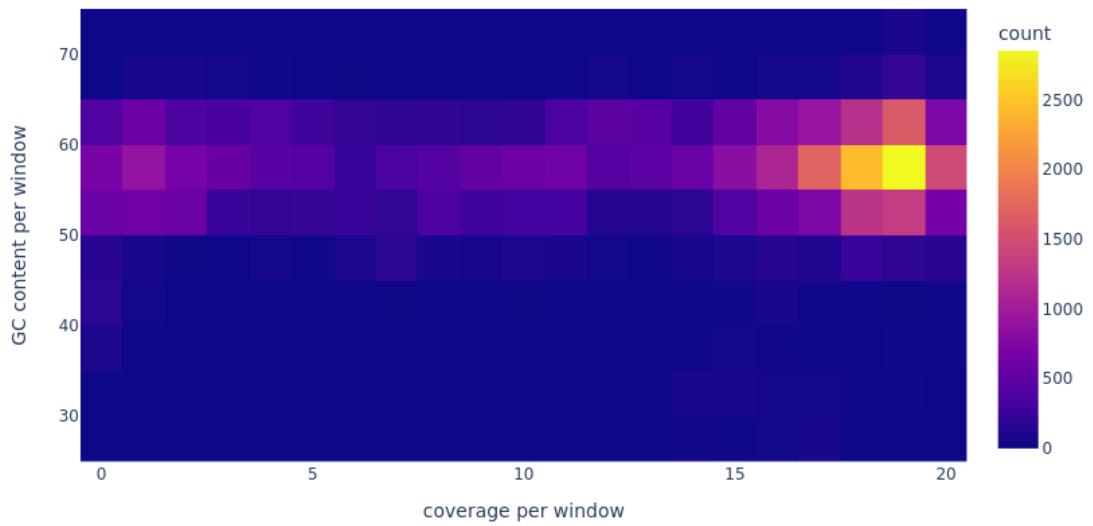
Average coverage: 63.5106896461674



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T22.4.4



# Report of *Agrobacterium tumefaciens* in T22.4.5

## Mapping stats of Illumina reads

75746405 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

19351 + 0 supplementary

0 + 0 duplicates

71673461 + 0 mapped (94.62% : N/A)

75727054 + 0 paired in sequencing

37863527 + 0 read1

37863527 + 0 read2

71262424 + 0 properly paired (94.10% : N/A)

71478502 + 0 with itself and mate mapped

175608 + 0 singletons (0.23% : N/A)

96846 + 0 with mate mapped to a different chr

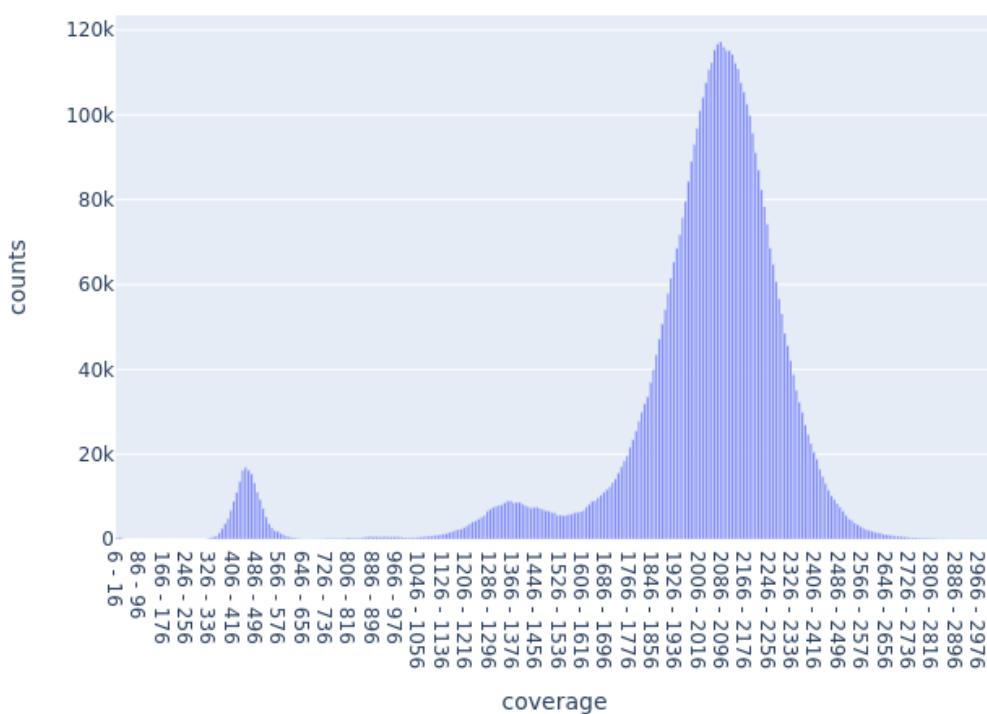
93595 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 1998.6835604136975

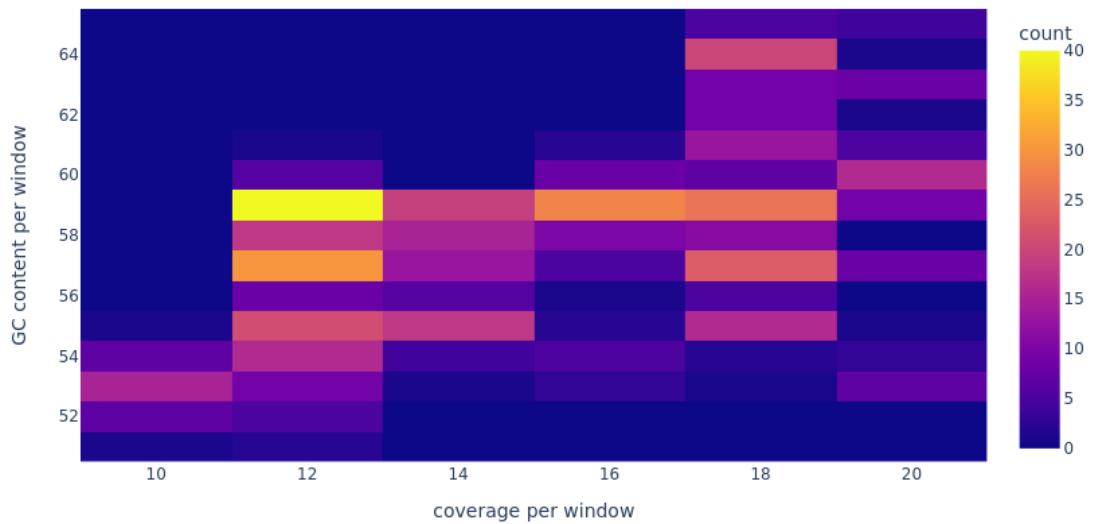
Agrobacterium tumefaciens in T22.4.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T22.4.5



# Report of Comamonas testosterone in T22.4.5

## Mapping stats of Illumina reads

75727561 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

507 + 0 supplementary

0 + 0 duplicates

1975016 + 0 mapped (2.61% : N/A)

75727054 + 0 paired in sequencing

37863527 + 0 read1

37863527 + 0 read2

1860298 + 0 properly paired (2.46% : N/A)

1861546 + 0 with itself and mate mapped

112963 + 0 singletons (0.15% : N/A)

16 + 0 with mate mapped to a different chr

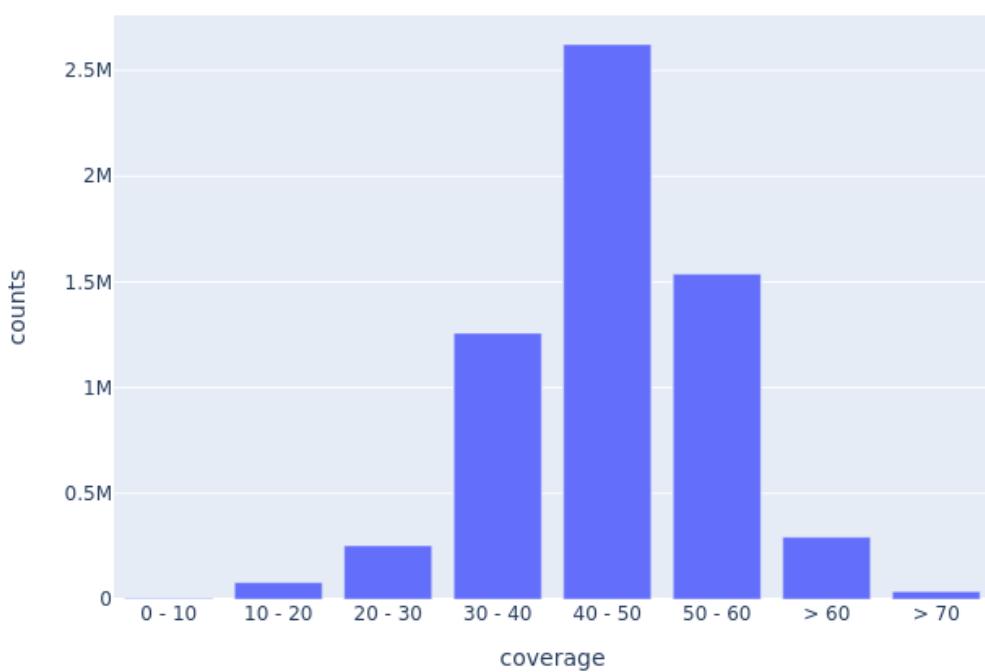
9 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 46.64673851499682

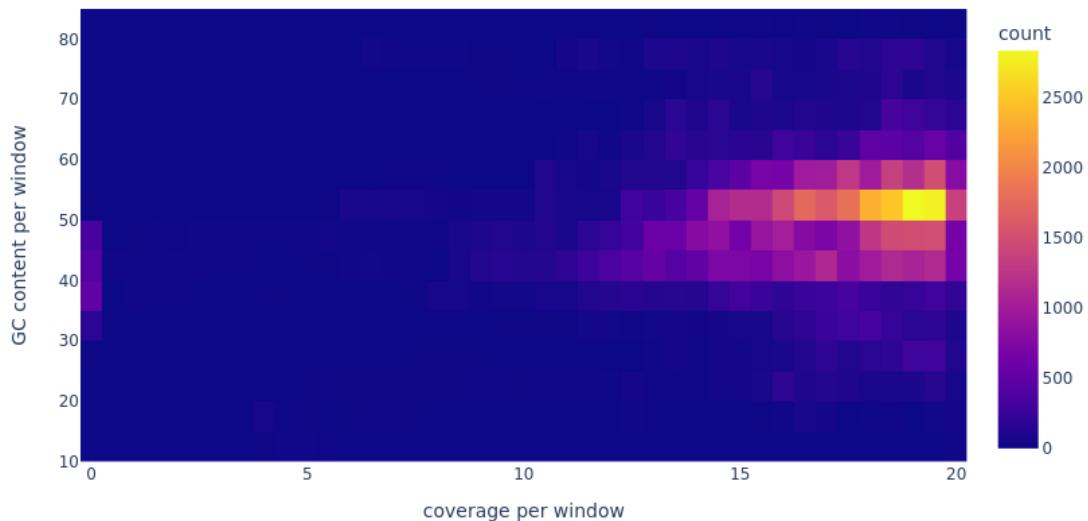
Comamonas testosterone in T22.4.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T22.4.5



# Report of *Microbacterium saperdae* in T22.4.5

## Mapping stats of Illumina reads

75727104 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

50 + 0 supplementary

0 + 0 duplicates

241119 + 0 mapped (0.32% : N/A)

75727054 + 0 paired in sequencing

37863527 + 0 read1

37863527 + 0 read2

201090 + 0 properly paired (0.27% : N/A)

202164 + 0 with itself and mate mapped

38905 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

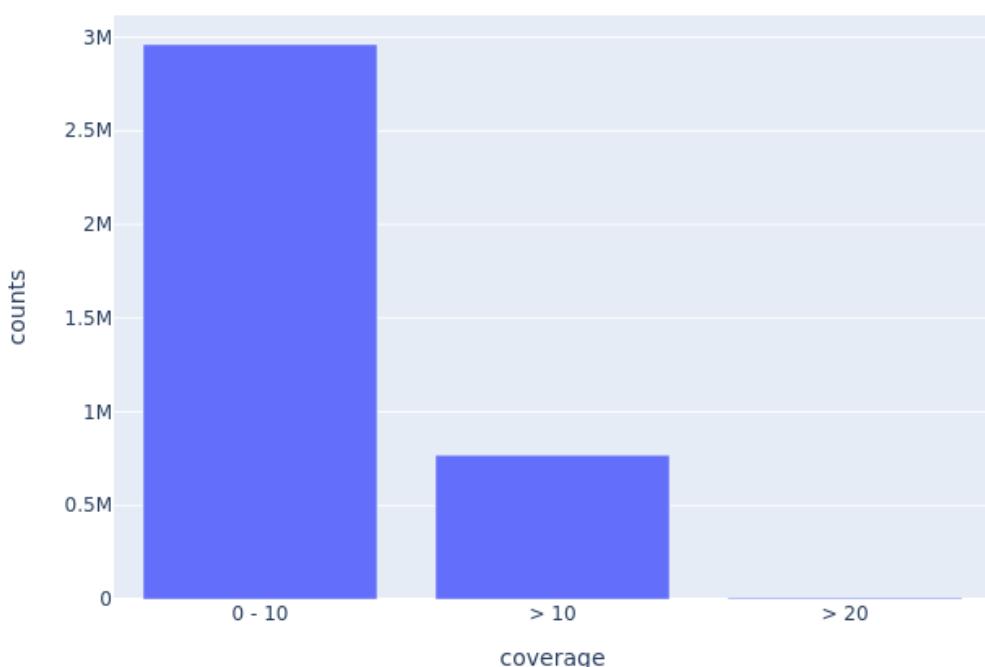
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 8.214091193926897

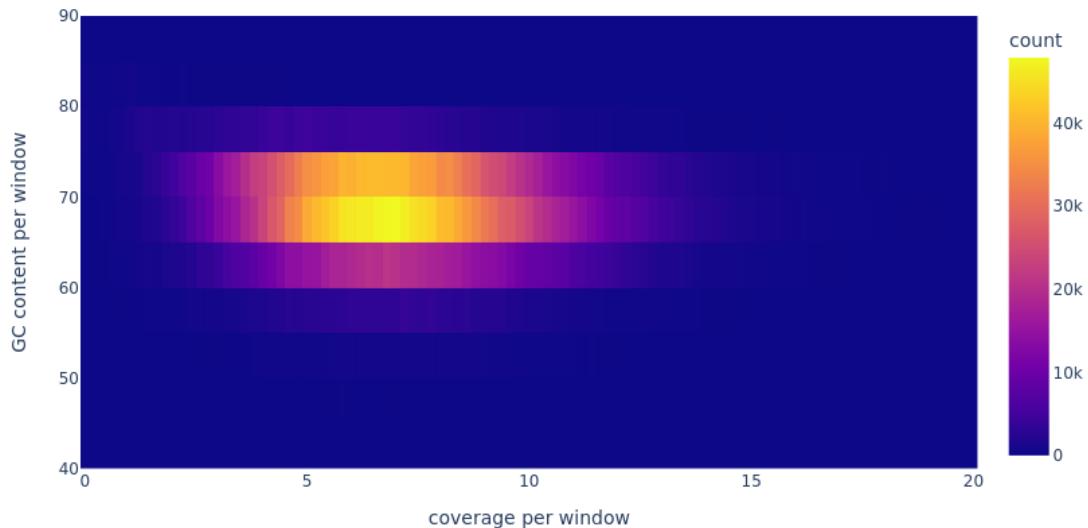
Microbacterium saperdae in T22.4.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T22.4.5



# Report of *Ochrobactrum anthropi* in T22.4.5

## Mapping stats of Illumina reads

75728538 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1484 + 0 supplementary

0 + 0 duplicates

3083666 + 0 mapped (4.07% : N/A)

75727054 + 0 paired in sequencing

37863527 + 0 read1

37863527 + 0 read2

2411654 + 0 properly paired (3.18% : N/A)

2425792 + 0 with itself and mate mapped

656390 + 0 singletons (0.87% : N/A)

8468 + 0 with mate mapped to a different chr

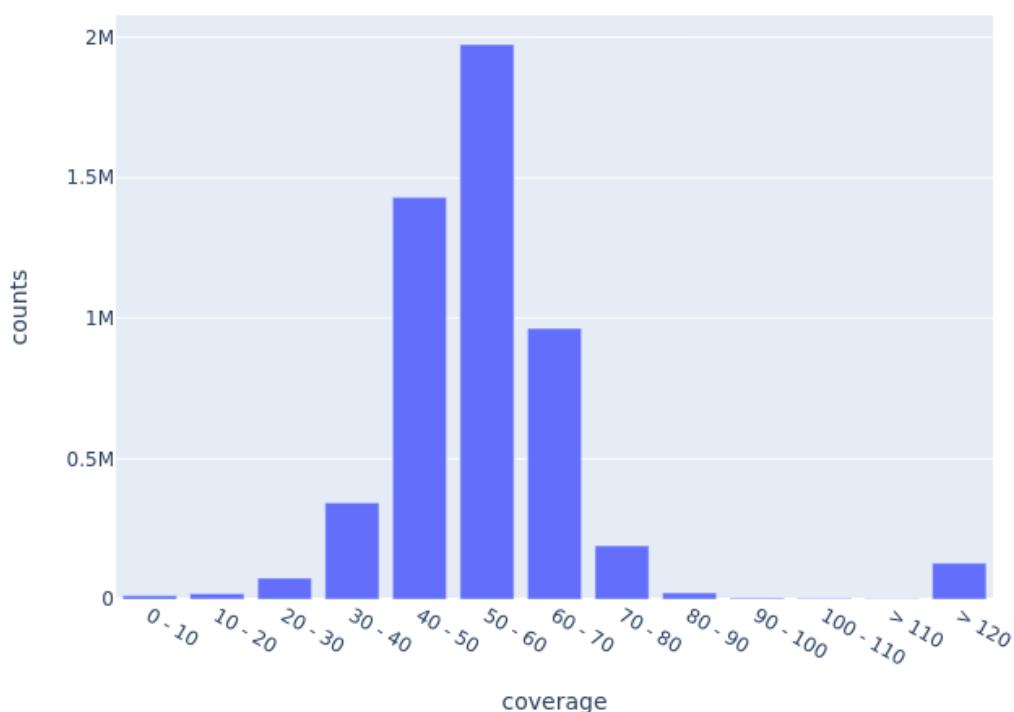
5759 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 78.26738575132967

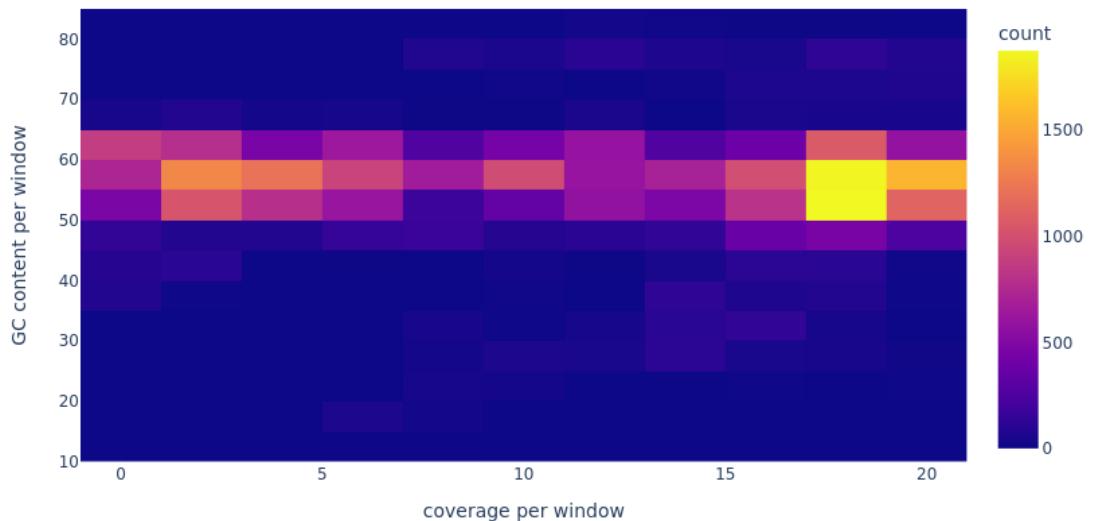
Ochrobactrum anthropi in T22.4.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T22.4.5



# Report of *Agrobacterium tumefaciens* in T33.1.1

## Mapping stats of Illumina reads

14569242 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

7746 + 0 supplementary

0 + 0 duplicates

14531707 + 0 mapped (99.74% : N/A)

14561496 + 0 paired in sequencing

7280748 + 0 read1

7280748 + 0 read2

14442732 + 0 properly paired (99.18% : N/A)

14518164 + 0 with itself and mate mapped

5797 + 0 singletons (0.04% : N/A)

36952 + 0 with mate mapped to a different chr

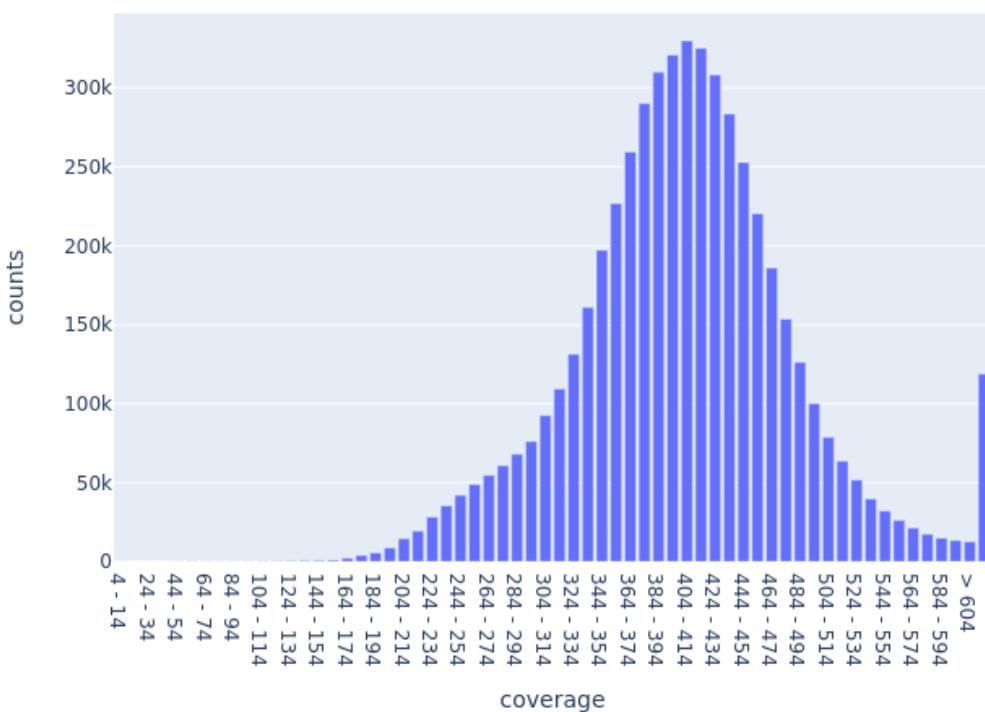
35679 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 408.7086371307946

Agrobacterium tumefaciens in T33.1.1

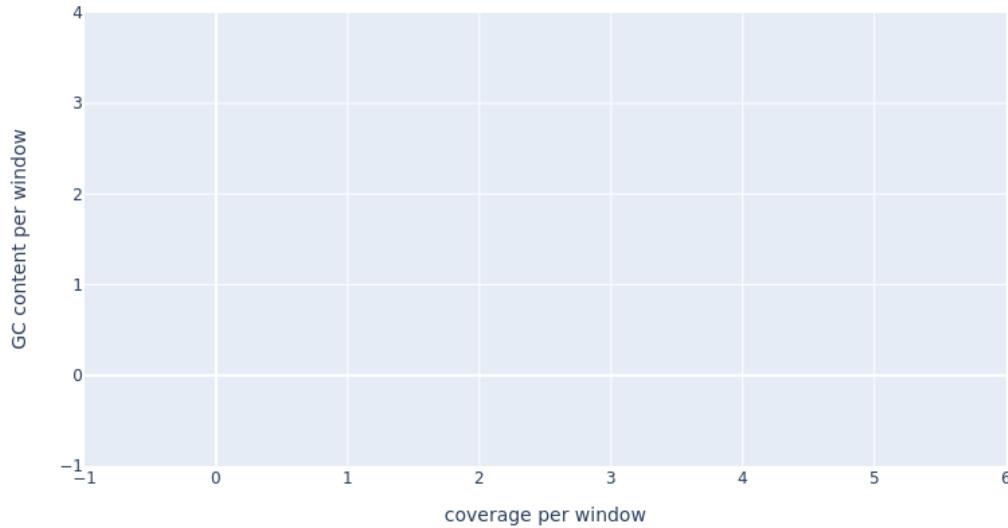


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T33.1.1



# Report of *Agrobacterium tumefaciens* in T33.1.2

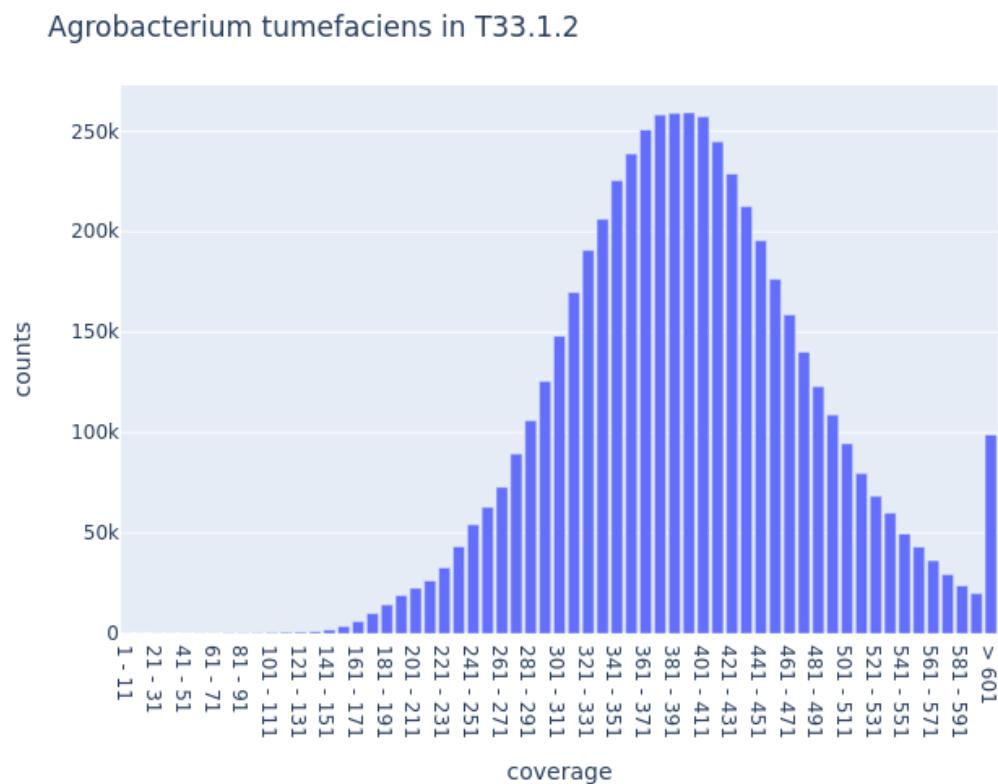
## Mapping stats of Illumina reads

14108800 + 0 in total (QC-passed reads + QC-failed reads)  
0 + 0 secondary  
16594 + 0 supplementary  
0 + 0 duplicates  
14077213 + 0 mapped (99.78% : N/A)  
14092206 + 0 paired in sequencing  
7046103 + 0 read1  
7046103 + 0 read2  
13969120 + 0 properly paired (99.13% : N/A)  
14055830 + 0 with itself and mate mapped  
4789 + 0 singletons (0.03% : N/A)  
42246 + 0 with mate mapped to a different chr  
40937 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 395.76057703148166

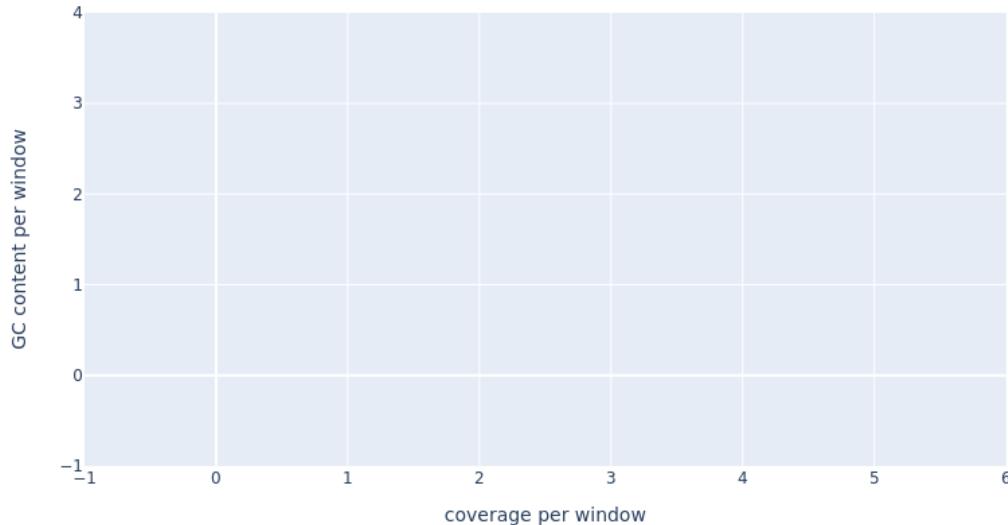


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T33.1.2



# Report of *Comamonas testosteronei* in T33.2.1.rep

## Mapping stats of Illumina reads

15659134 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

11488 + 0 supplementary

0 + 0 duplicates

15650236 + 0 mapped (99.94% : N/A)

15647646 + 0 paired in sequencing

7823823 + 0 read1

7823823 + 0 read2

15583512 + 0 properly paired (99.59% : N/A)

15633440 + 0 with itself and mate mapped

5308 + 0 singletons (0.03% : N/A)

1104 + 0 with mate mapped to a different chr

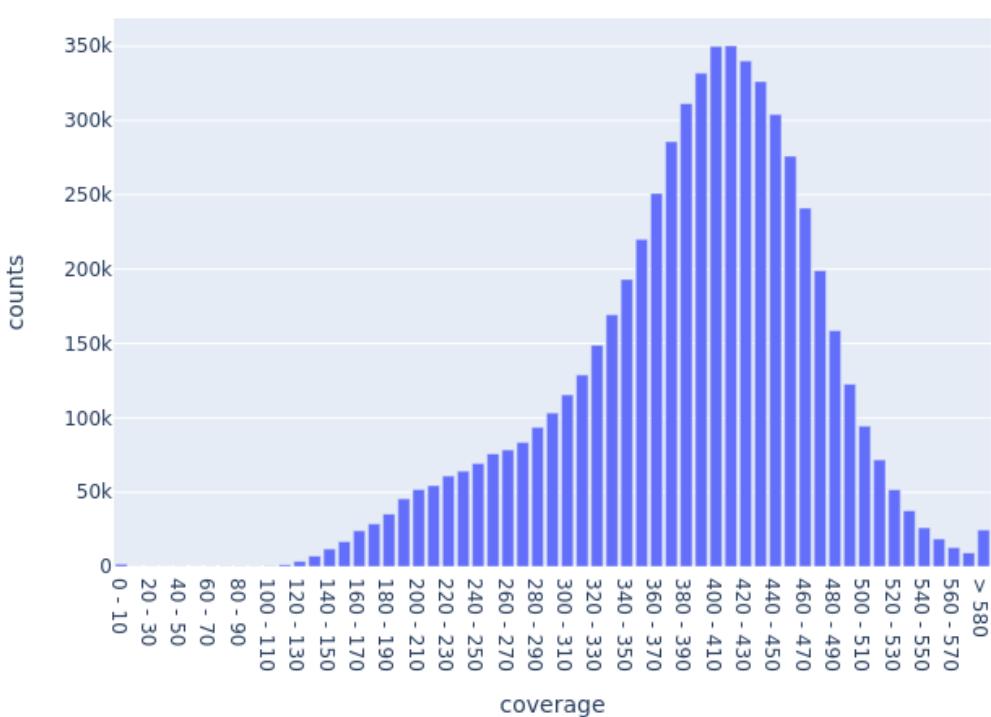
1043 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 386.9933179836733

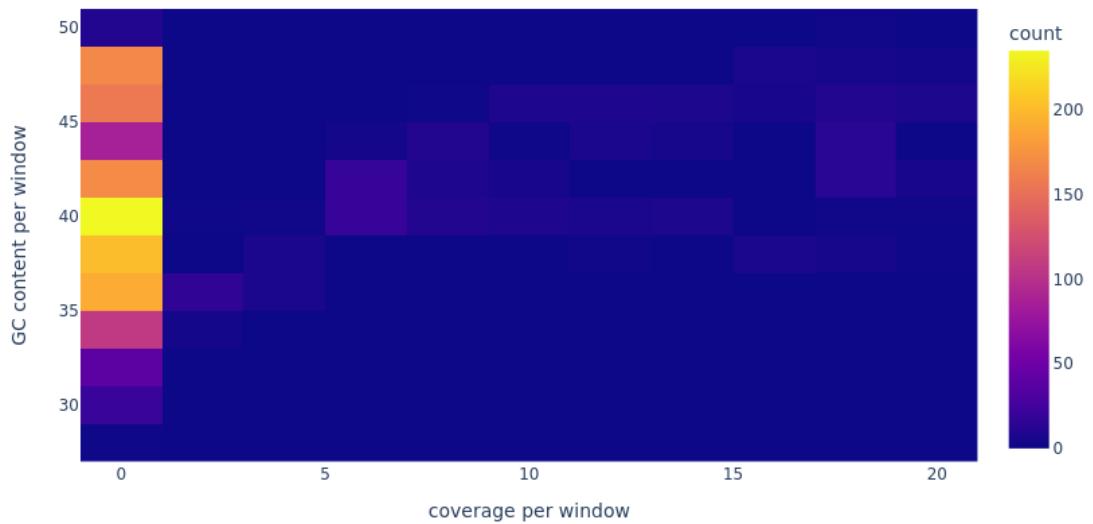
Comamonas testosteronei in T33.2.1.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.2.1.rep



# Report of *Comamonas testosteronei* in T33.2.2.rep

## Mapping stats of Illumina reads

14250790 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

5148 + 0 supplementary

0 + 0 duplicates

14242104 + 0 mapped (99.94% : N/A)

14245642 + 0 paired in sequencing

7122821 + 0 read1

7122821 + 0 read2

14160304 + 0 properly paired (99.40% : N/A)

14231740 + 0 with itself and mate mapped

5216 + 0 singletons (0.04% : N/A)

4472 + 0 with mate mapped to a different chr

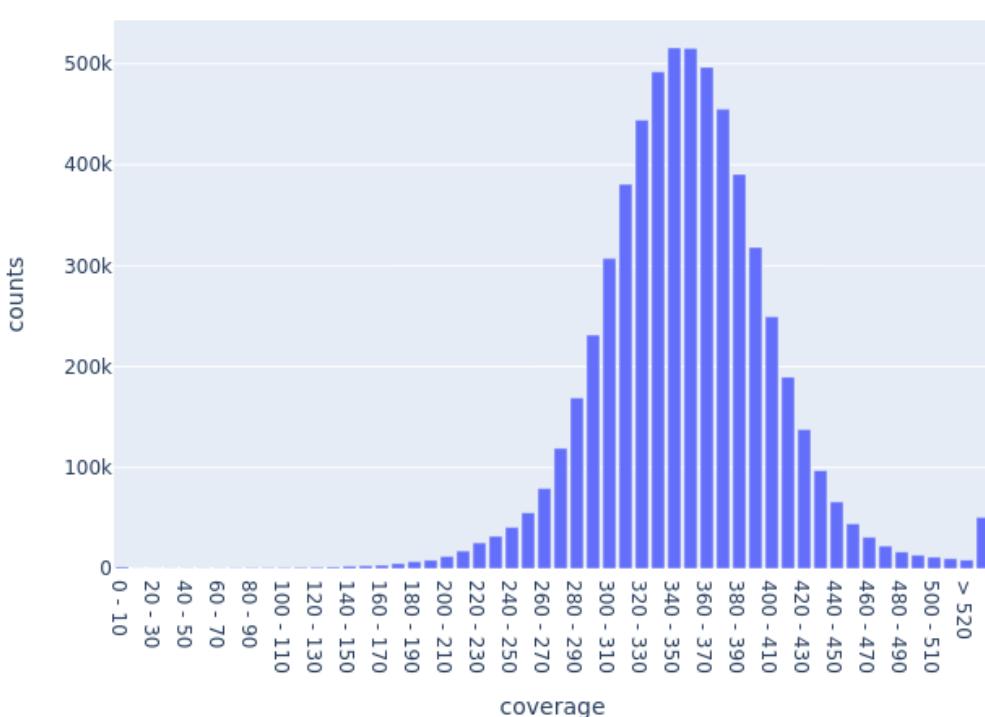
4026 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 352.20805944259666

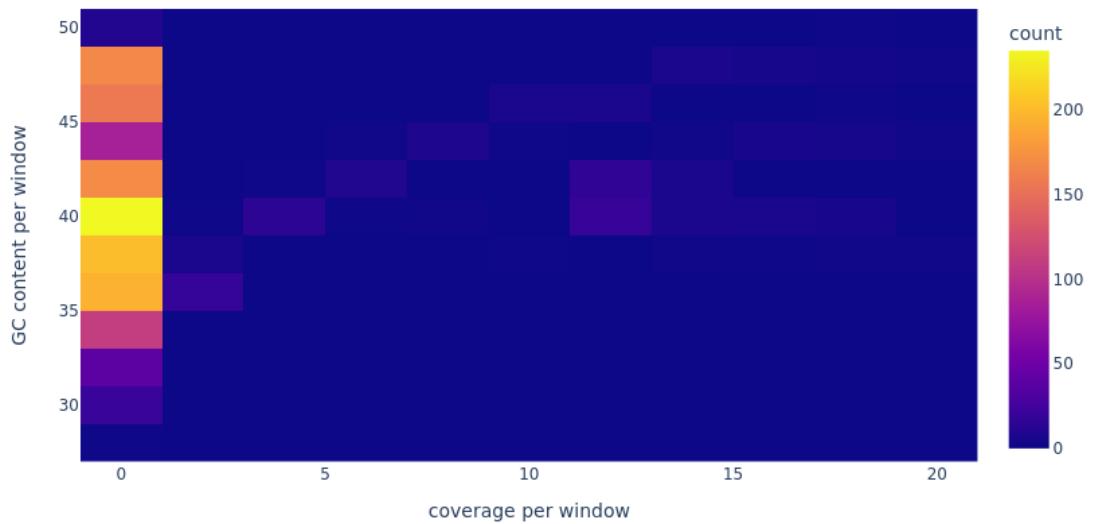
Comamonas testosteronei in T33.2.2.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.2.2.rep



# Report of *Comamonas testosteronei* in T33.2.3.rep

## Mapping stats of Illumina reads

15319298 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

6716 + 0 supplementary

0 + 0 duplicates

15309249 + 0 mapped (99.93% : N/A)

15312582 + 0 paired in sequencing

7656291 + 0 read1

7656291 + 0 read2

15207766 + 0 properly paired (99.32% : N/A)

15296974 + 0 with itself and mate mapped

5559 + 0 singletons (0.04% : N/A)

5308 + 0 with mate mapped to a different chr

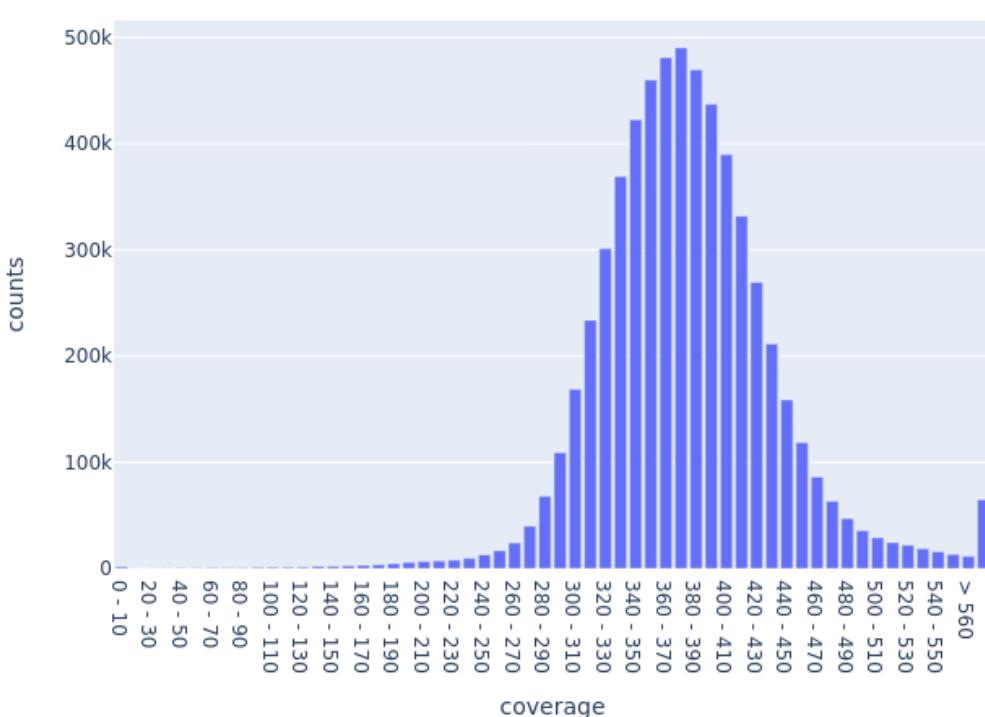
5047 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 378.5815845825819

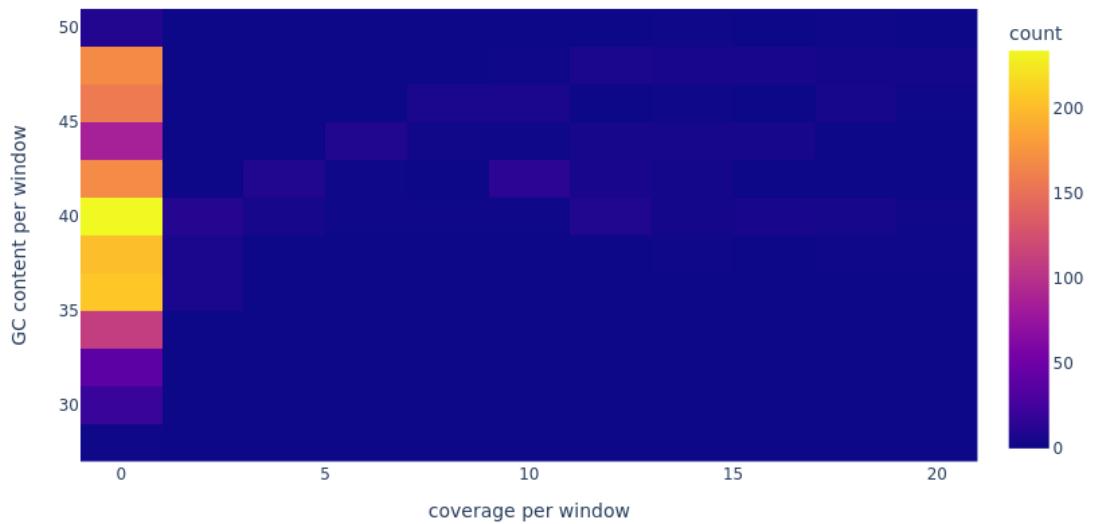
Comamonas testosteronei in T33.2.3.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.2.3.rep



# Report of *Comamonas testosteronei* in T33.2.4.rep

## Mapping stats of Illumina reads

13557878 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

26864 + 0 supplementary

0 + 0 duplicates

13549440 + 0 mapped (99.94% : N/A)

13531014 + 0 paired in sequencing

6765507 + 0 read1

6765507 + 0 read2

13395784 + 0 properly paired (99.00% : N/A)

13517236 + 0 with itself and mate mapped

5340 + 0 singletons (0.04% : N/A)

4118 + 0 with mate mapped to a different chr

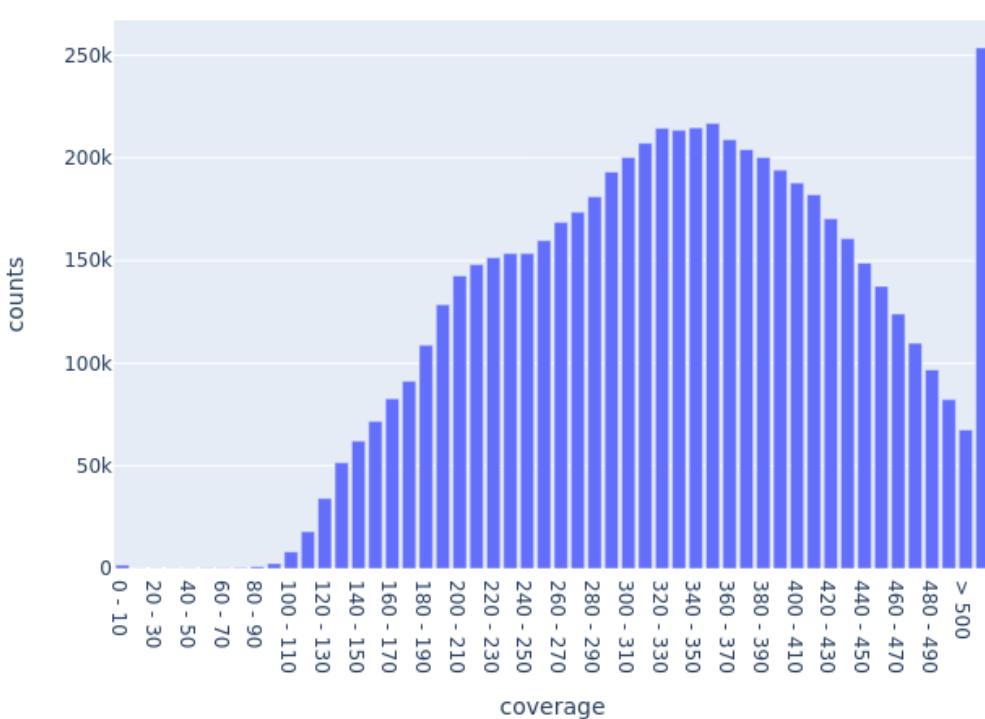
3949 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 334.531525669537

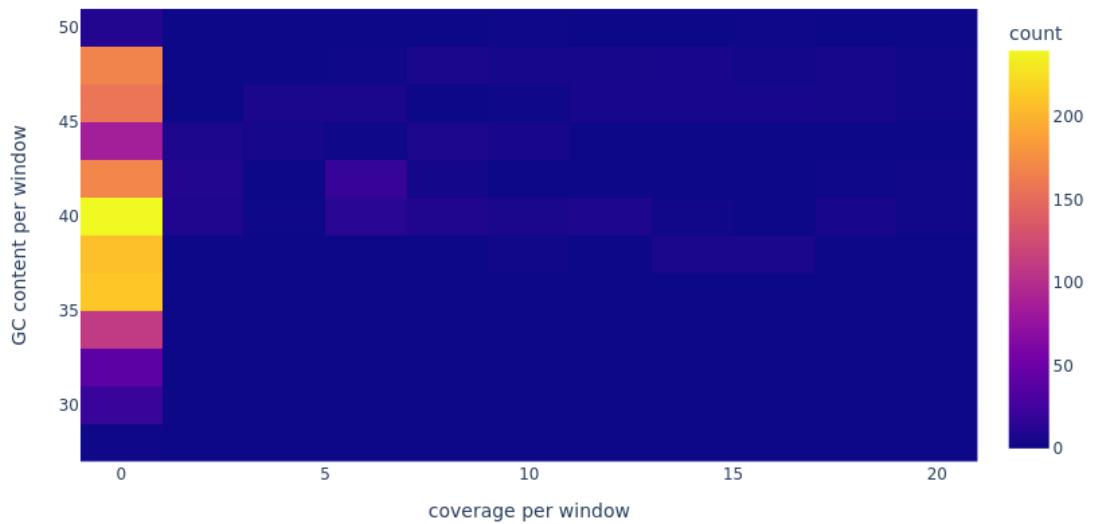
Comamonas testosteronei in T33.2.4.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.2.4.rep



# Report of Comamonas testosteronei in T33.2.5.rep

## Mapping stats of Illumina reads

15521864 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

6722 + 0 supplementary

0 + 0 duplicates

2779331 + 0 mapped (17.91% : N/A)

15515142 + 0 paired in sequencing

7757571 + 0 read1

7757571 + 0 read2

2676756 + 0 properly paired (17.25% : N/A)

2698758 + 0 with itself and mate mapped

73851 + 0 singletons (0.48% : N/A)

544 + 0 with mate mapped to a different chr

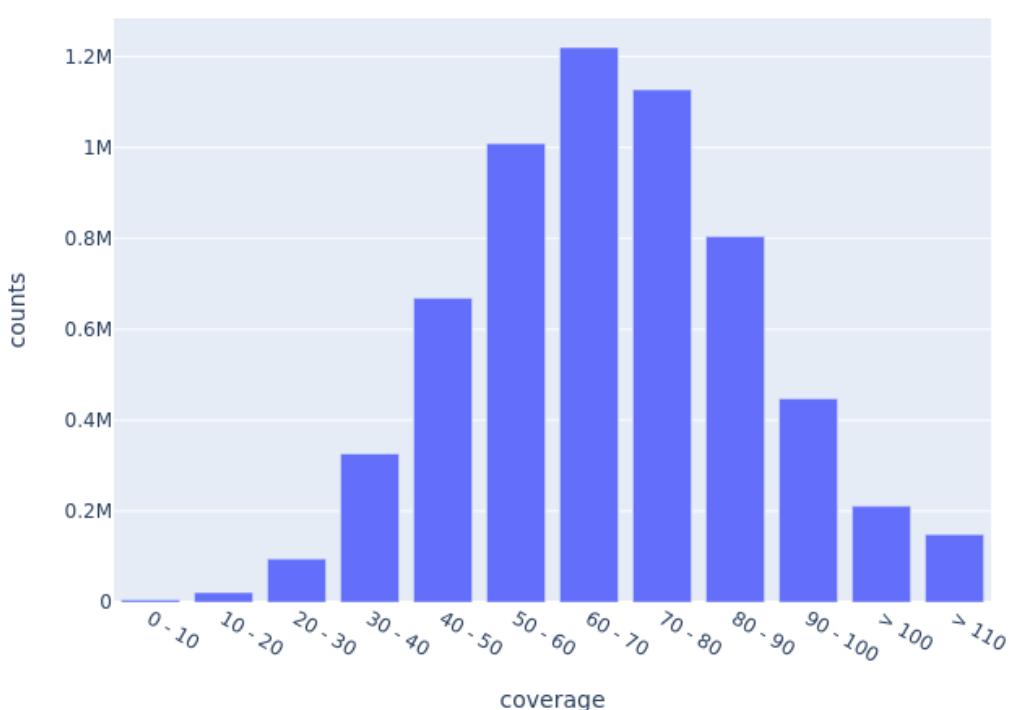
509 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 67.84691927261085

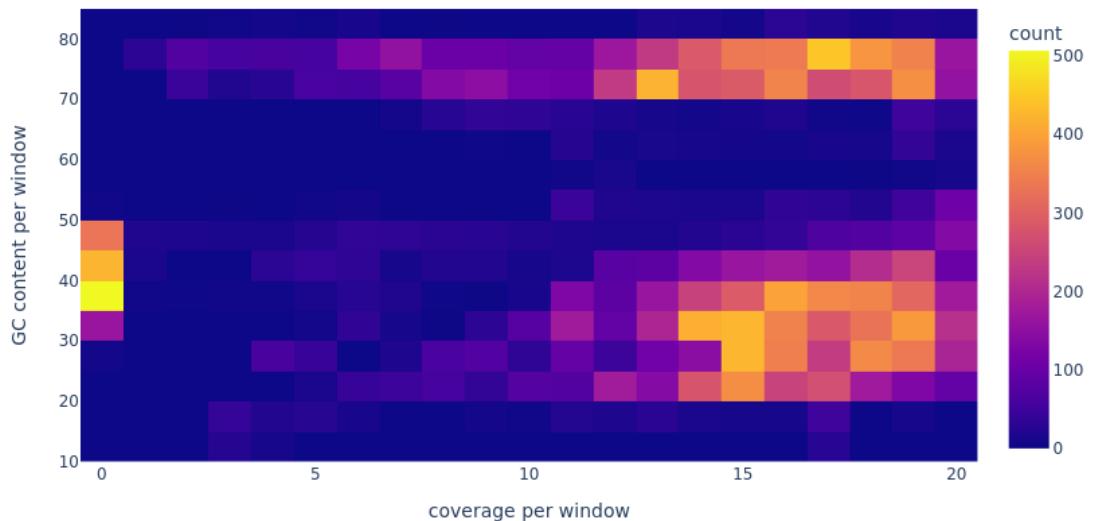
Comamonas testosteronei in T33.2.5.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.2.5.rep



# Report of *Agrobacterium tumefaciens* in T33.3.1

## Mapping stats of Illumina reads

150633419 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

103951 + 0 supplementary

0 + 0 duplicates

142081227 + 0 mapped (94.32% : N/A)

150529468 + 0 paired in sequencing

75264734 + 0 read1

75264734 + 0 read2

141140642 + 0 properly paired (93.76% : N/A)

141875954 + 0 with itself and mate mapped

101322 + 0 singletons (0.07% : N/A)

324596 + 0 with mate mapped to a different chr

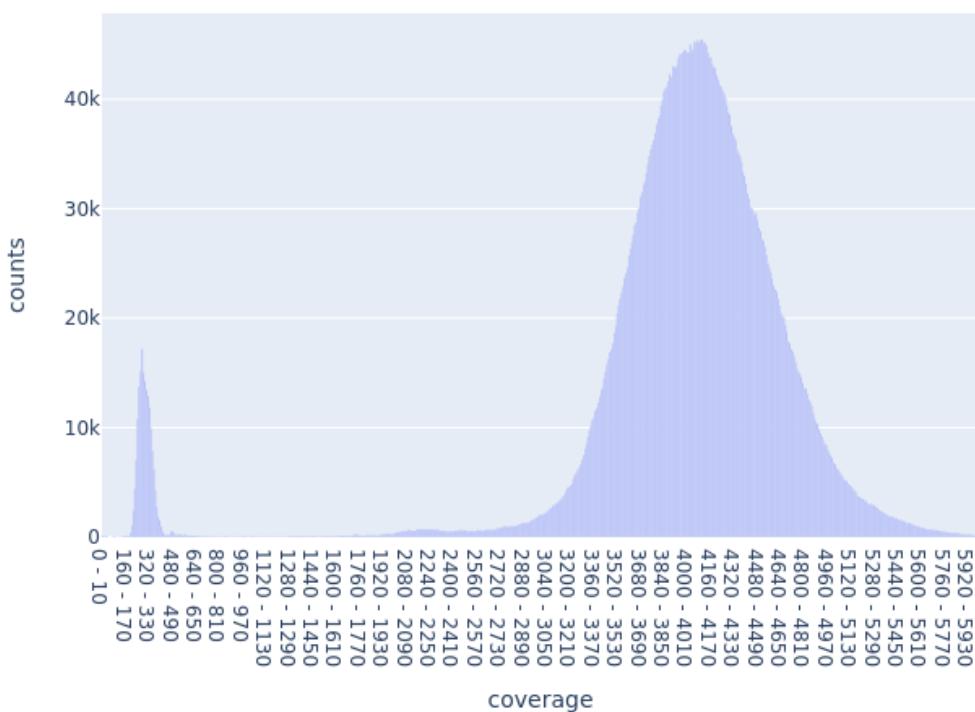
308575 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 3991.2383967084893

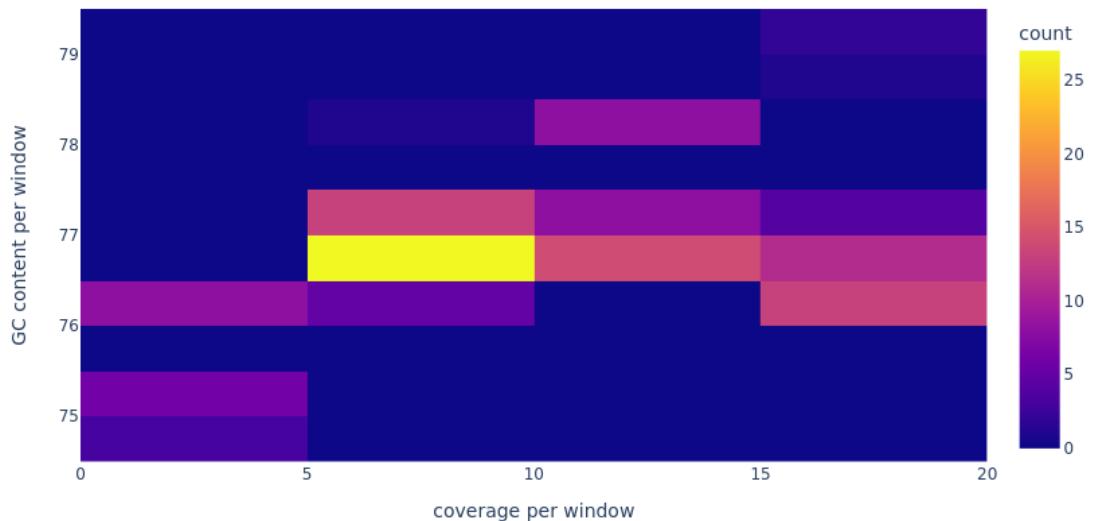
Agrobacterium tumefaciens in T33.3.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T33.3.1



# Report of Comamonas testosterone in T33.3.1

## Mapping stats of Illumina reads

150530972 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1504 + 0 supplementary

0 + 0 duplicates

5579901 + 0 mapped (3.71% : N/A)

150529468 + 0 paired in sequencing

75264734 + 0 read1

75264734 + 0 read2

5357866 + 0 properly paired (3.56% : N/A)

5363590 + 0 with itself and mate mapped

214807 + 0 singletons (0.14% : N/A)

96 + 0 with mate mapped to a different chr

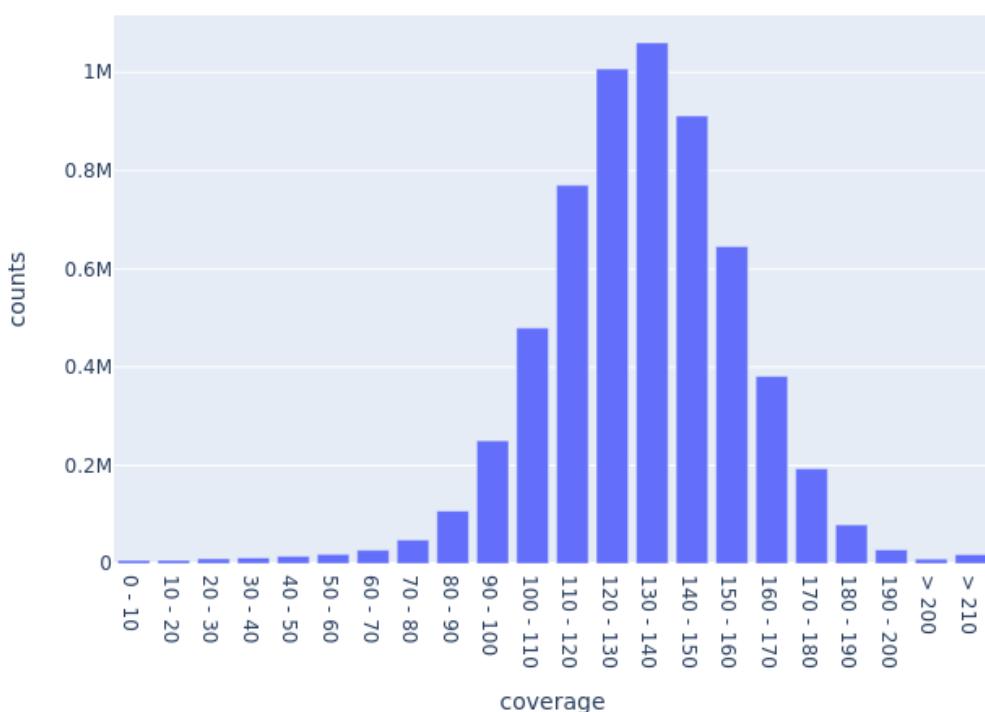
65 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 134.6651710910755

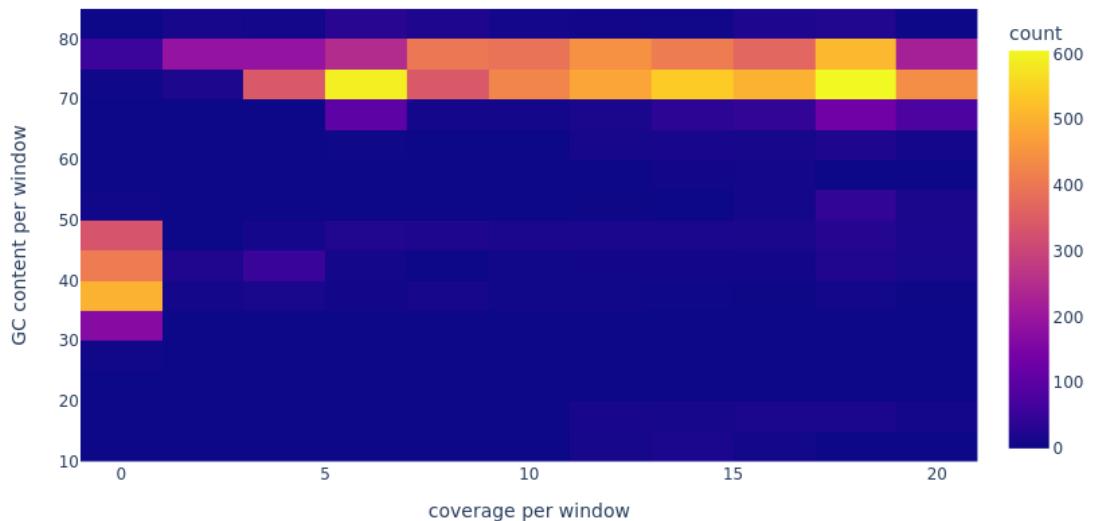
Comamonas testosterone in T33.3.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.3.1



# Report of *Microbacterium saperdae* in T33.3.1

## Mapping stats of Illumina reads

150530335 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

867 + 0 supplementary

0 + 0 duplicates

3005027 + 0 mapped (2.00% : N/A)

150529468 + 0 paired in sequencing

75264734 + 0 read1

75264734 + 0 read2

2917052 + 0 properly paired (1.94% : N/A)

2921522 + 0 with itself and mate mapped

82638 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

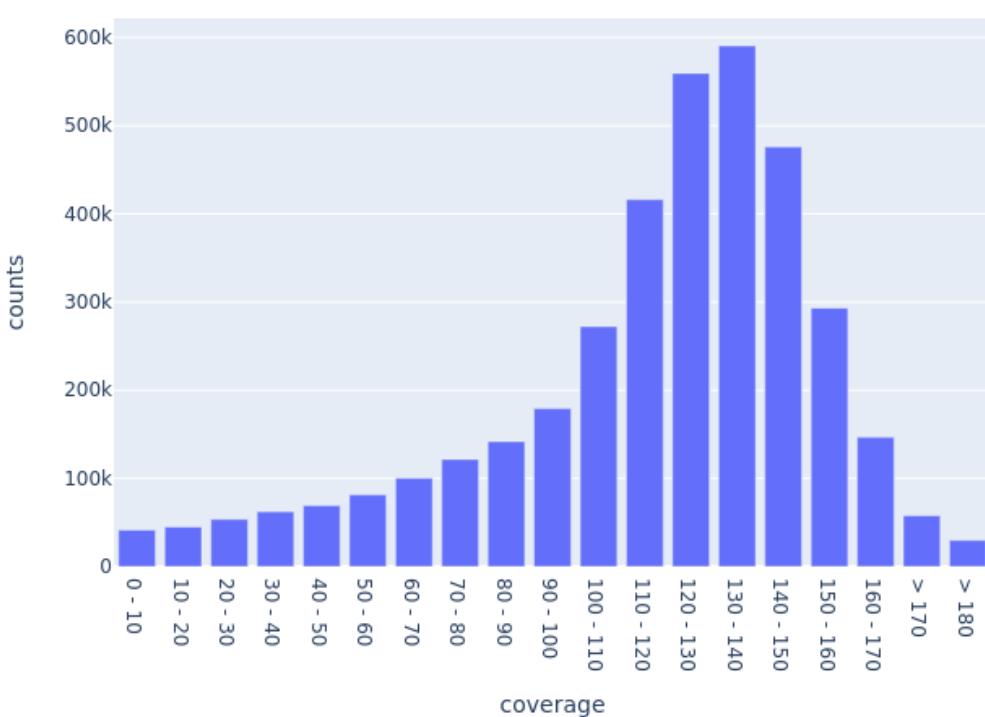
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 118.27661731504111

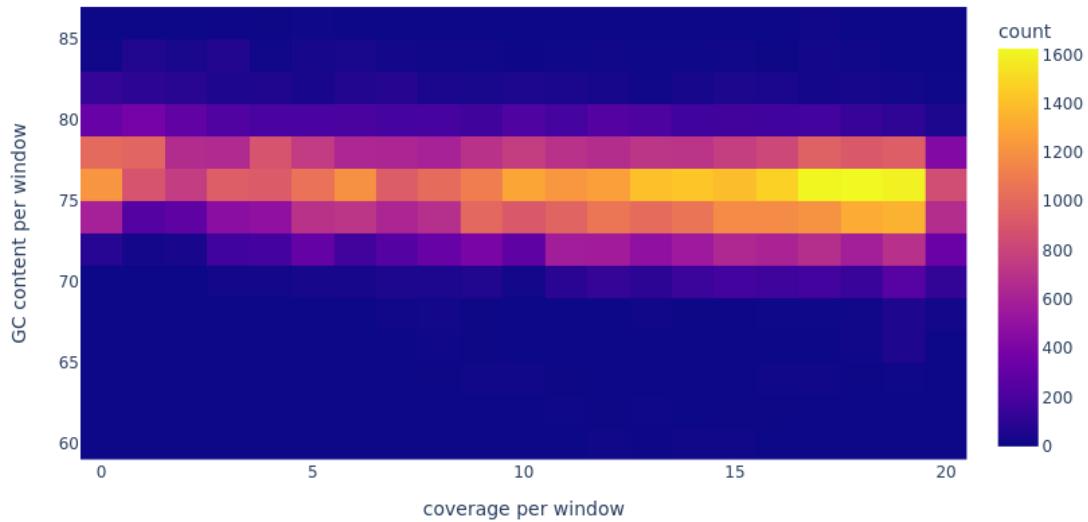
Microbacterium saperdae in T33.3.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T33.3.1



# Report of *Agrobacterium tumefaciens* in T33.3.2

## Mapping stats of Illumina reads

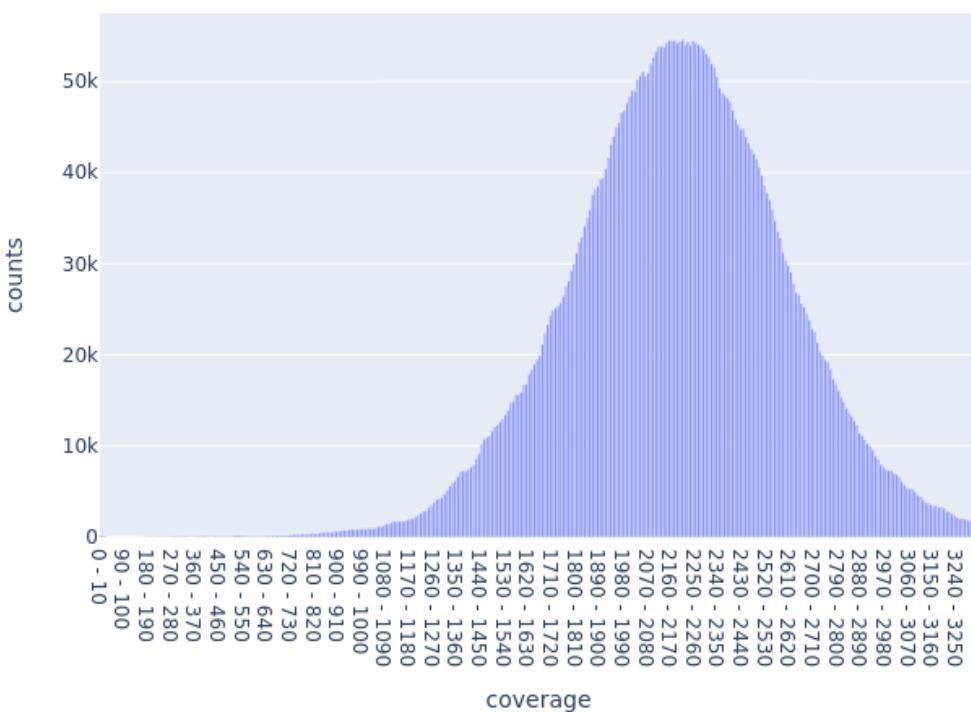
83503226 + 0 in total (QC-passed reads + QC-failed reads)  
0 + 0 secondary  
37844 + 0 supplementary  
0 + 0 duplicates  
78277807 + 0 mapped (93.74% : N/A)  
83465382 + 0 paired in sequencing  
41732691 + 0 read1  
41732691 + 0 read2  
77915032 + 0 properly paired (93.35% : N/A)  
78195916 + 0 with itself and mate mapped  
44047 + 0 singletons (0.05% : N/A)  
128572 + 0 with mate mapped to a different chr  
123390 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 2201.831296238025

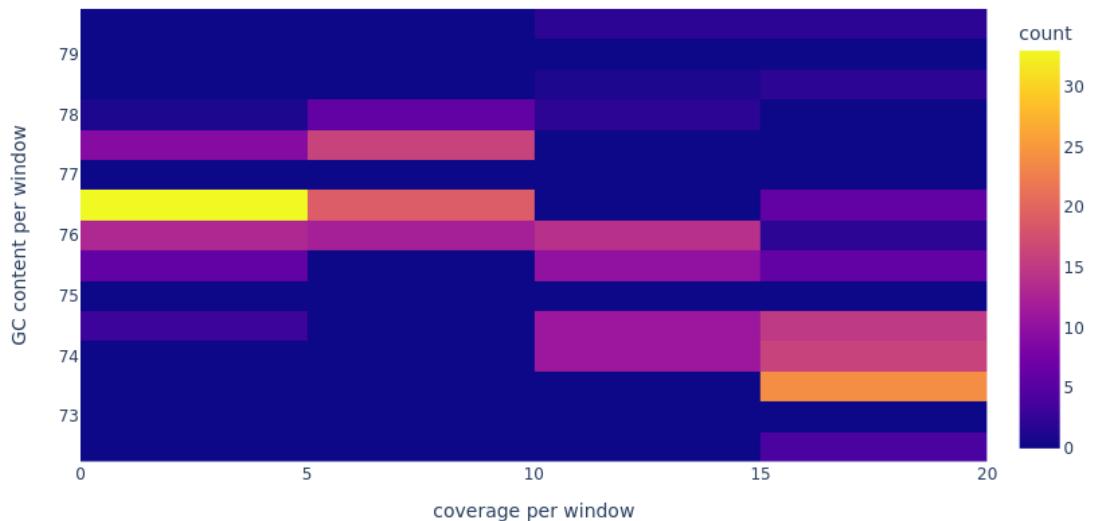
Agrobacterium tumefaciens in T33.3.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T33.3.2



# Report of Comamonas testosterone in T33.3.2

## Mapping stats of Illumina reads

83465624 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

242 + 0 supplementary

0 + 0 duplicates

2753169 + 0 mapped (3.30% : N/A)

83465382 + 0 paired in sequencing

41732691 + 0 read1

41732691 + 0 read2

2637410 + 0 properly paired (3.16% : N/A)

2639372 + 0 with itself and mate mapped

113555 + 0 singletons (0.14% : N/A)

18 + 0 with mate mapped to a different chr

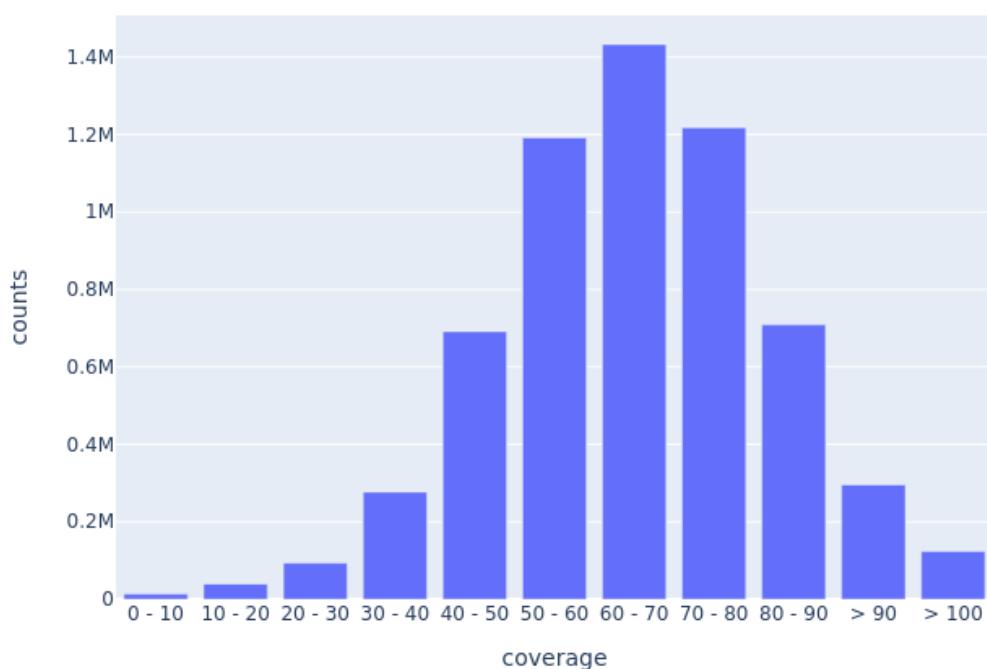
13 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 66.24400963054478

Comamonas testosterone in T33.3.2

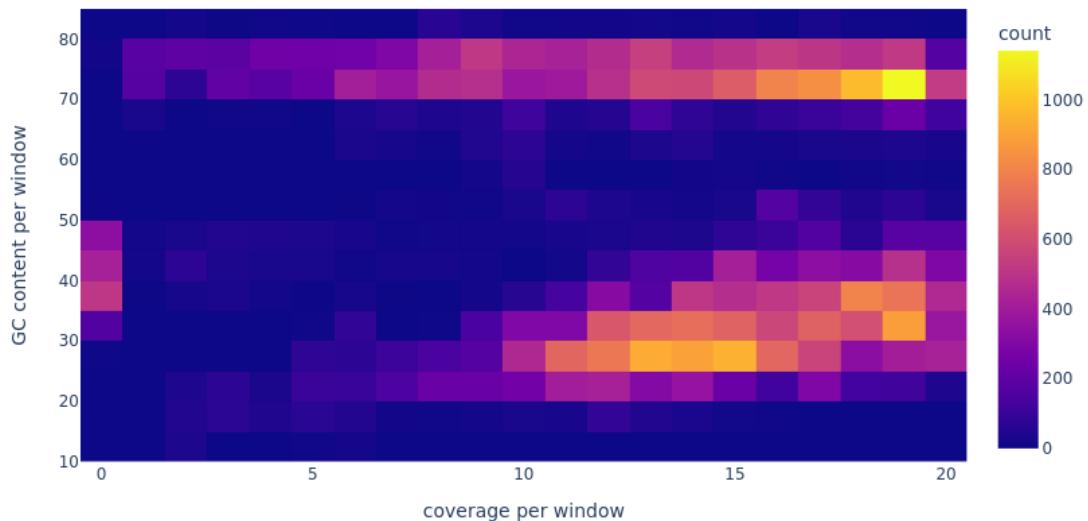


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.3.2



# Report of *Microbacterium saperdae* in T33.3.2

## Mapping stats of Illumina reads

83465690 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

308 + 0 supplementary

0 + 0 duplicates

2539931 + 0 mapped (3.04% : N/A)

83465382 + 0 paired in sequencing

41732691 + 0 read1

41732691 + 0 read2

2491878 + 0 properly paired (2.99% : N/A)

2494416 + 0 with itself and mate mapped

45207 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

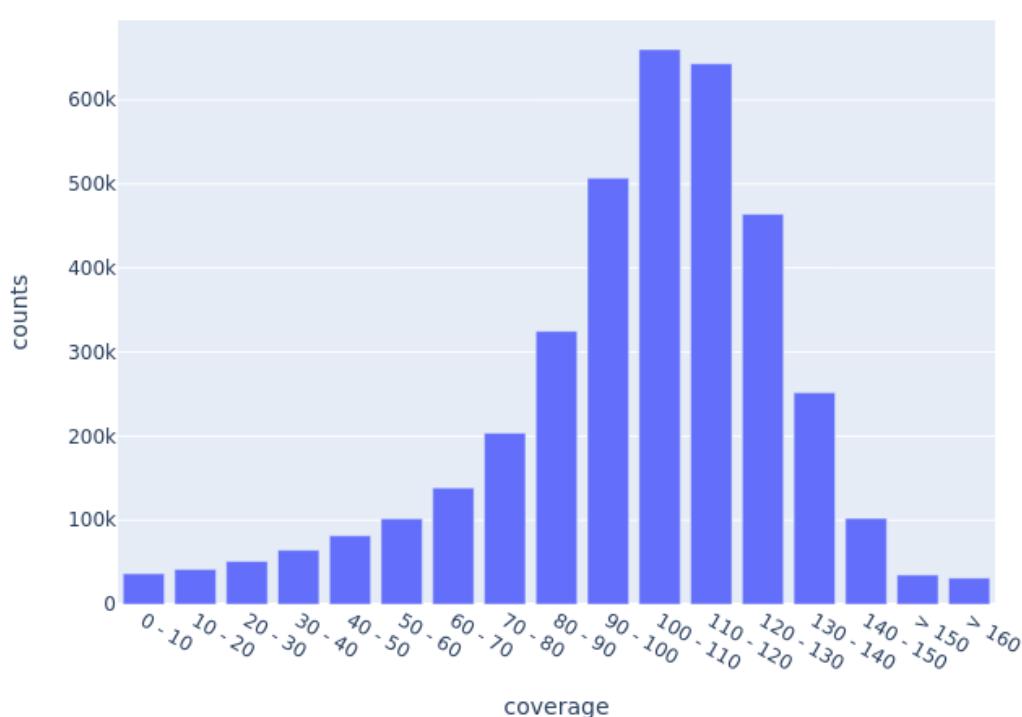
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 100.71999877989981

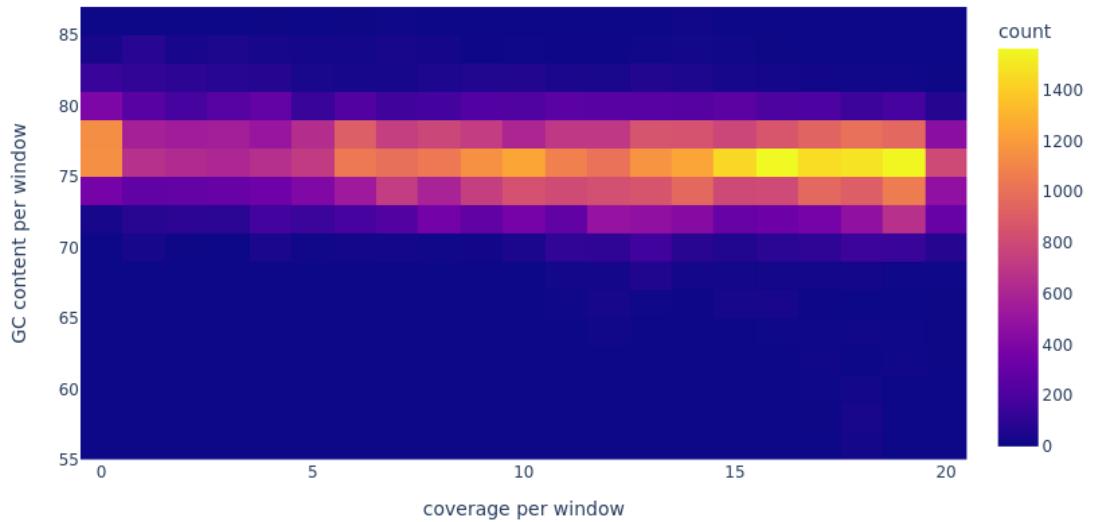
Microbacterium saperdae in T33.3.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T33.3.2



# Report of *Agrobacterium tumefaciens* in T33.3.3

## Mapping stats of Illumina reads

147846985 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

49359 + 0 supplementary

0 + 0 duplicates

129901865 + 0 mapped (87.86% : N/A)

147797626 + 0 paired in sequencing

73898813 + 0 read1

73898813 + 0 read2

129087638 + 0 properly paired (87.34% : N/A)

129714226 + 0 with itself and mate mapped

138280 + 0 singletons (0.09% : N/A)

295686 + 0 with mate mapped to a different chr

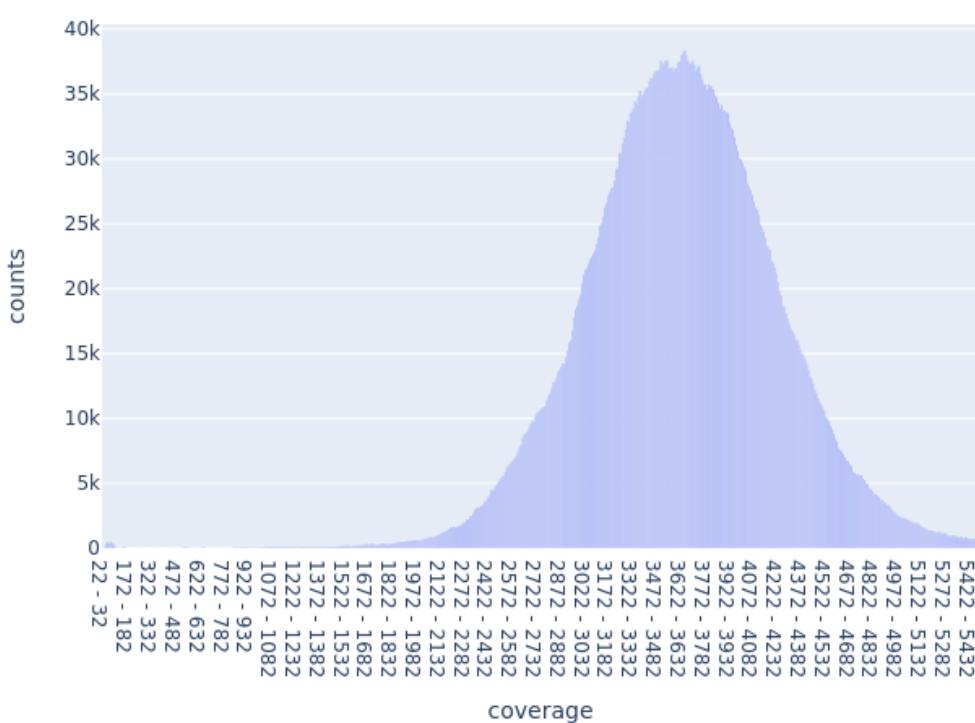
284462 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 3653.050507362093

Agrobacterium tumefaciens in T33.3.3

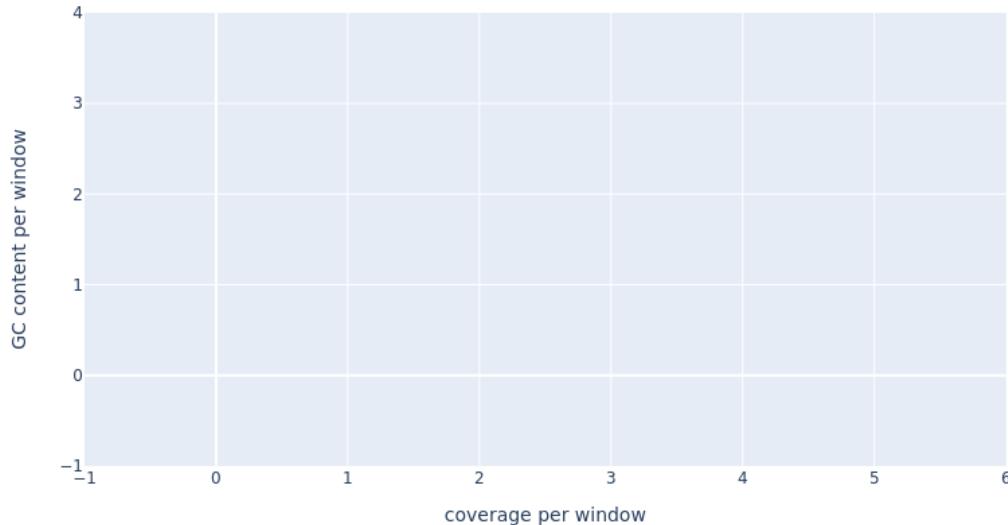


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T33.3.3



# Report of Comamonas testosterone in T33.3.3

## Mapping stats of Illumina reads

147798566 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

940 + 0 supplementary

0 + 0 duplicates

8529168 + 0 mapped (5.77% : N/A)

147797626 + 0 paired in sequencing

73898813 + 0 read1

73898813 + 0 read2

8299290 + 0 properly paired (5.62% : N/A)

8306792 + 0 with itself and mate mapped

221436 + 0 singletons (0.15% : N/A)

264 + 0 with mate mapped to a different chr

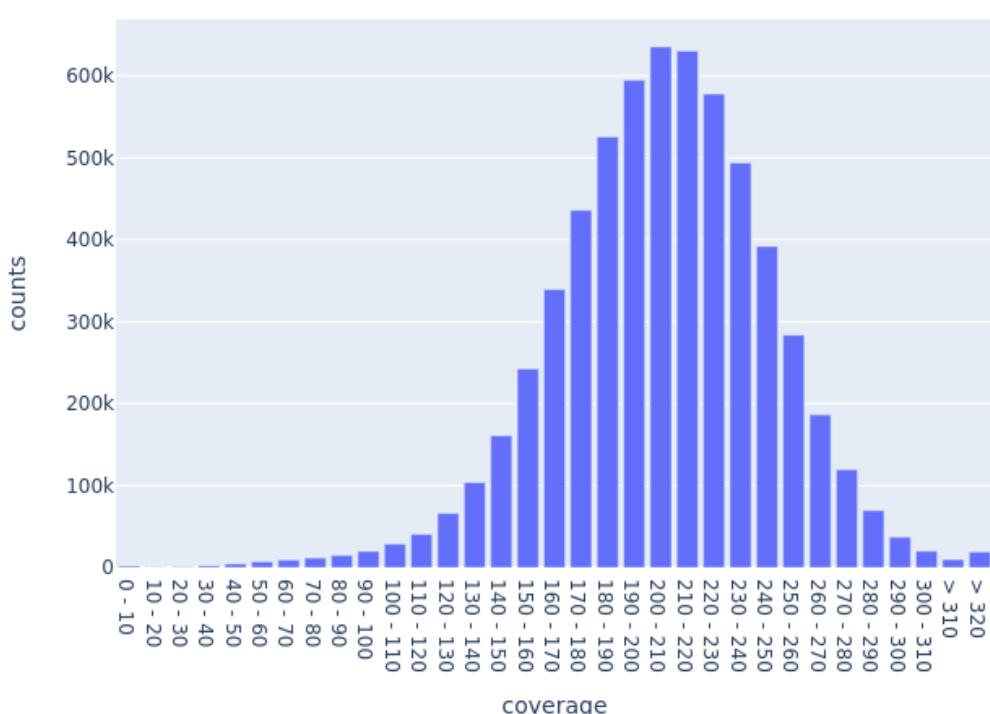
189 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 207.81357822007166

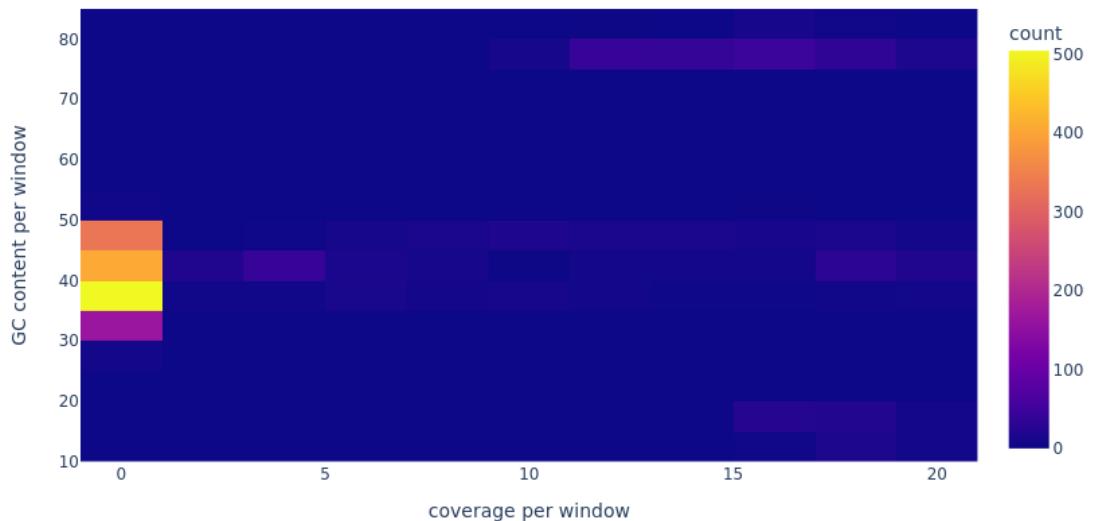
Comamonas testosterone in T33.3.3



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.3.3



# Report of *Microbacterium saperdae* in T33.3.3

## Mapping stats of Illumina reads

147799340 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1714 + 0 supplementary

0 + 0 duplicates

9527760 + 0 mapped (6.45% : N/A)

147797626 + 0 paired in sequencing

73898813 + 0 read1

73898813 + 0 read2

9405676 + 0 properly paired (6.36% : N/A)

9416402 + 0 with itself and mate mapped

109644 + 0 singletons (0.07% : N/A)

0 + 0 with mate mapped to a different chr

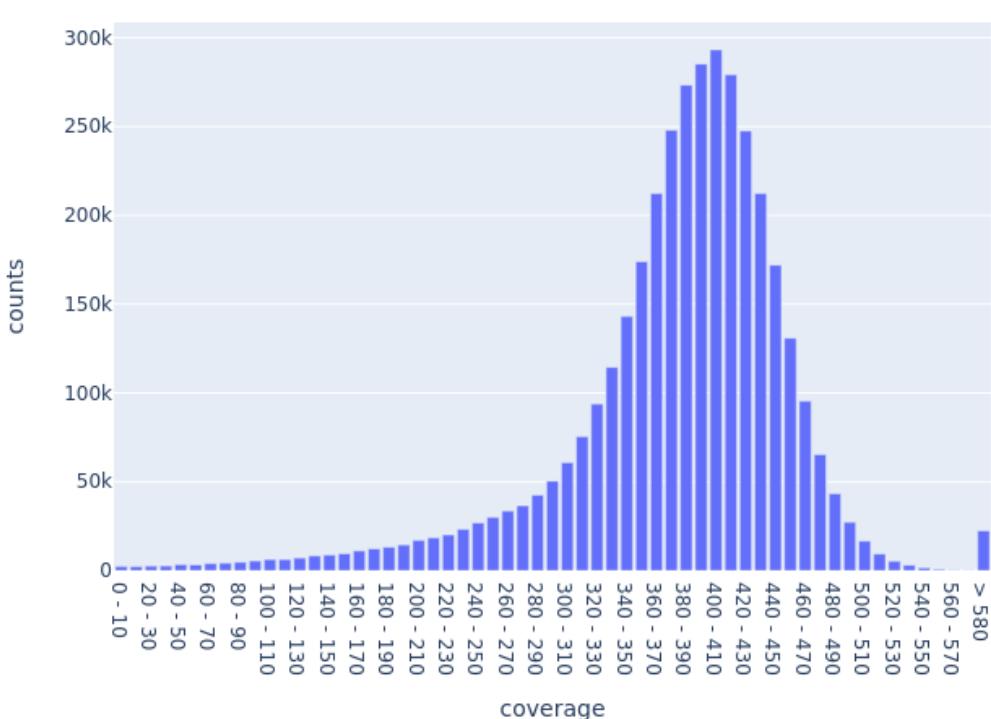
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 380.7904146146597

Microbacterium saperdae in T33.3.3

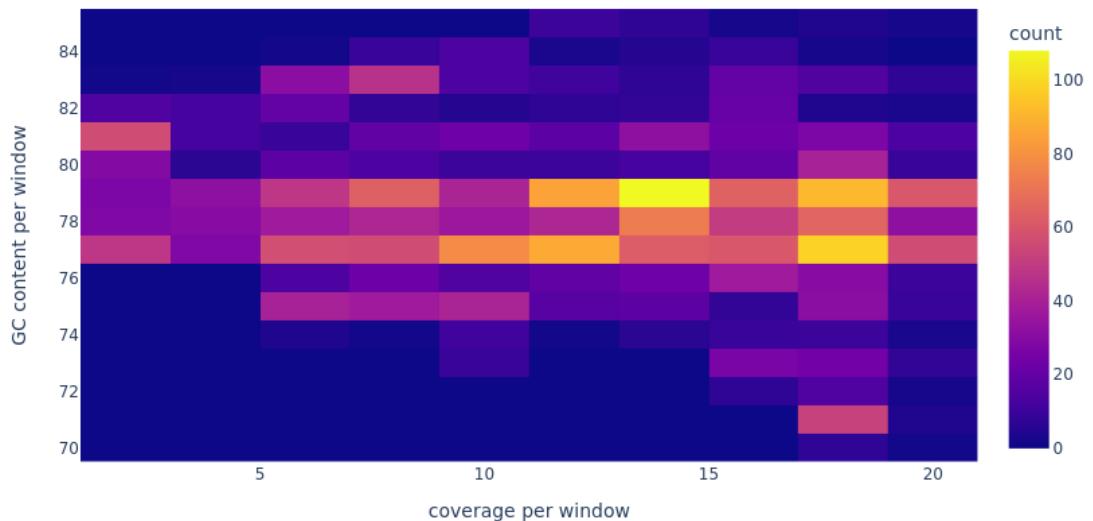


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T33.3.3



# Report of *Agrobacterium tumefaciens* in T33.3.4

## Mapping stats of Illumina reads

169362136 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

199254 + 0 supplementary

0 + 0 duplicates

158770805 + 0 mapped (93.75% : N/A)

169162882 + 0 paired in sequencing

84581441 + 0 read1

84581441 + 0 read2

157288214 + 0 properly paired (92.98% : N/A)

158440844 + 0 with itself and mate mapped

130707 + 0 singletons (0.08% : N/A)

553106 + 0 with mate mapped to a different chr

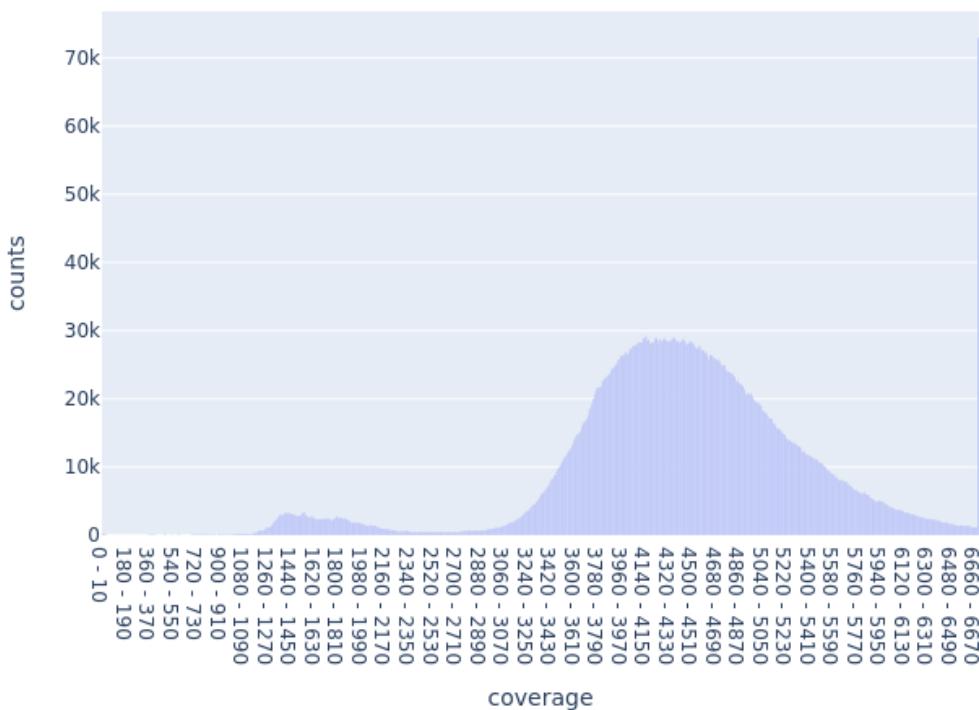
532351 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 4454.345789052615

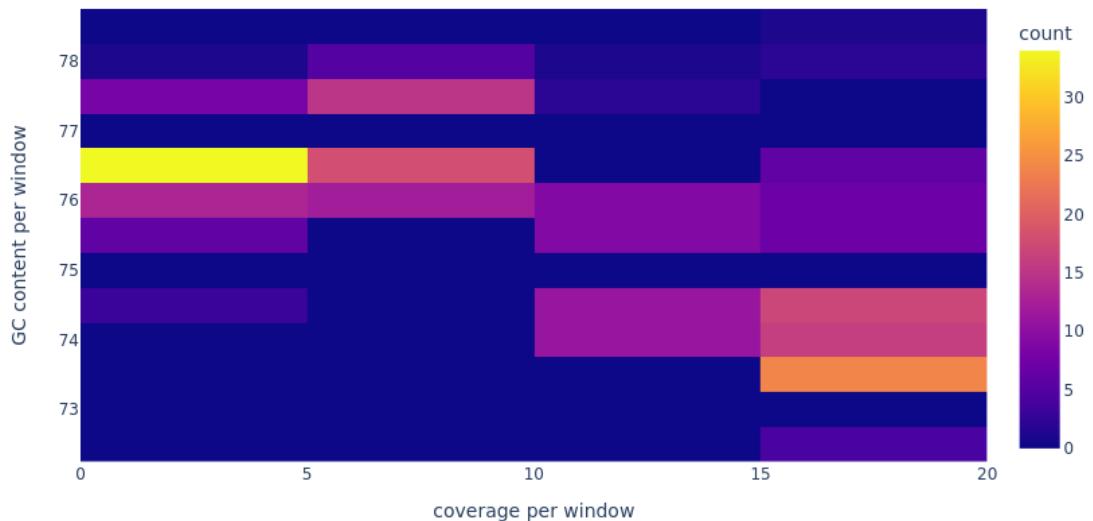
Agrobacterium tumefaciens in T33.3.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T33.3.4



# Report of Comamonas testosterone in T33.3.4

## Mapping stats of Illumina reads

169163742 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

860 + 0 supplementary

0 + 0 duplicates

5817057 + 0 mapped (3.44% : N/A)

169162882 + 0 paired in sequencing

84581441 + 0 read1

84581441 + 0 read2

5562410 + 0 properly paired (3.29% : N/A)

5567382 + 0 with itself and mate mapped

248815 + 0 singletons (0.15% : N/A)

78 + 0 with mate mapped to a different chr

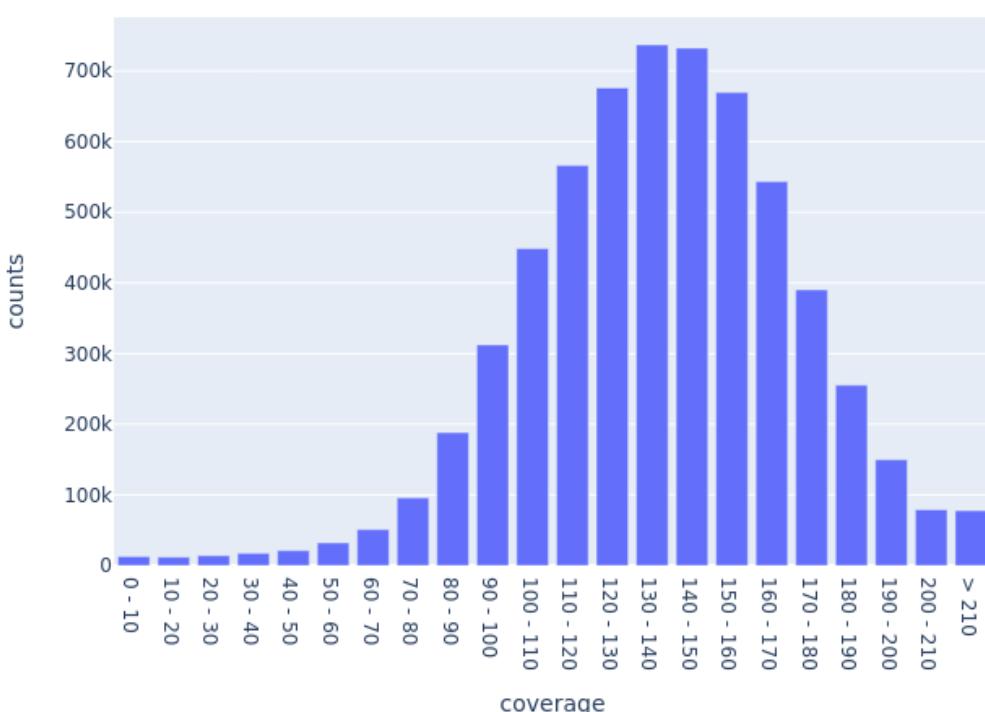
54 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 140.0849403005165

Comamonas testosterone in T33.3.4

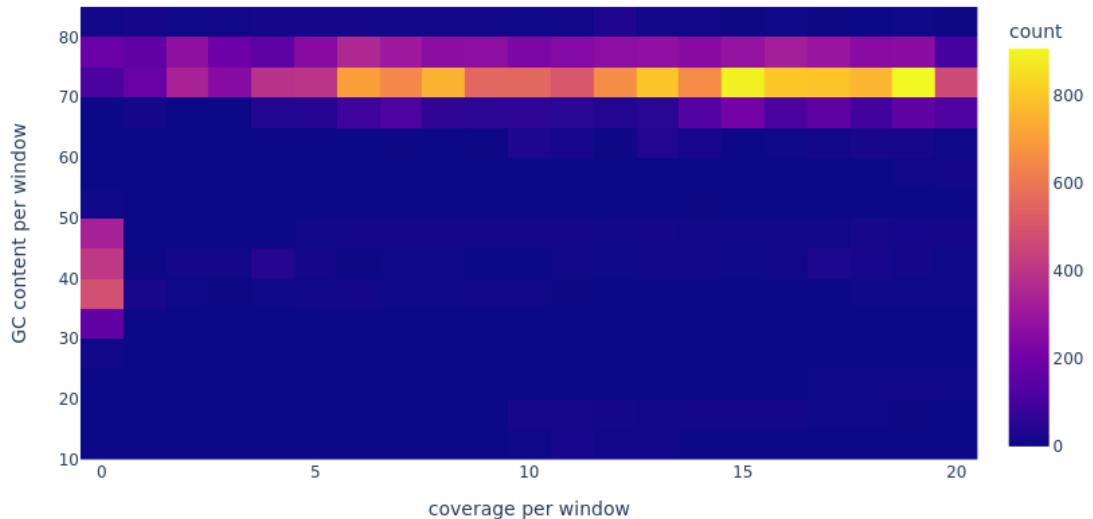


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.3.4



# Report of *Microbacterium saperdae* in T33.3.4

## Mapping stats of Illumina reads

169163485 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

603 + 0 supplementary

0 + 0 duplicates

4729399 + 0 mapped (2.80% : N/A)

169162882 + 0 paired in sequencing

84581441 + 0 read1

84581441 + 0 read2

4619730 + 0 properly paired (2.73% : N/A)

4624602 + 0 with itself and mate mapped

104194 + 0 singletons (0.06% : N/A)

0 + 0 with mate mapped to a different chr

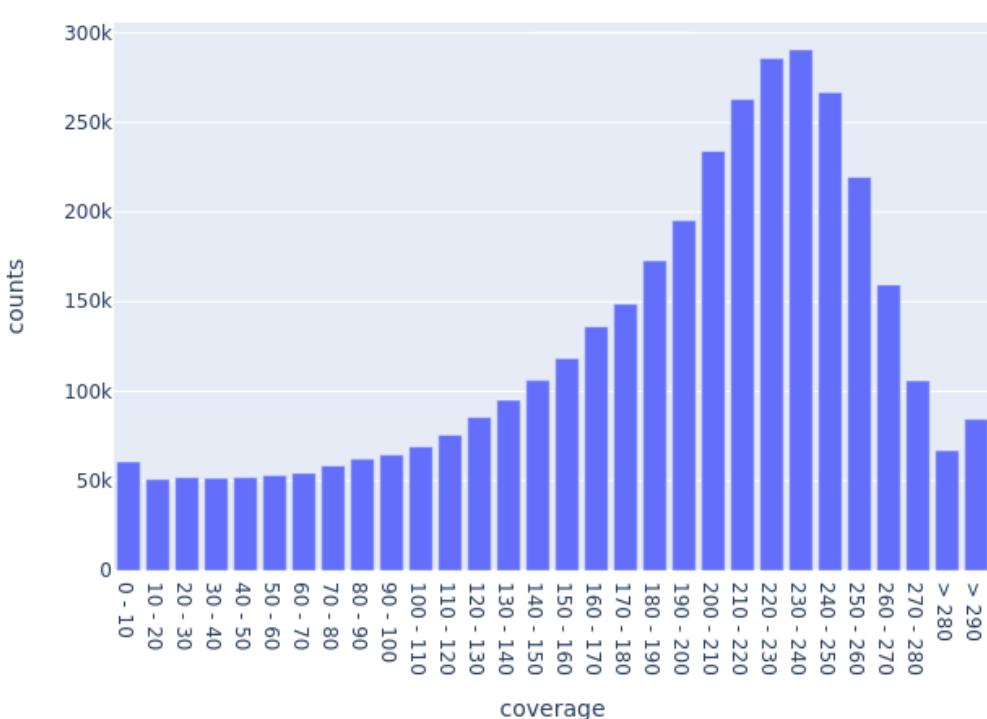
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 187.34635406772304

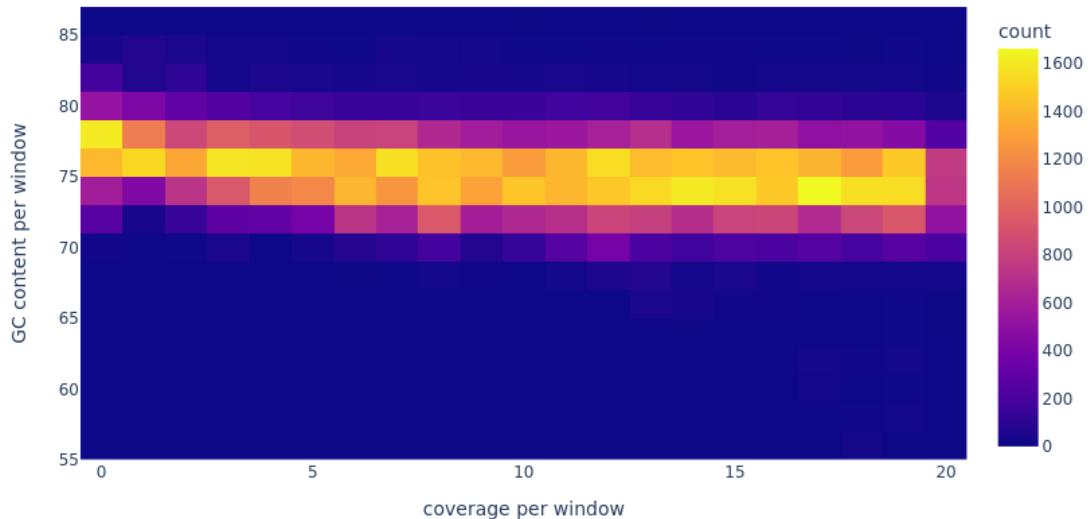
Microbacterium saperdae in T33.3.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T33.3.4



# Report of *Agrobacterium tumefaciens* in T33.3.5

## Mapping stats of Illumina reads

161953047 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

72369 + 0 supplementary

0 + 0 duplicates

145980991 + 0 mapped (90.14% : N/A)

161880678 + 0 paired in sequencing

80940339 + 0 read1

80940339 + 0 read2

145274304 + 0 properly paired (89.74% : N/A)

145723416 + 0 with itself and mate mapped

185206 + 0 singletons (0.11% : N/A)

197972 + 0 with mate mapped to a different chr

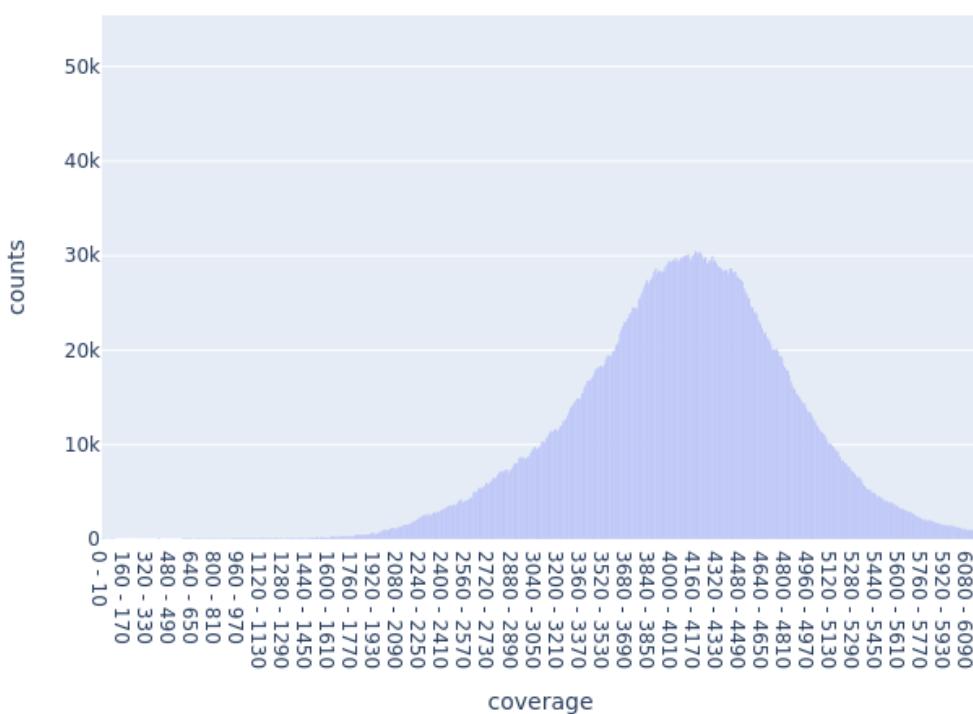
190318 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

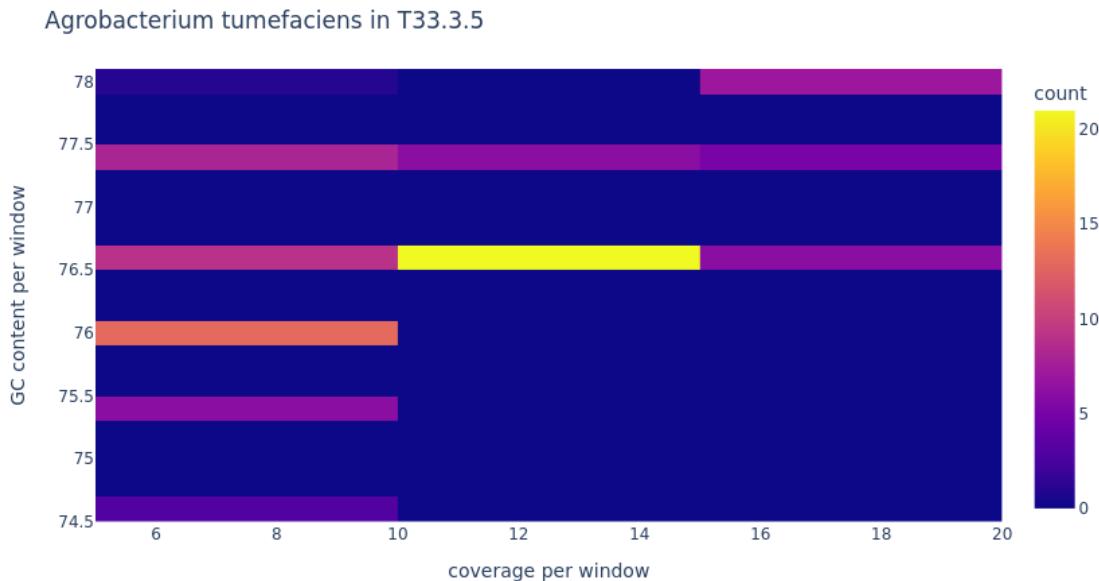
Average coverage: 4102.524761771749

Agrobacterium tumefaciens in T33.3.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.



# Report of Comamonas testosterone in T33.3.5

## Mapping stats of Illumina reads

161881303 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

625 + 0 supplementary

0 + 0 duplicates

6149497 + 0 mapped (3.80% : N/A)

161880678 + 0 paired in sequencing

80940339 + 0 read1

80940339 + 0 read2

5917340 + 0 properly paired (3.66% : N/A)

5921278 + 0 with itself and mate mapped

227594 + 0 singletons (0.14% : N/A)

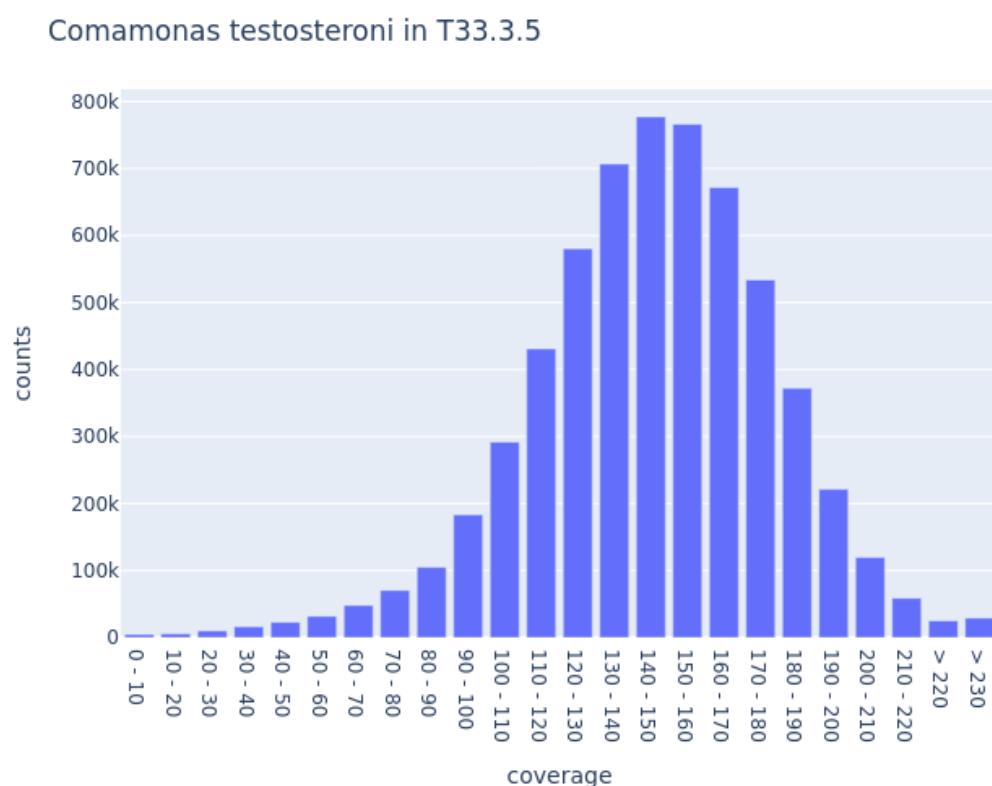
42 + 0 with mate mapped to a different chr

32 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

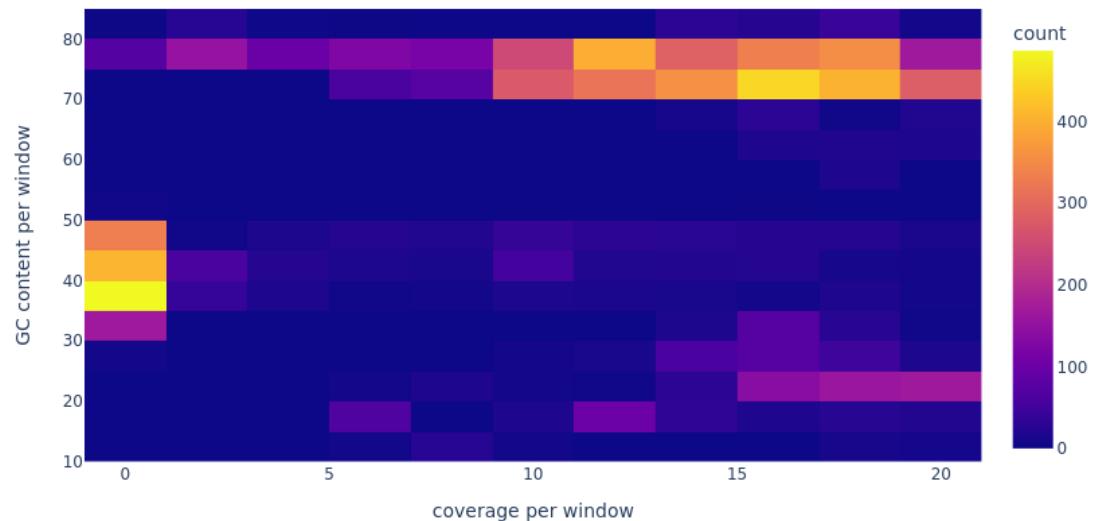
Average coverage: 148.36829865141803



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.3.5



# Report of *Microbacterium saperdae* in T33.3.5

## Mapping stats of Illumina reads

161880773 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

95 + 0 supplementary

0 + 0 duplicates

1292500 + 0 mapped (0.80% : N/A)

161880678 + 0 paired in sequencing

80940339 + 0 read1

80940339 + 0 read2

1208870 + 0 properly paired (0.75% : N/A)

1211212 + 0 with itself and mate mapped

81193 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

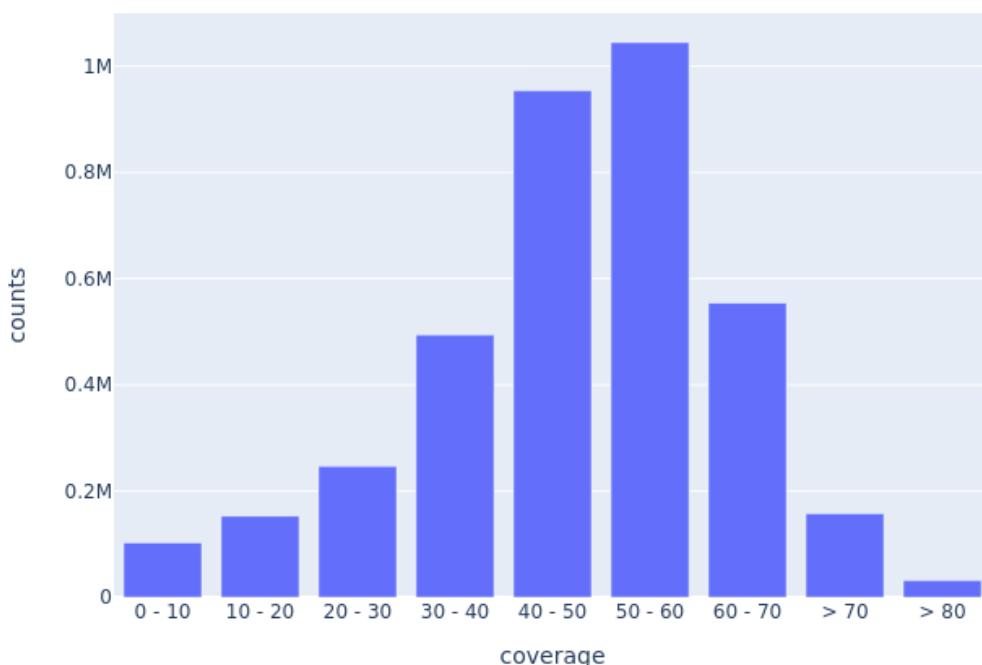
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 49.04336038067126

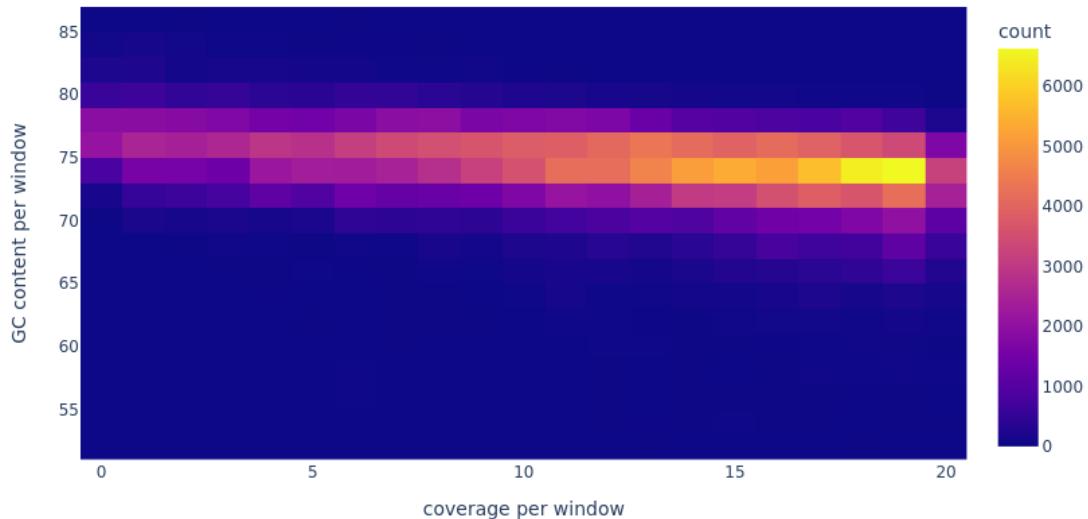
Microbacterium saperdae in T33.3.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T33.3.5



# Report of *Agrobacterium tumefaciens* in T33.4.1

## Mapping stats of Illumina reads

168326014 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

50996 + 0 supplementary

0 + 0 duplicates

151734065 + 0 mapped (90.14% : N/A)

168275018 + 0 paired in sequencing

84137509 + 0 read1

84137509 + 0 read2

150921868 + 0 properly paired (89.69% : N/A)

151500908 + 0 with itself and mate mapped

182161 + 0 singletons (0.11% : N/A)

270772 + 0 with mate mapped to a different chr

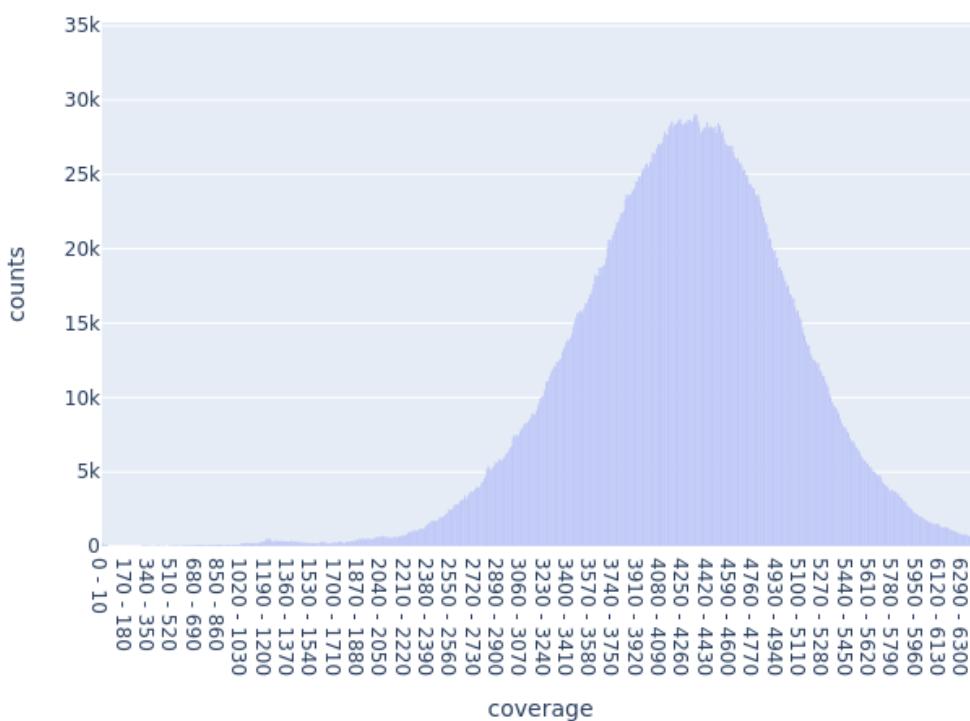
258659 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 4264.944674506927

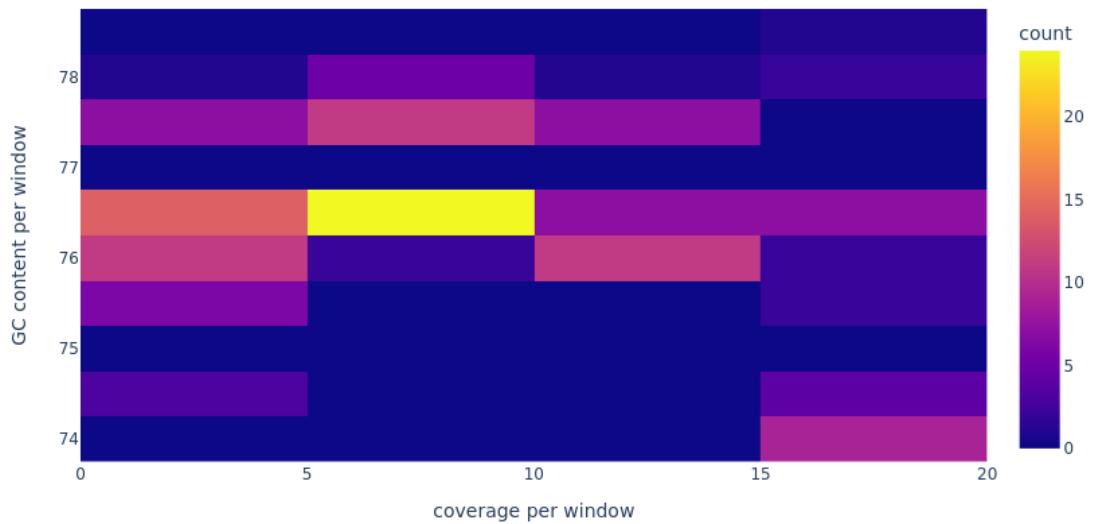
Agrobacterium tumefaciens in T33.4.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T33.4.1



# Report of Comamonas testosterone in T33.4.1

## Mapping stats of Illumina reads

168276013 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

995 + 0 supplementary

0 + 0 duplicates

9874459 + 0 mapped (5.87% : N/A)

168275018 + 0 paired in sequencing

84137509 + 0 read1

84137509 + 0 read2

9617148 + 0 properly paired (5.72% : N/A)

9624088 + 0 with itself and mate mapped

249376 + 0 singletons (0.15% : N/A)

126 + 0 with mate mapped to a different chr

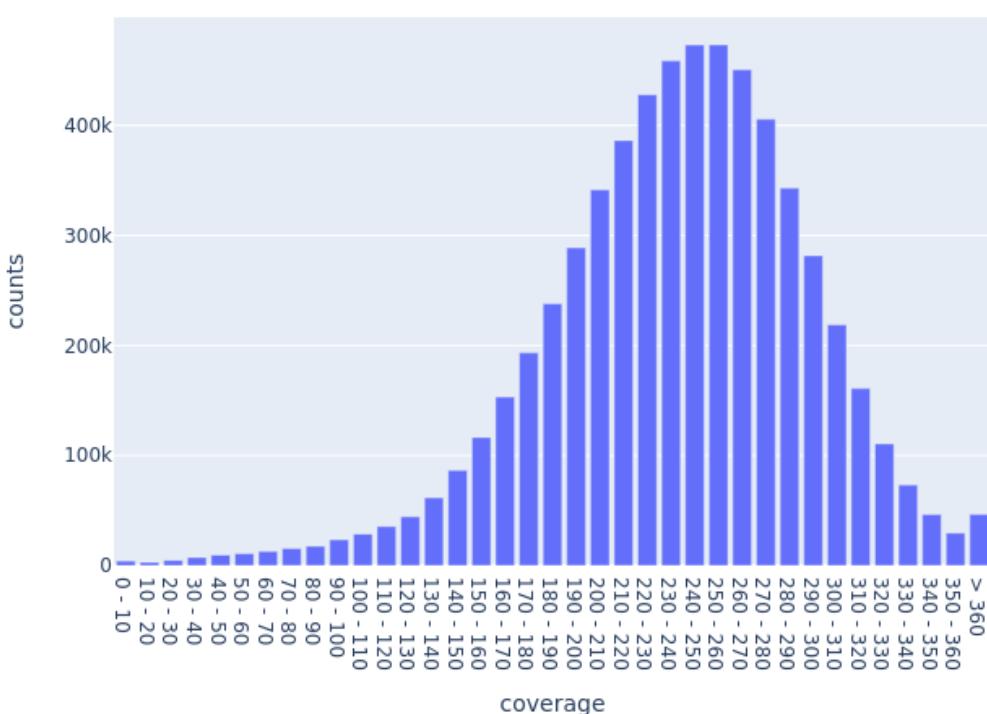
100 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 240.54847740718833

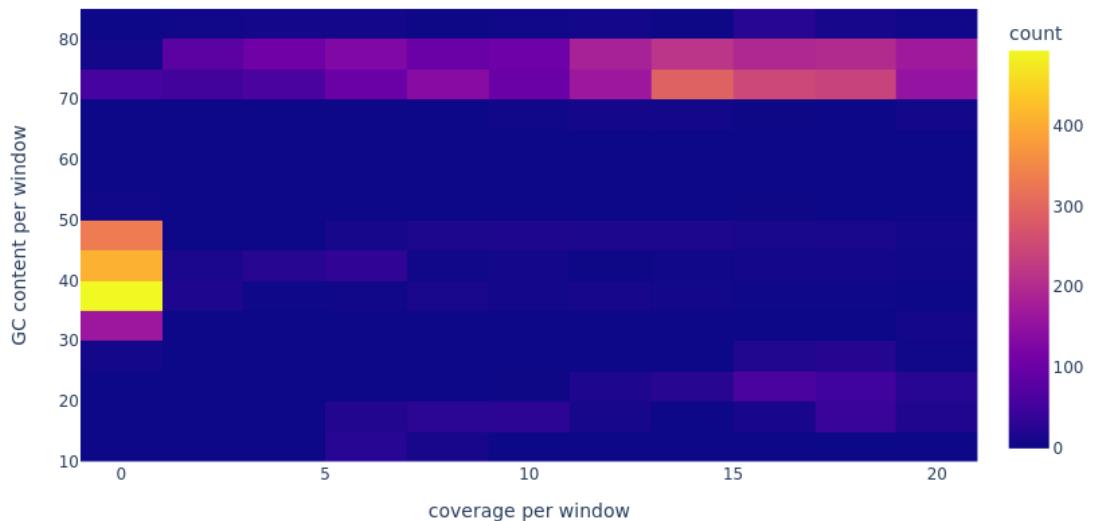
Comamonas testosterone in T33.4.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.4.1



# Report of *Microbacterium saperdae* in T33.4.1

## Mapping stats of Illumina reads

168275028 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

10 + 0 supplementary

0 + 0 duplicates

131190 + 0 mapped (0.08% : N/A)

168275018 + 0 paired in sequencing

84137509 + 0 read1

84137509 + 0 read2

46070 + 0 properly paired (0.03% : N/A)

47970 + 0 with itself and mate mapped

83210 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

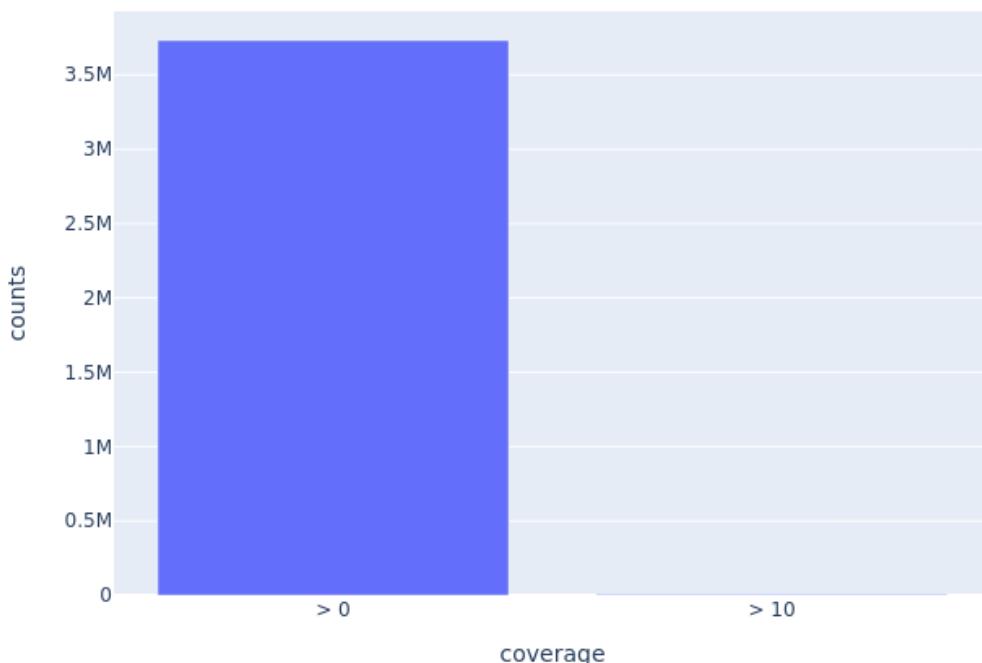
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 2.2236577426327084

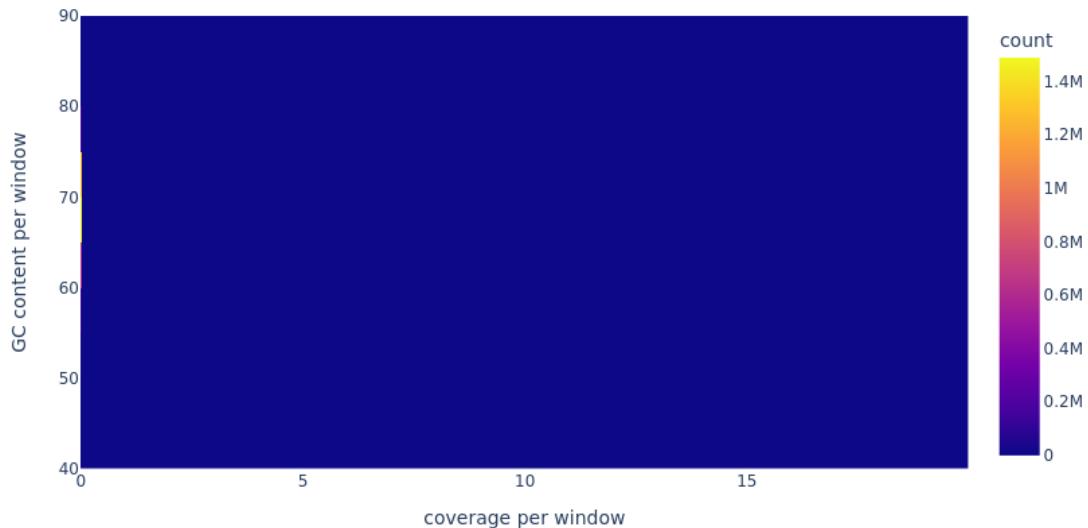
Microbacterium saperdae in T33.4.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T33.4.1



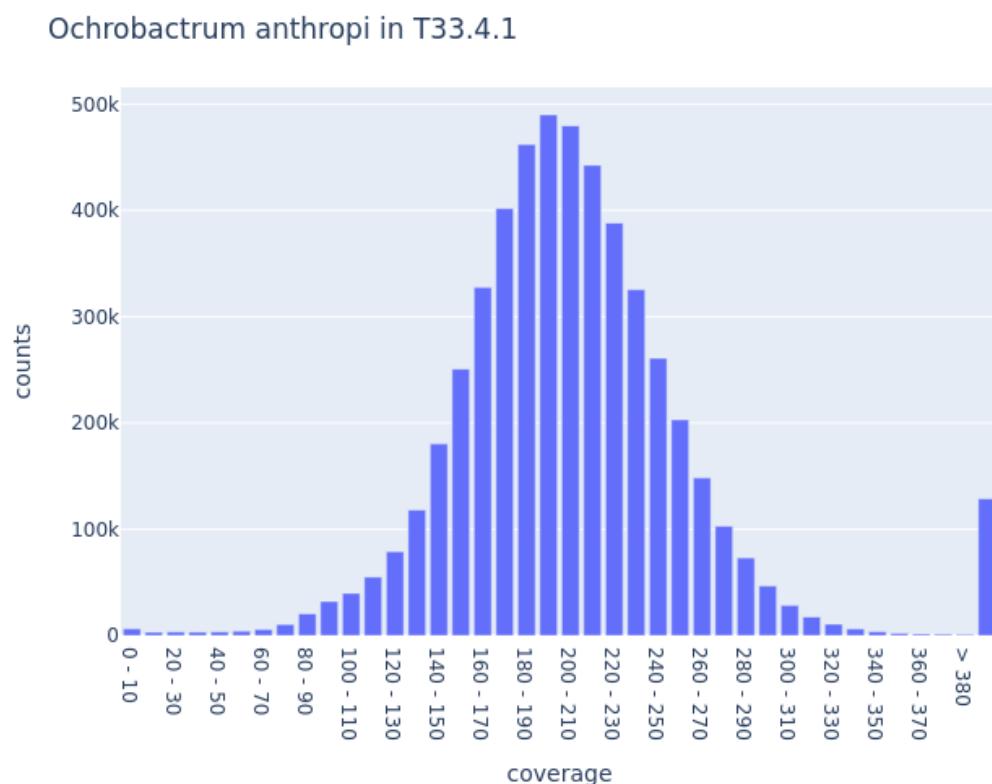
# Report of *Ochrobactrum anthropi* in T33.4.1

## Mapping stats of Illumina reads

168278699 + 0 in total (QC-passed reads + QC-failed reads)  
0 + 0 secondary  
3681 + 0 supplementary  
0 + 0 duplicates  
9563954 + 0 mapped (5.68% : N/A)  
168275018 + 0 paired in sequencing  
84137509 + 0 read1  
84137509 + 0 read2  
8120600 + 0 properly paired (4.83% : N/A)  
8156836 + 0 with itself and mate mapped  
1403437 + 0 singletons (0.83% : N/A)  
21088 + 0 with mate mapped to a different chr  
14392 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.  
Average coverage: 254.90299533710478

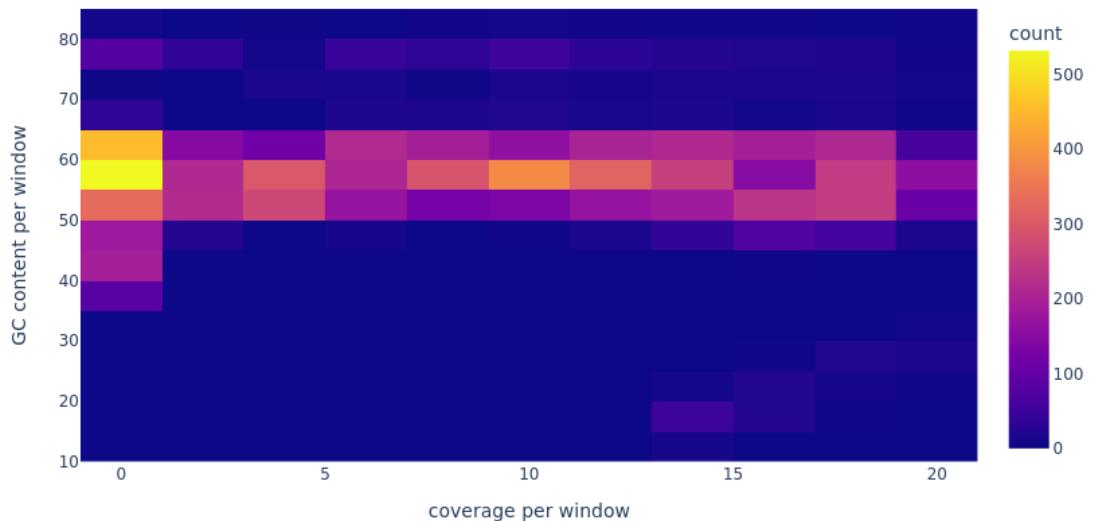


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T33.4.1



# Report of *Agrobacterium tumefaciens* in T33.4.2

## Mapping stats of Illumina reads

162967524 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

45606 + 0 supplementary

0 + 0 duplicates

150648547 + 0 mapped (92.44% : N/A)

162921918 + 0 paired in sequencing

81460959 + 0 read1

81460959 + 0 read2

149858390 + 0 properly paired (91.98% : N/A)

150461372 + 0 with itself and mate mapped

141569 + 0 singletons (0.09% : N/A)

291896 + 0 with mate mapped to a different chr

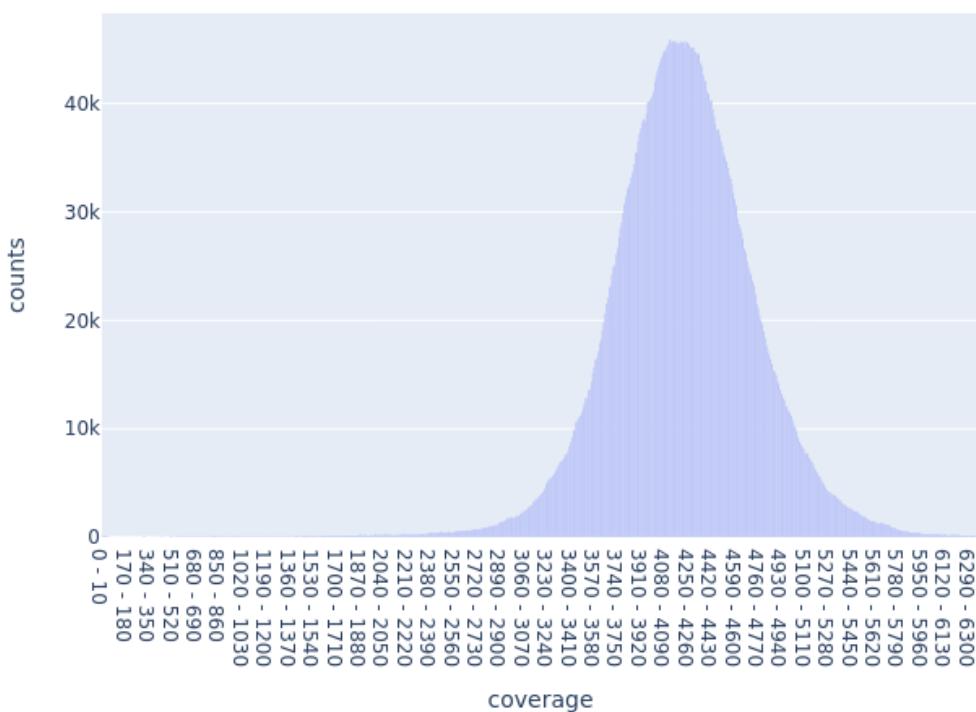
280562 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

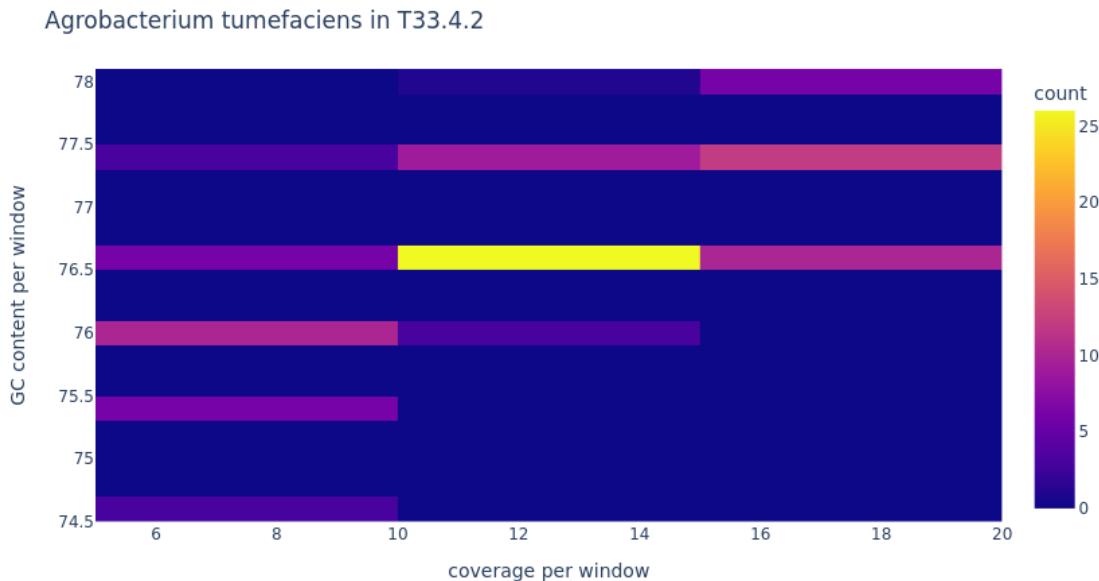
Average coverage: 4234.465802955457

Agrobacterium tumefaciens in T33.4.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.



# Report of Comamonas testosterone in T33.4.2

## Mapping stats of Illumina reads

162922710 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

792 + 0 supplementary

0 + 0 duplicates

6853779 + 0 mapped (4.21% : N/A)

162921918 + 0 paired in sequencing

81460959 + 0 read1

81460959 + 0 read2

6604584 + 0 properly paired (4.05% : N/A)

6608938 + 0 with itself and mate mapped

244049 + 0 singletons (0.15% : N/A)

104 + 0 with mate mapped to a different chr

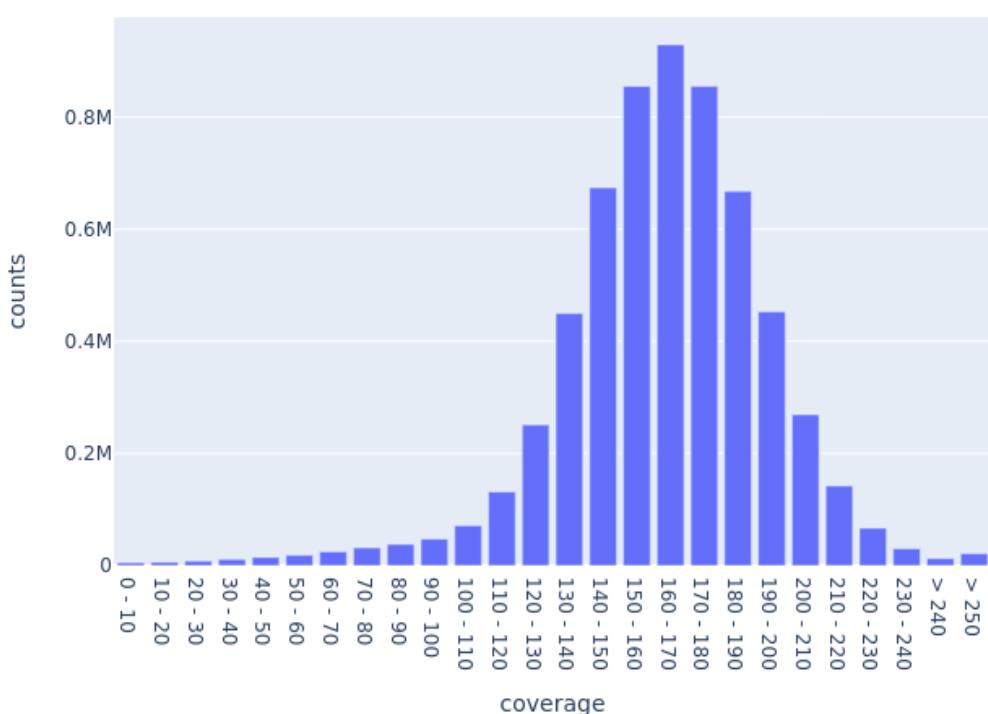
87 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 165.81848470948037

Comamonas testosterone in T33.4.2

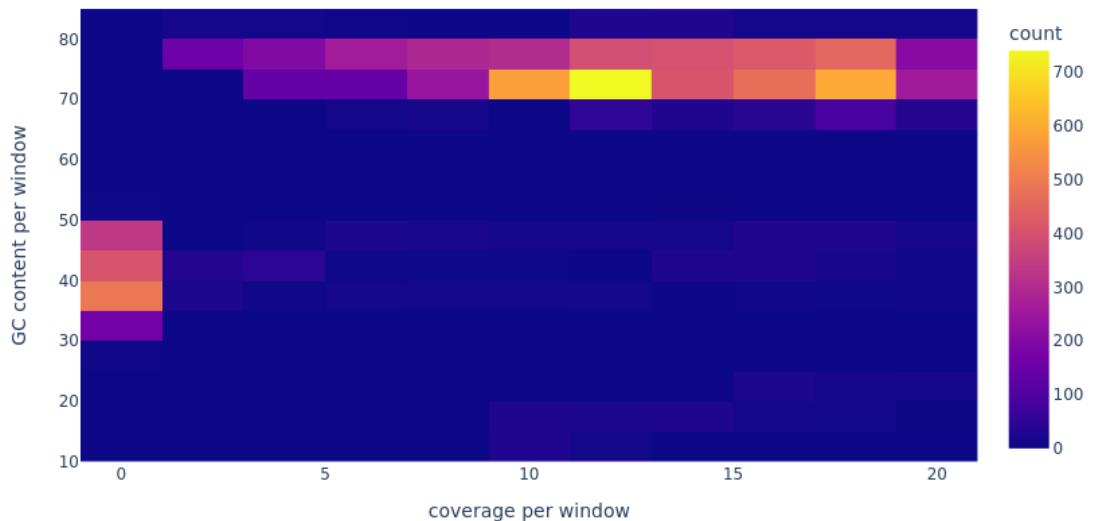


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.4.2



# Report of *Microbacterium saperdae* in T33.4.2

## Mapping stats of Illumina reads

162922192 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

274 + 0 supplementary

0 + 0 duplicates

2497334 + 0 mapped (1.53% : N/A)

162921918 + 0 paired in sequencing

81460959 + 0 read1

81460959 + 0 read2

2405208 + 0 properly paired (1.48% : N/A)

2408094 + 0 with itself and mate mapped

88966 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

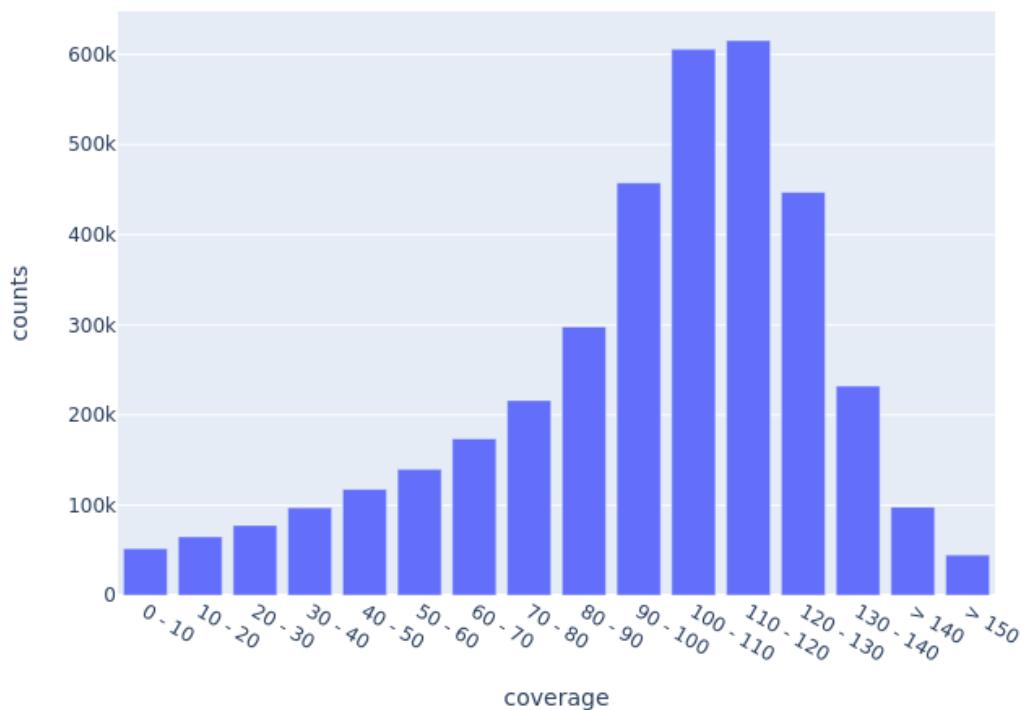
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 97.57000485364416

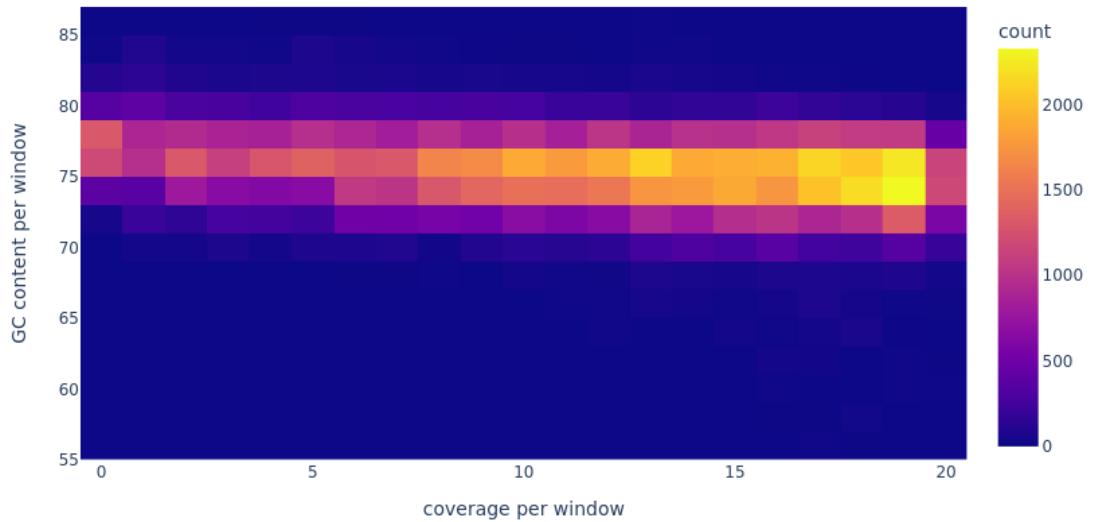
Microbacterium saperdae in T33.4.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T33.4.2



# Report of *Ochrobactrum anthropi* in T33.4.2

## Mapping stats of Illumina reads

162925382 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

3464 + 0 supplementary

0 + 0 duplicates

5752283 + 0 mapped (3.53% : N/A)

162921918 + 0 paired in sequencing

81460959 + 0 read1

81460959 + 0 read2

4345048 + 0 properly paired (2.67% : N/A)

4375468 + 0 with itself and mate mapped

1373351 + 0 singletons (0.84% : N/A)

18734 + 0 with mate mapped to a different chr

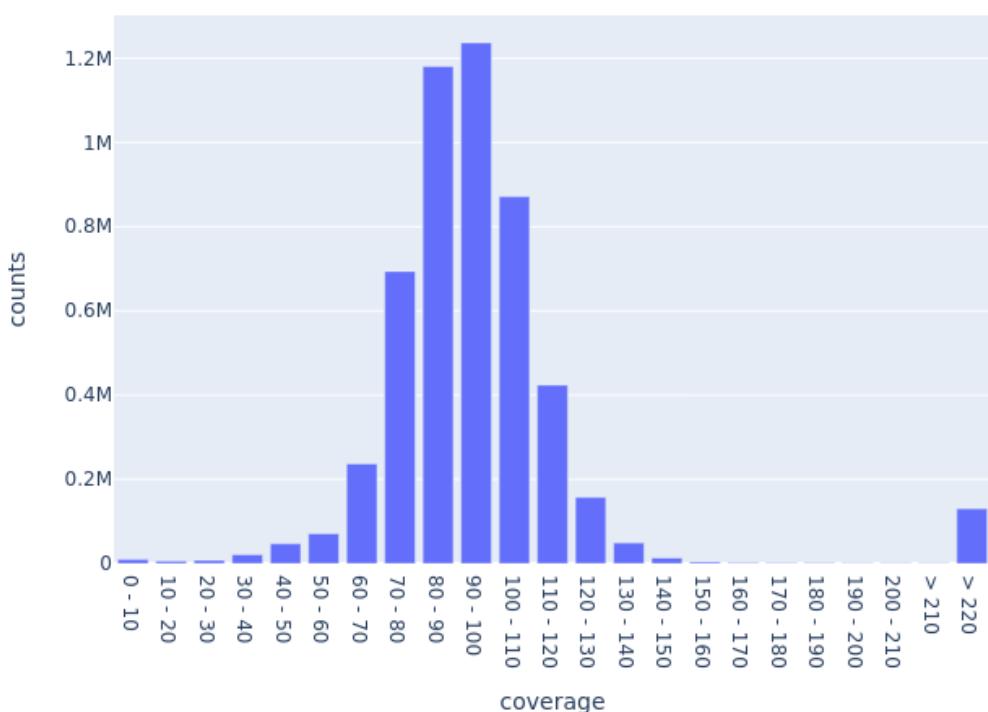
12779 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 144.44154628994679

Ochrobactrum anthropi in T33.4.2

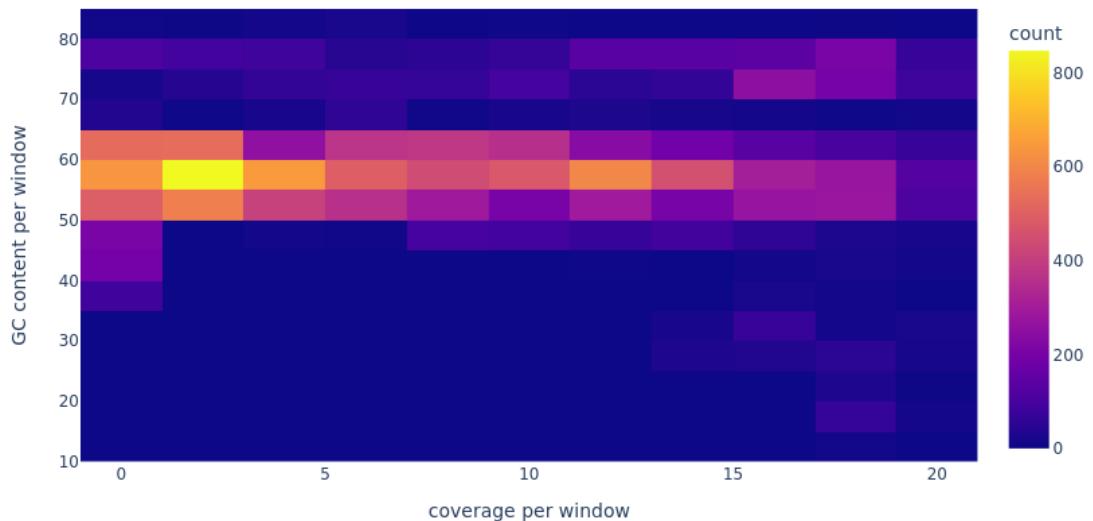


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T33.4.2



# Report of *Agrobacterium tumefaciens* in T33.4.3.rep

## Mapping stats of Illumina reads

172204634 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

67856 + 0 supplementary

0 + 0 duplicates

163472159 + 0 mapped (94.93% : N/A)

172136778 + 0 paired in sequencing

86068389 + 0 read1

86068389 + 0 read2

162634686 + 0 properly paired (94.48% : N/A)

163292602 + 0 with itself and mate mapped

111701 + 0 singletons (0.06% : N/A)

313610 + 0 with mate mapped to a different chr

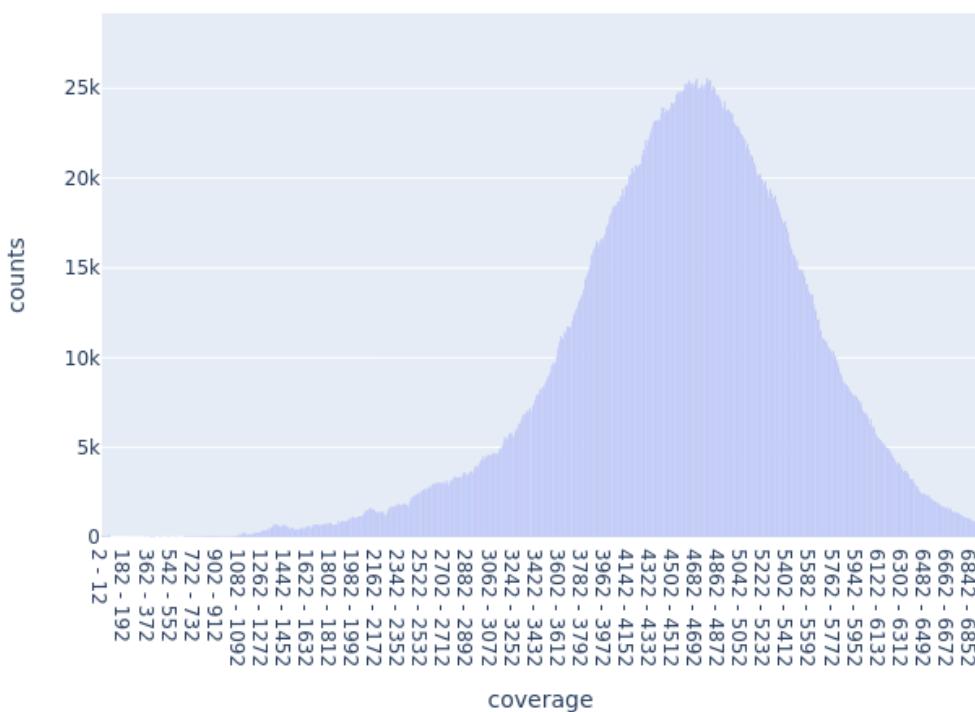
299113 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

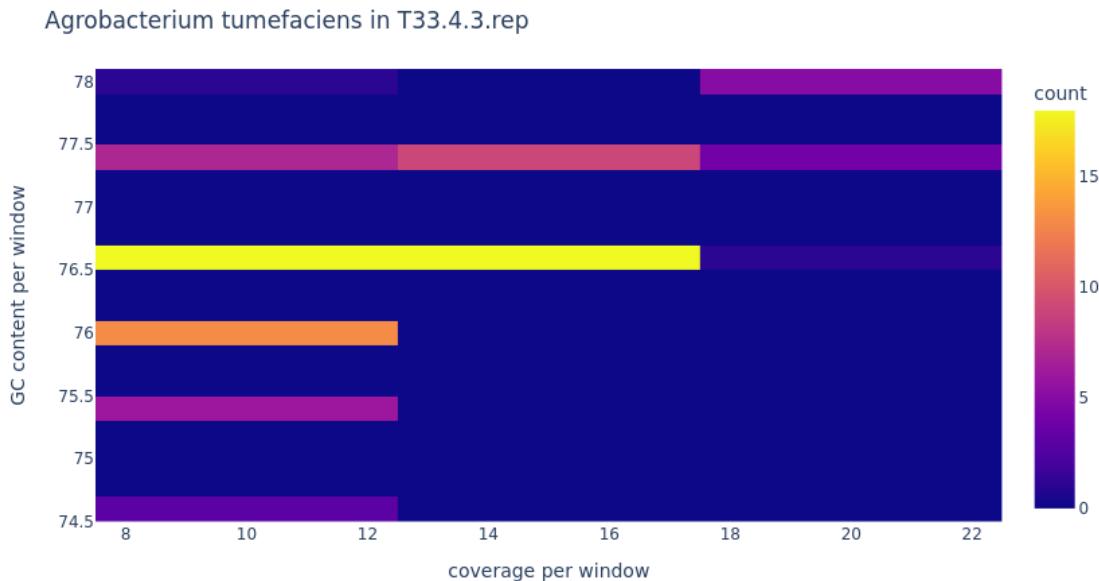
Average coverage: 4596.847622541225

Agrobacterium tumefaciens in T33.4.3.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.



# Report of Comamonas testosteronei in T33.4.3.rep

## Mapping stats of Illumina reads

172137509 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

731 + 0 supplementary

0 + 0 duplicates

6579735 + 0 mapped (3.82% : N/A)

172136778 + 0 paired in sequencing

86068389 + 0 read1

86068389 + 0 read2

6337872 + 0 properly paired (3.68% : N/A)

6342254 + 0 with itself and mate mapped

236750 + 0 singletons (0.14% : N/A)

58 + 0 with mate mapped to a different chr

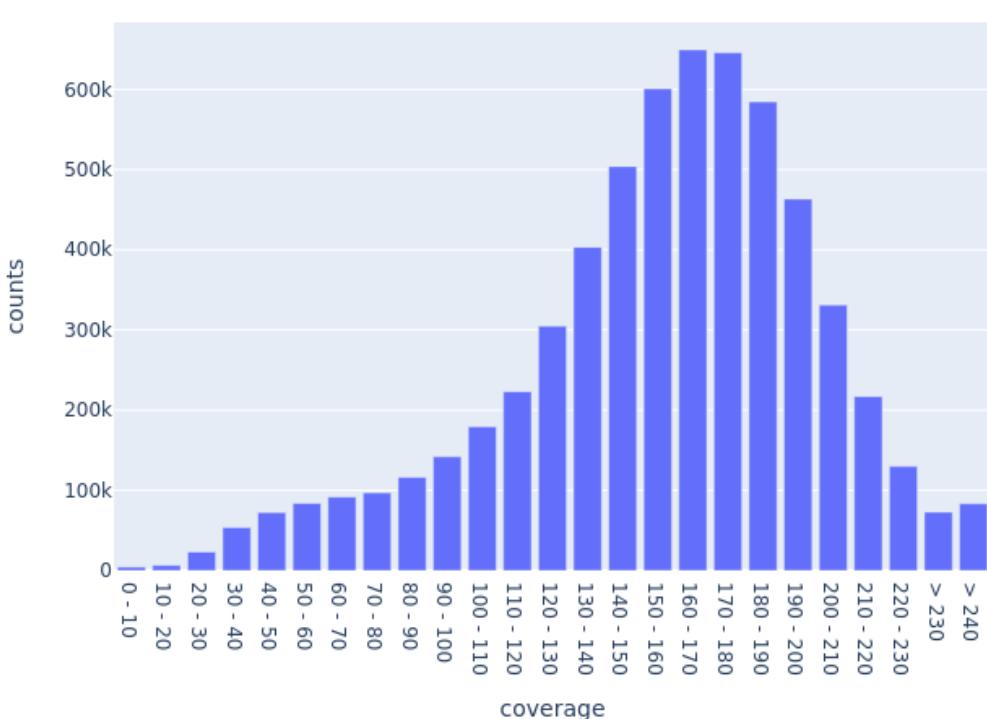
42 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 159.06899047086225

Comamonas testosteronei in T33.4.3.rep

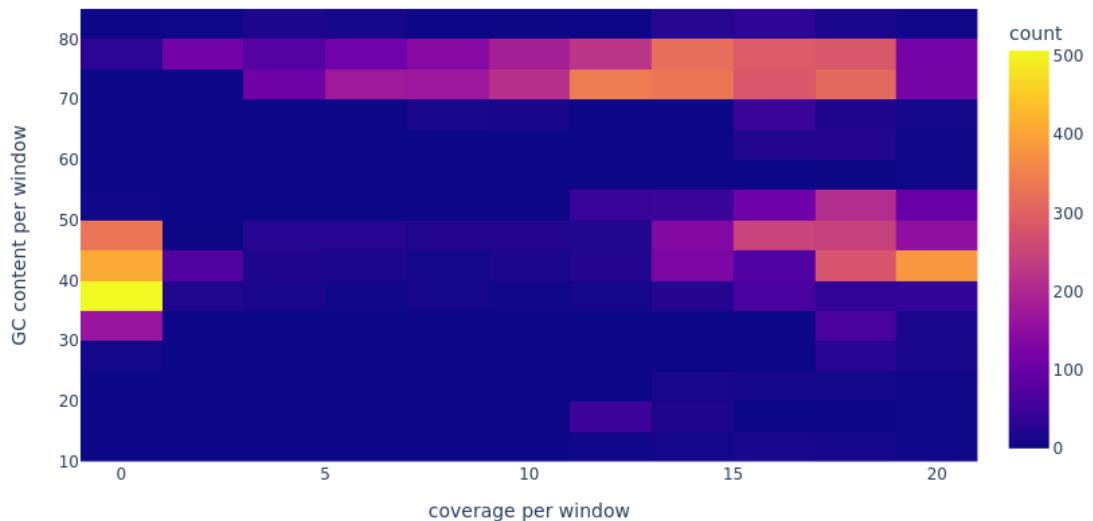


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.4.3.rep



# Report of *Microbacterium saperdae* in T33.4.3.rep

## Mapping stats of Illumina reads

172136872 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

94 + 0 supplementary

0 + 0 duplicates

1253290 + 0 mapped (0.73% : N/A)

172136778 + 0 paired in sequencing

86068389 + 0 read1

86068389 + 0 read2

1170886 + 0 properly paired (0.68% : N/A)

1173292 + 0 with itself and mate mapped

79904 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

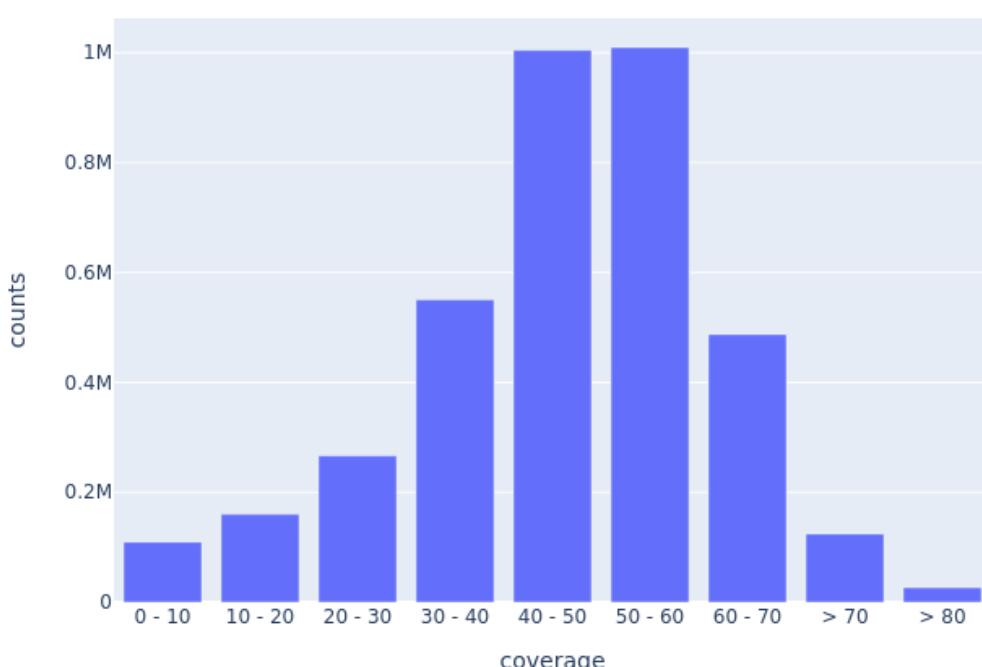
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 47.63973224152204

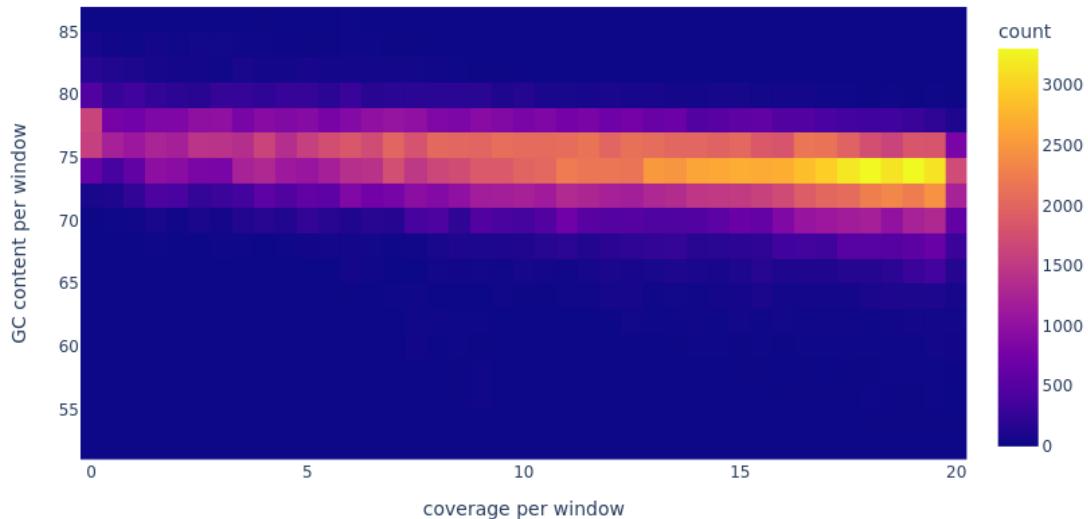
Microbacterium saperdae in T33.4.3.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T33.4.3.rep



# Report of *Ochrobactrum anthropi* in T33.4.3.rep

## Mapping stats of Illumina reads

172140174 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

3396 + 0 supplementary

0 + 0 duplicates

3761168 + 0 mapped (2.18% : N/A)

172136778 + 0 paired in sequencing

86068389 + 0 read1

86068389 + 0 read2

2241390 + 0 properly paired (1.30% : N/A)

2278600 + 0 with itself and mate mapped

1479172 + 0 singletons (0.86% : N/A)

24260 + 0 with mate mapped to a different chr

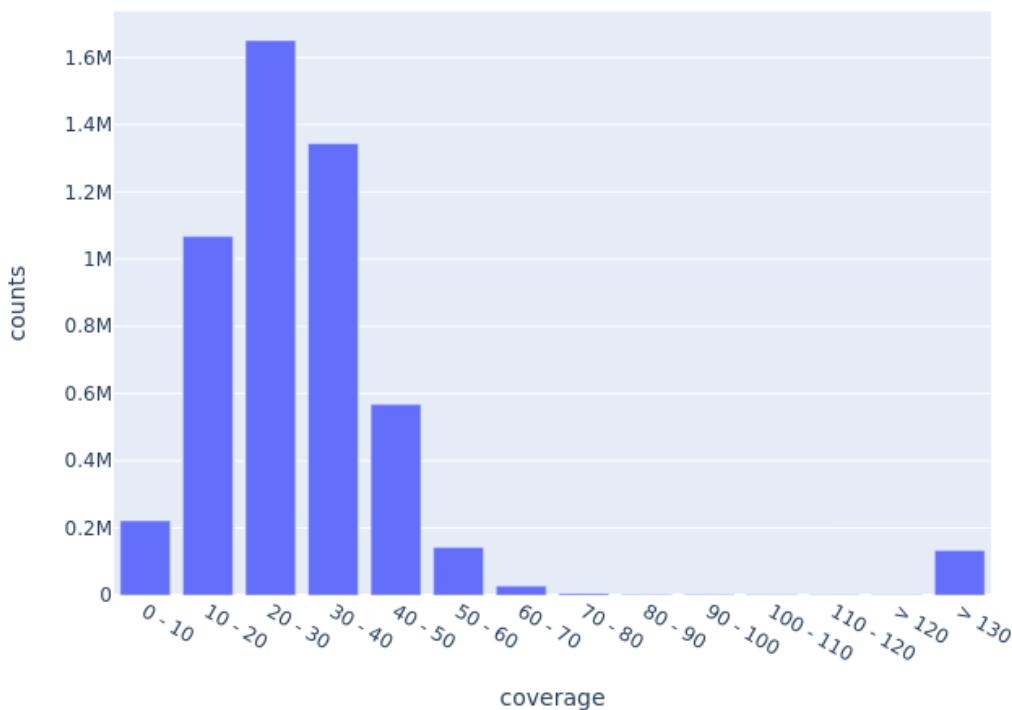
16648 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 84.2713269181851

Ochrobactrum anthropi in T33.4.3.rep

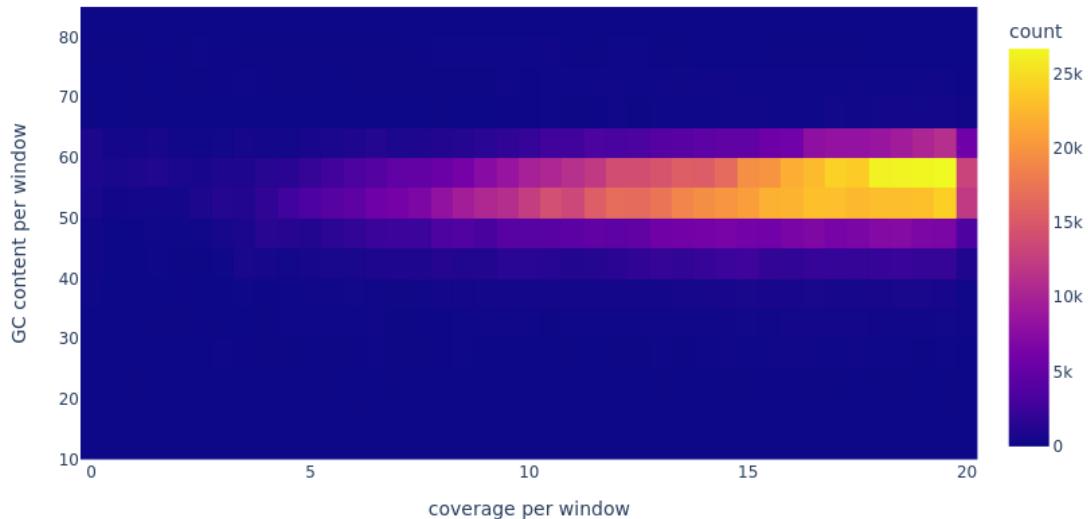


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T33.4.3.rep



# Report of *Agrobacterium tumefaciens* in T33.4.4

## Mapping stats of Illumina reads

170582827 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

50393 + 0 supplementary

0 + 0 duplicates

152173571 + 0 mapped (89.21% : N/A)

170532434 + 0 paired in sequencing

85266217 + 0 read1

85266217 + 0 read2

151162188 + 0 properly paired (88.64% : N/A)

151890838 + 0 with itself and mate mapped

232340 + 0 singletons (0.14% : N/A)

358818 + 0 with mate mapped to a different chr

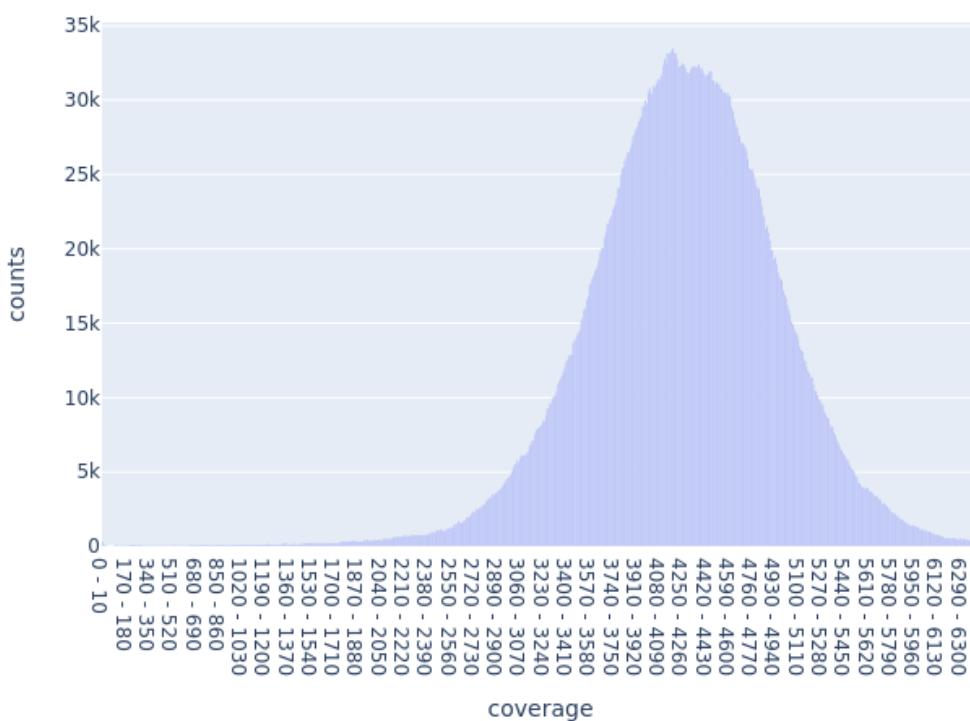
347676 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 4276.235694292301

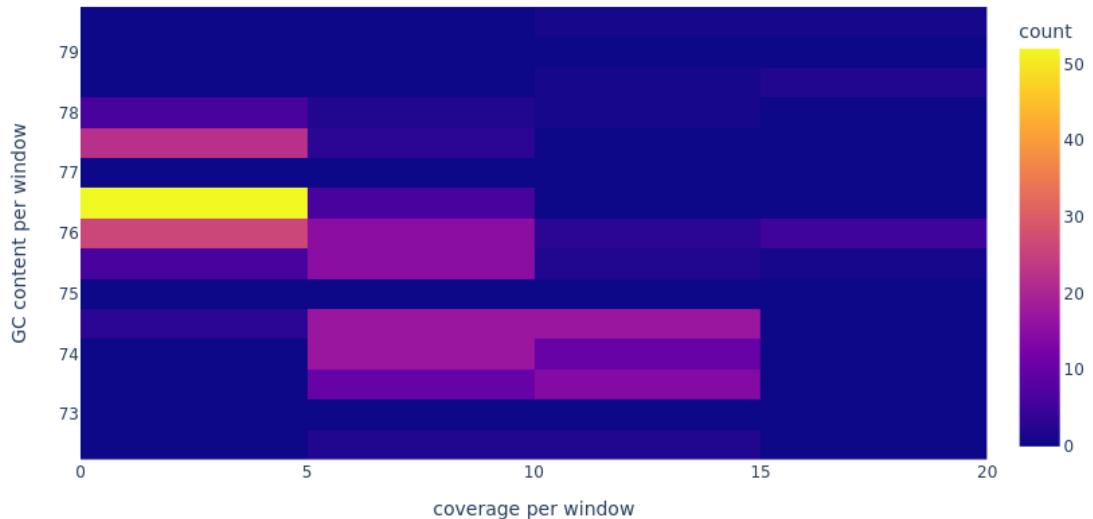
Agrobacterium tumefaciens in T33.4.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T33.4.4



# Report of Comamonas testosterone in T33.4.4

## Mapping stats of Illumina reads

170533687 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1253 + 0 supplementary

0 + 0 duplicates

9095310 + 0 mapped (5.33% : N/A)

170532434 + 0 paired in sequencing

85266217 + 0 read1

85266217 + 0 read2

8825300 + 0 properly paired (5.18% : N/A)

8832218 + 0 with itself and mate mapped

261839 + 0 singletons (0.15% : N/A)

656 + 0 with mate mapped to a different chr

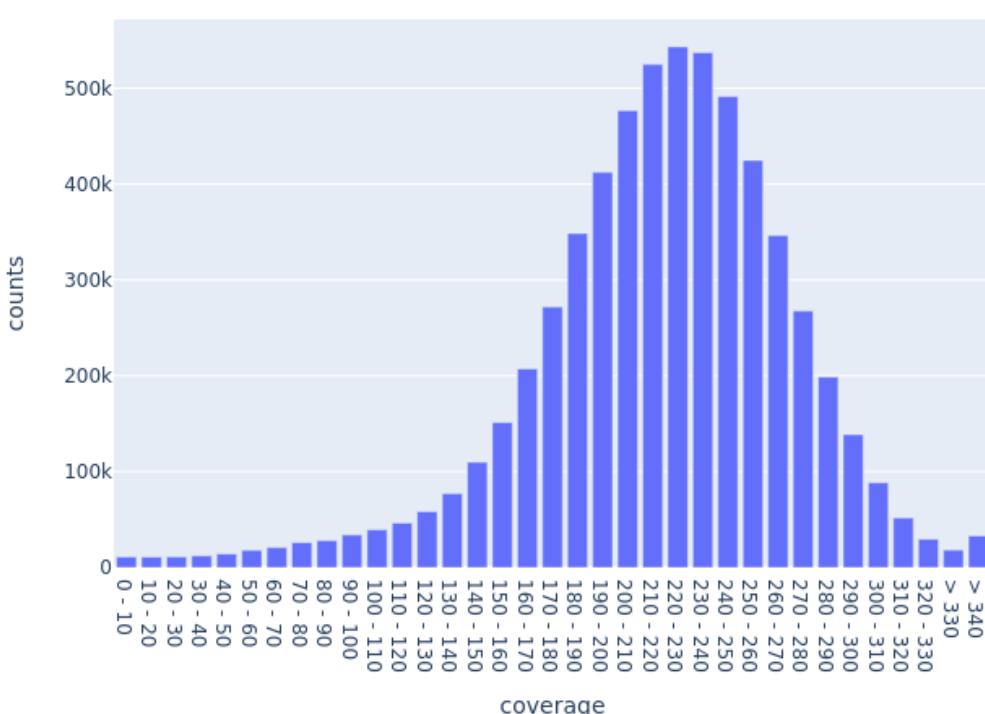
378 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 221.17606610094586

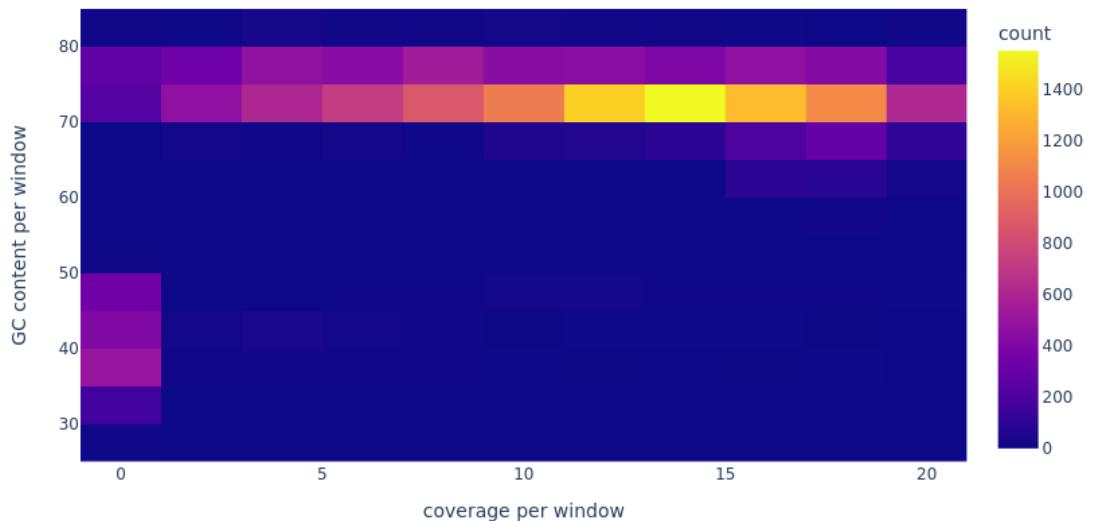
Comamonas testosterone in T33.4.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.4.4



# Report of *Microbacterium saperdae* in T33.4.4

## Mapping stats of Illumina reads

170532443 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

9 + 0 supplementary

0 + 0 duplicates

135793 + 0 mapped (0.08% : N/A)

170532434 + 0 paired in sequencing

85266217 + 0 read1

85266217 + 0 read2

49542 + 0 properly paired (0.03% : N/A)

51574 + 0 with itself and mate mapped

84210 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

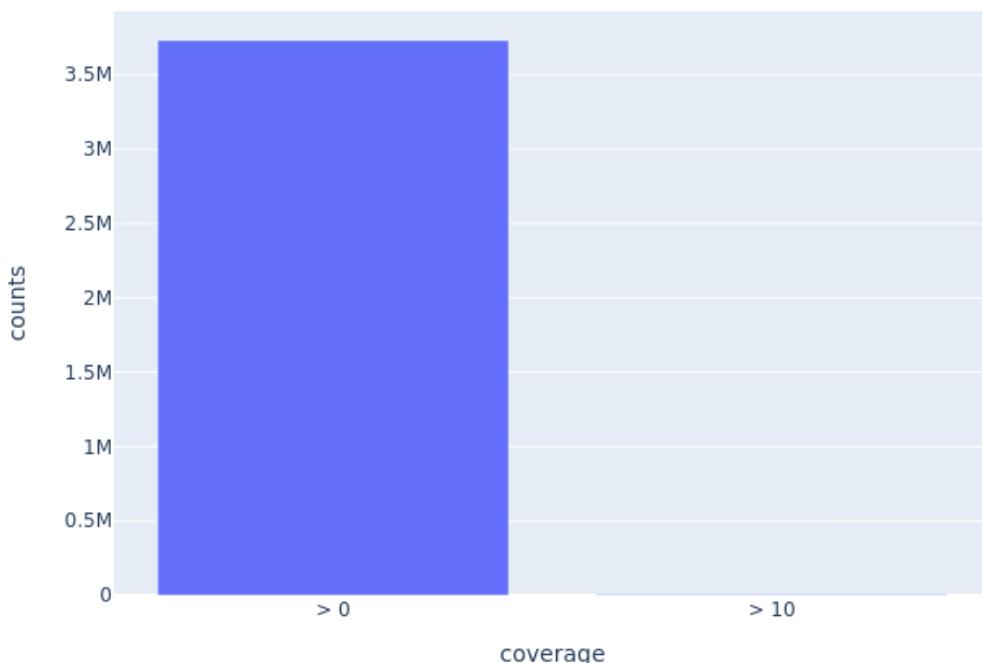
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 2.3352045995636534

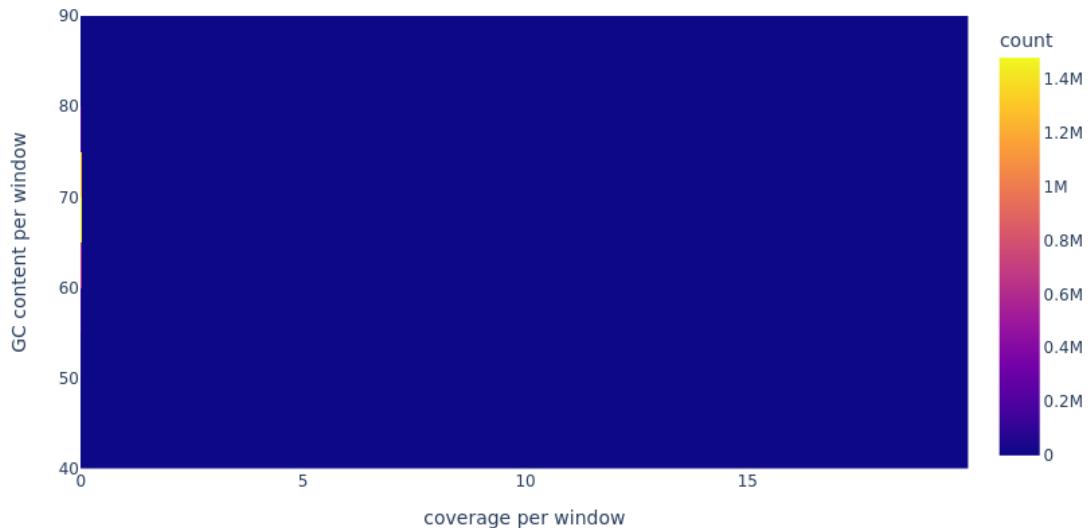
Microbacterium saperdae in T33.4.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T33.4.4



# Report of *Ochrobactrum anthropi* in T33.4.4

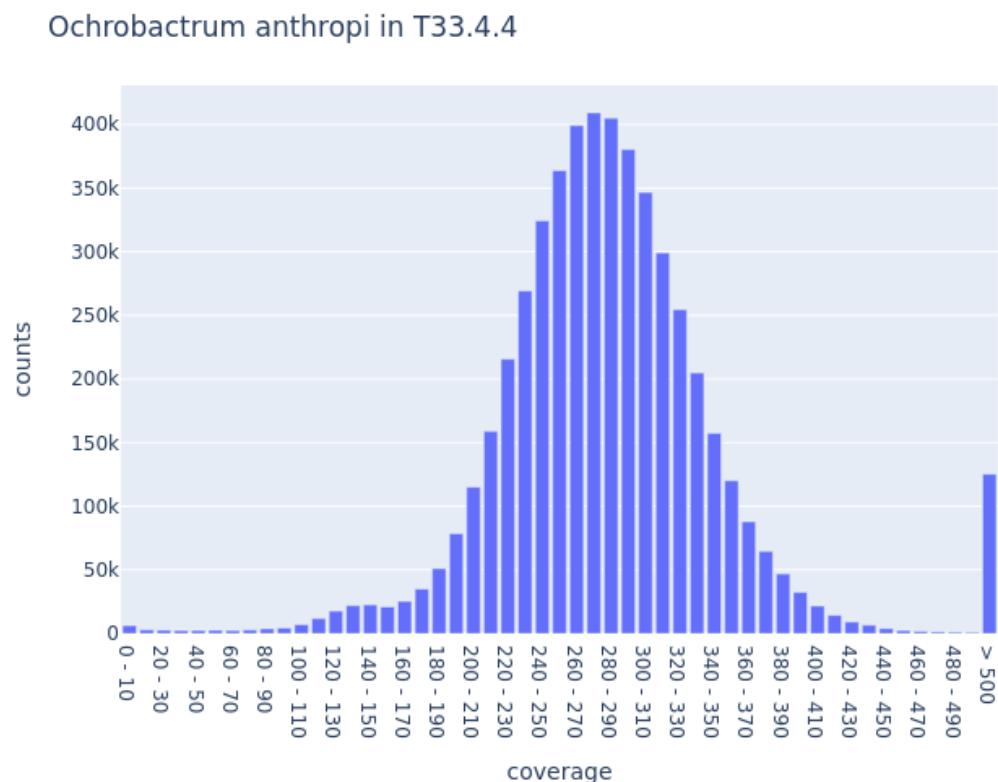
## Mapping stats of Illumina reads

170536253 + 0 in total (QC-passed reads + QC-failed reads)  
0 + 0 secondary  
3819 + 0 supplementary  
0 + 0 duplicates  
12178159 + 0 mapped (7.14% : N/A)  
170532434 + 0 paired in sequencing  
85266217 + 0 read1  
85266217 + 0 read2  
10728956 + 0 properly paired (6.29% : N/A)  
10766750 + 0 with itself and mate mapped  
1407590 + 0 singletons (0.83% : N/A)  
21018 + 0 with mate mapped to a different chr  
14816 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 331.2300754323164

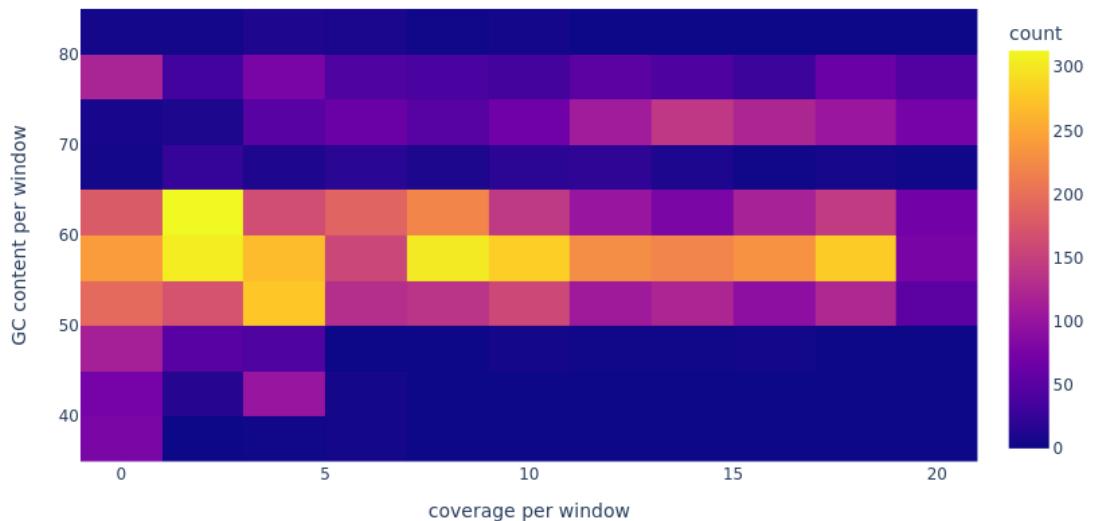


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T33.4.4



# Report of *Agrobacterium tumefaciens* in T33.4.5

## Mapping stats of Illumina reads

162638901 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

49319 + 0 supplementary

0 + 0 duplicates

154469756 + 0 mapped (94.98% : N/A)

162589582 + 0 paired in sequencing

81294791 + 0 read1

81294791 + 0 read2

153773820 + 0 properly paired (94.58% : N/A)

154323704 + 0 with itself and mate mapped

96733 + 0 singletons (0.06% : N/A)

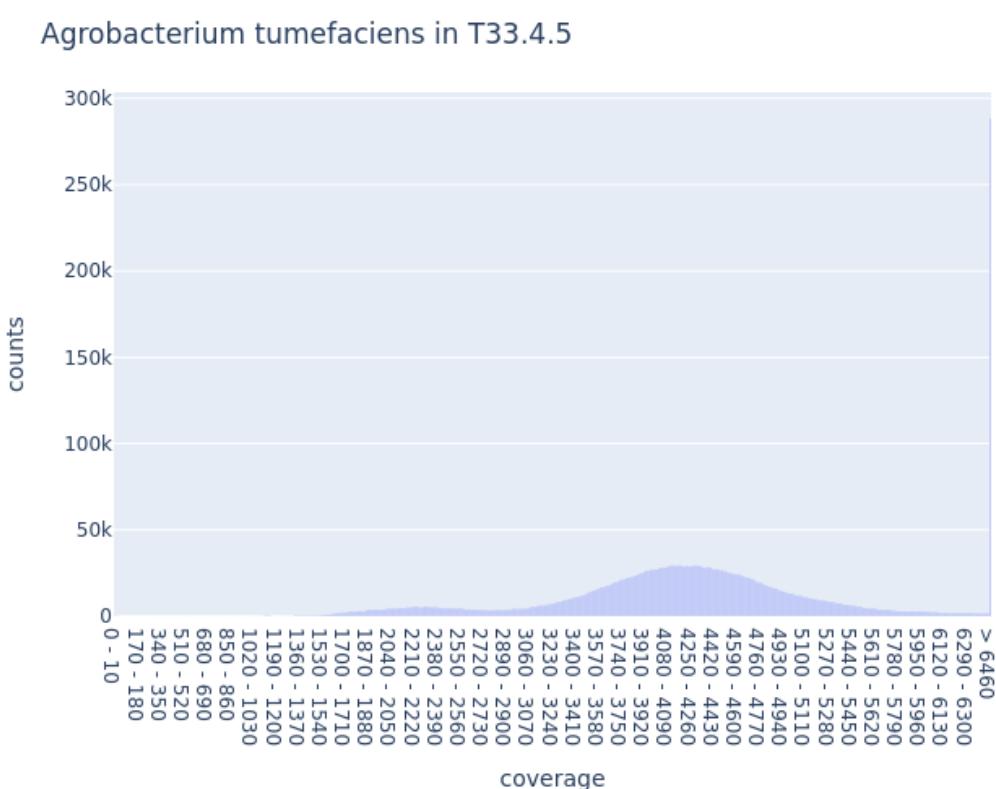
257138 + 0 with mate mapped to a different chr

245895 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

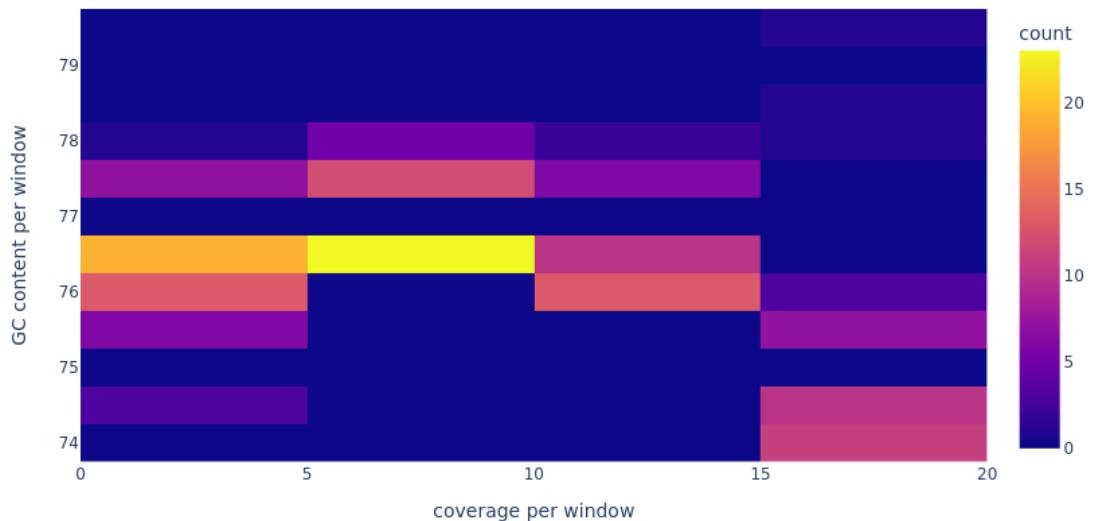
Average coverage: 4307.62842693539



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T33.4.5



# Report of Comamonas testosterone in T33.4.5

## Mapping stats of Illumina reads

162590059 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

477 + 0 supplementary

0 + 0 duplicates

6377940 + 0 mapped (3.92% : N/A)

162589582 + 0 paired in sequencing

81294791 + 0 read1

81294791 + 0 read2

6141348 + 0 properly paired (3.78% : N/A)

6145082 + 0 with itself and mate mapped

232381 + 0 singletons (0.14% : N/A)

44 + 0 with mate mapped to a different chr

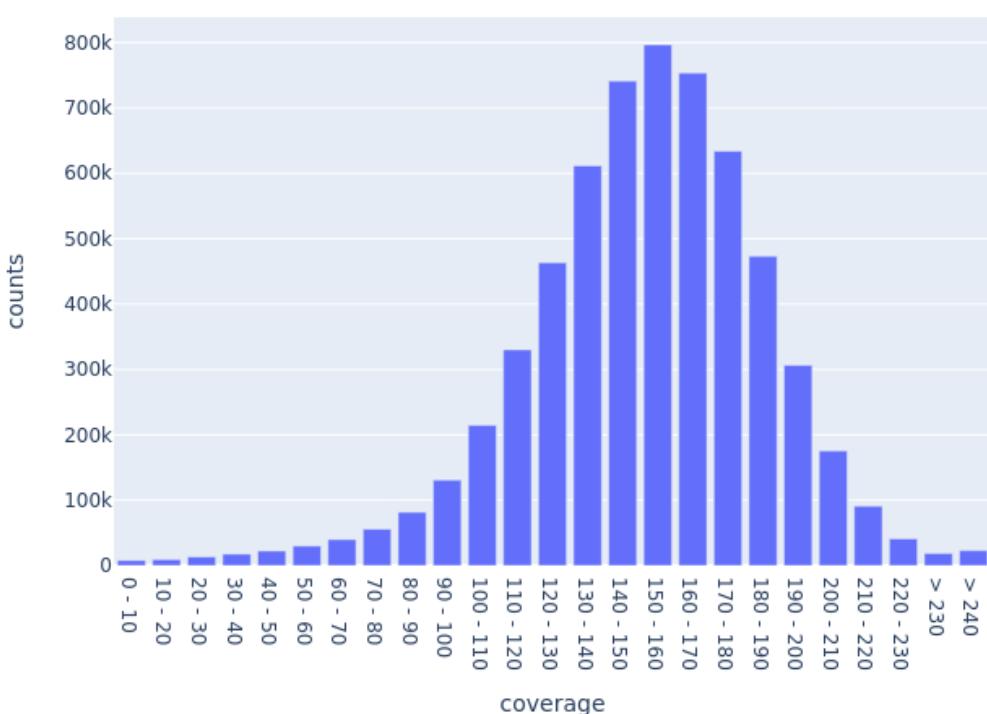
24 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 154.1577549832021

Comamonas testosterone in T33.4.5

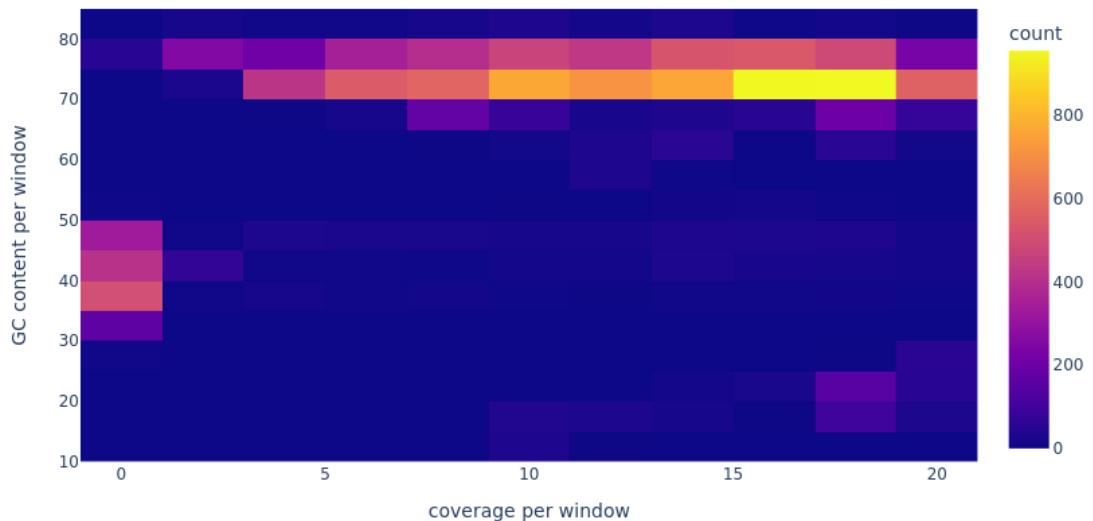


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T33.4.5



# Report of *Microbacterium saperdae* in T33.4.5

## Mapping stats of Illumina reads

162589639 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

57 + 0 supplementary

0 + 0 duplicates

981341 + 0 mapped (0.60% : N/A)

162589582 + 0 paired in sequencing

81294791 + 0 read1

81294791 + 0 read2

896970 + 0 properly paired (0.55% : N/A)

899128 + 0 with itself and mate mapped

82156 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

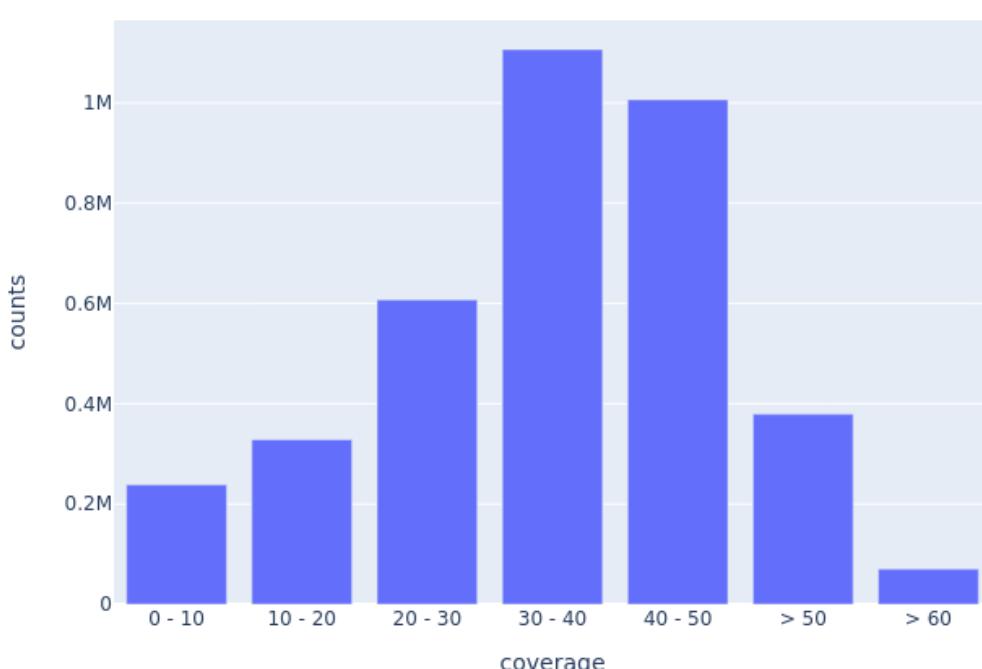
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 36.561879146935915

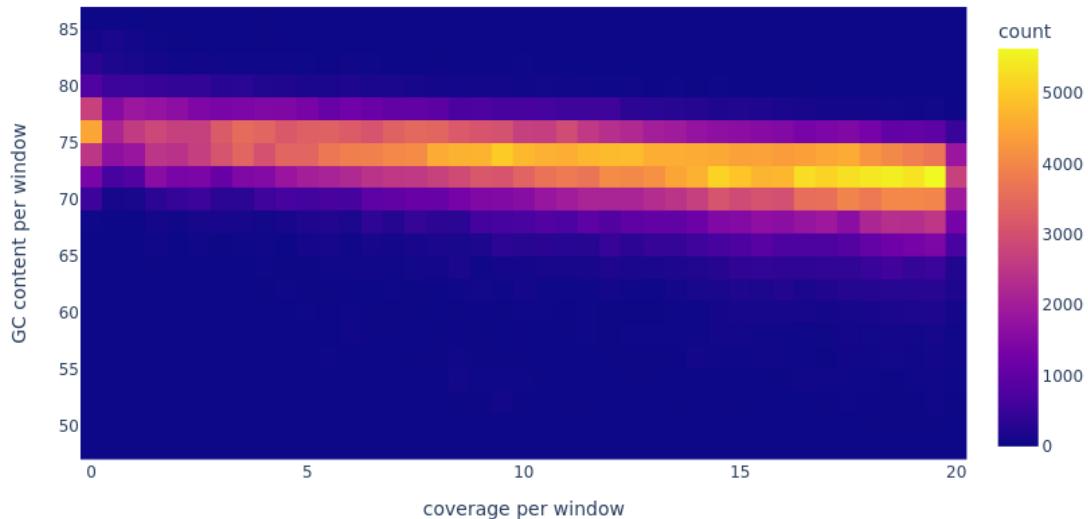
Microbacterium saperdae in T33.4.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T33.4.5



# Report of *Ochrobactrum anthropi* in T33.4.5

## Mapping stats of Illumina reads

162593478 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

3896 + 0 supplementary

0 + 0 duplicates

3494051 + 0 mapped (2.15% : N/A)

162589582 + 0 paired in sequencing

81294791 + 0 read1

81294791 + 0 read2

2053486 + 0 properly paired (1.26% : N/A)

2085760 + 0 with itself and mate mapped

1404395 + 0 singletons (0.86% : N/A)

20656 + 0 with mate mapped to a different chr

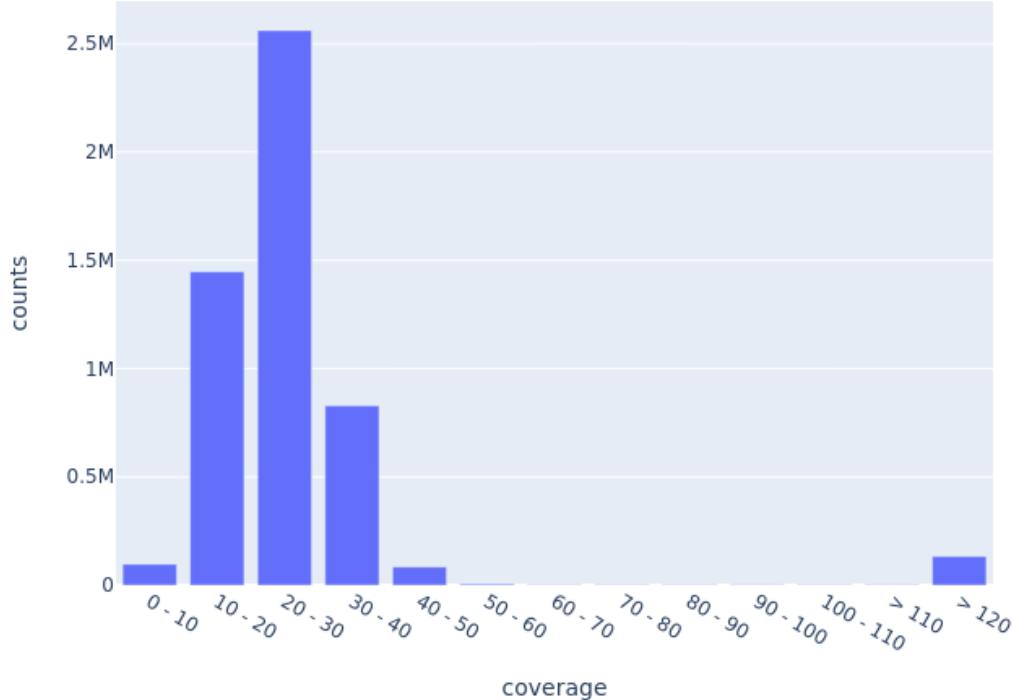
14248 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 77.67680419999091

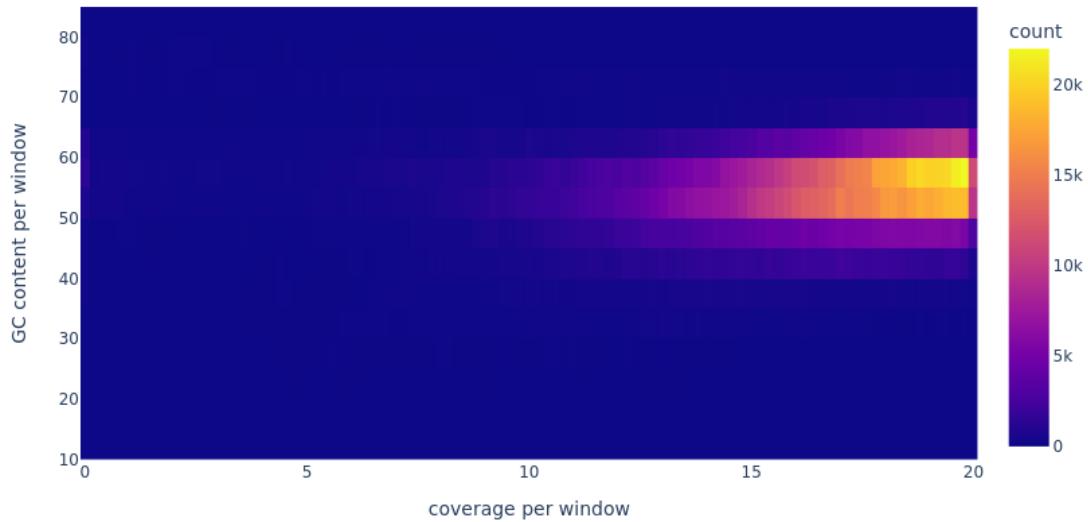
Ochrobactrum anthropi in T33.4.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T33.4.5



# Report of *Agrobacterium tumefaciens* in T44.1.1

## Mapping stats of Illumina reads

12610576 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

9686 + 0 supplementary

0 + 0 duplicates

12578283 + 0 mapped (99.74% : N/A)

12600890 + 0 paired in sequencing

6300445 + 0 read1

6300445 + 0 read2

12512374 + 0 properly paired (99.30% : N/A)

12563612 + 0 with itself and mate mapped

4985 + 0 singletons (0.04% : N/A)

22130 + 0 with mate mapped to a different chr

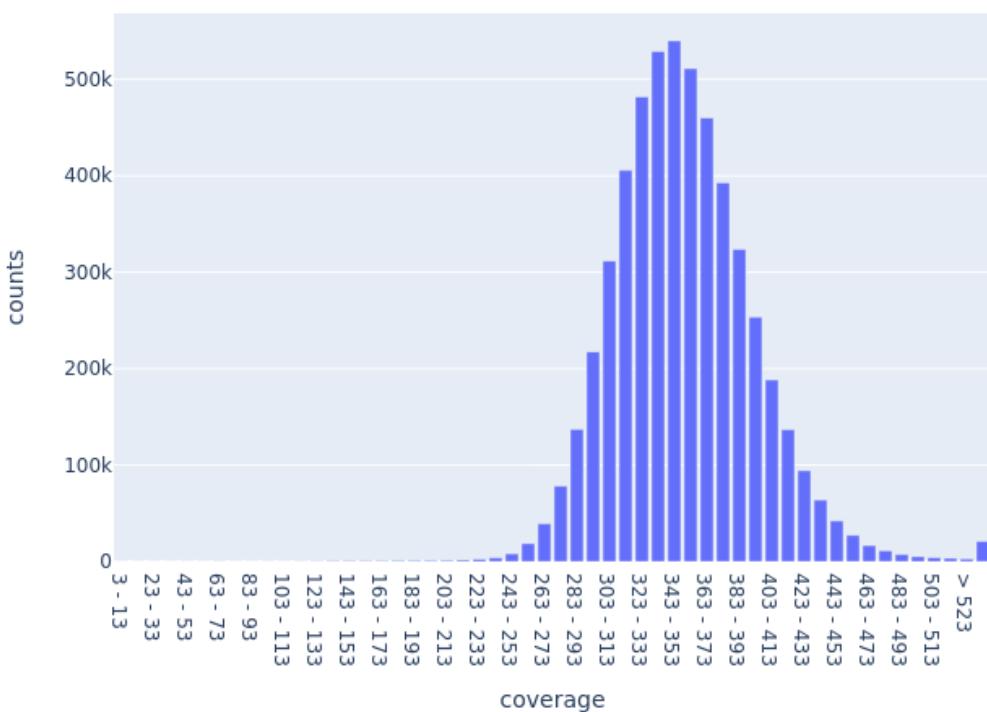
21130 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 353.7067173570691

Agrobacterium tumefaciens in T44.1.1

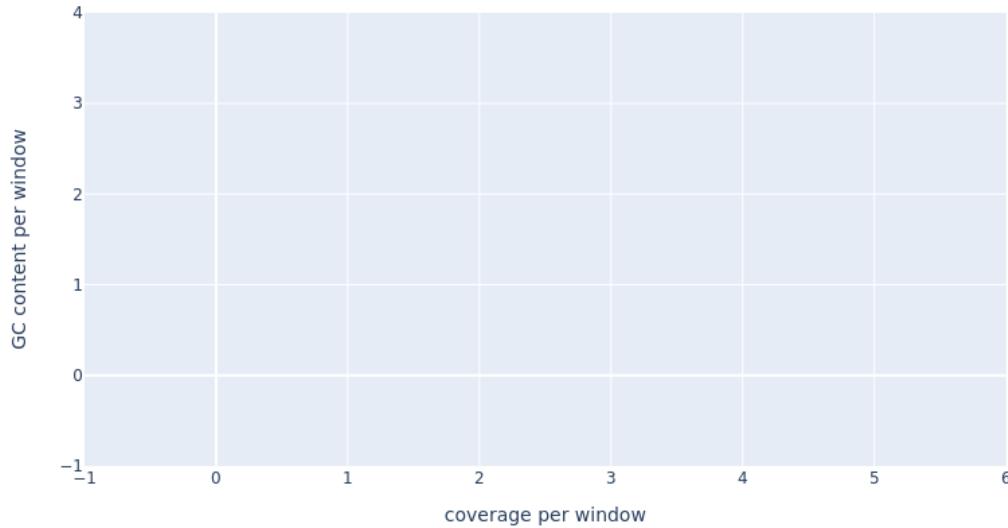


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T44.1.1



# Report of *Agrobacterium tumefaciens* in T44.1.2

## Mapping stats of Illumina reads

14383150 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

19230 + 0 supplementary

0 + 0 duplicates

14331904 + 0 mapped (99.64% : N/A)

14363920 + 0 paired in sequencing

7181960 + 0 read1

7181960 + 0 read2

14219866 + 0 properly paired (99.00% : N/A)

14306188 + 0 with itself and mate mapped

6486 + 0 singletons (0.05% : N/A)

41966 + 0 with mate mapped to a different chr

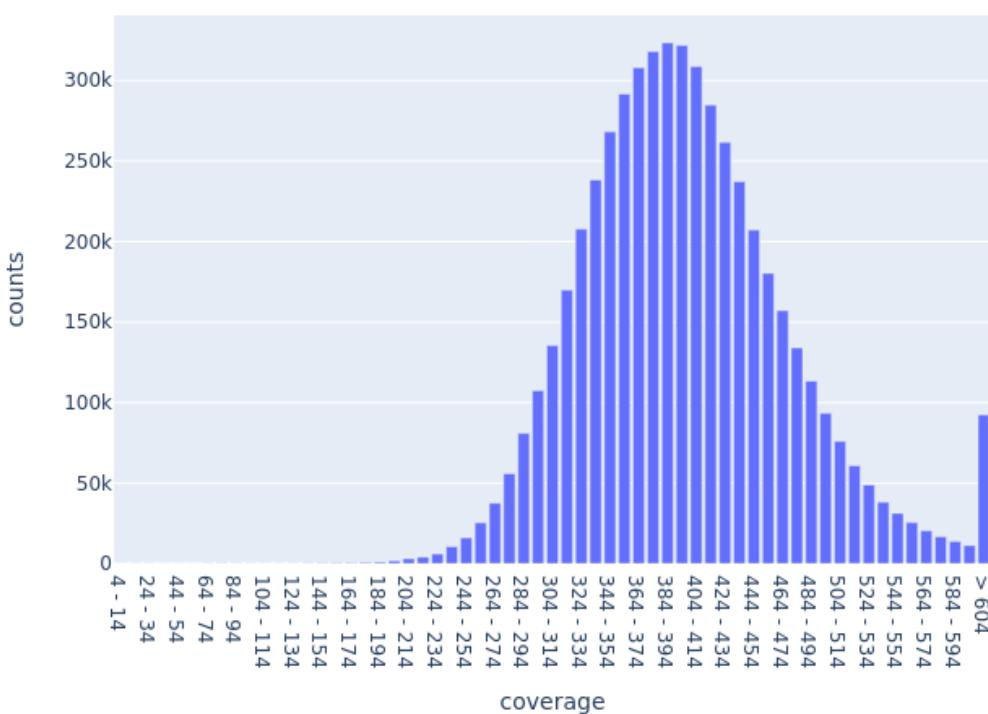
40285 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 402.6912137071994

Agrobacterium tumefaciens in T44.1.2

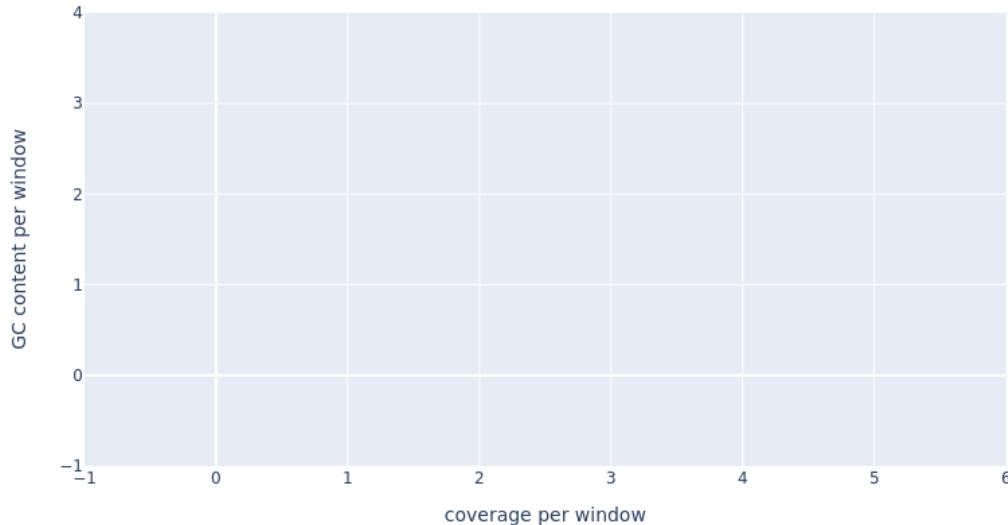


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T44.1.2



# Report of Comamonas testosterone in T44.2.1

## Mapping stats of Illumina reads

14429326 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

4060 + 0 supplementary

0 + 0 duplicates

14419331 + 0 mapped (99.93% : N/A)

14425266 + 0 paired in sequencing

7212633 + 0 read1

7212633 + 0 read2

14363636 + 0 properly paired (99.57% : N/A)

14410108 + 0 with itself and mate mapped

5163 + 0 singletons (0.04% : N/A)

2378 + 0 with mate mapped to a different chr

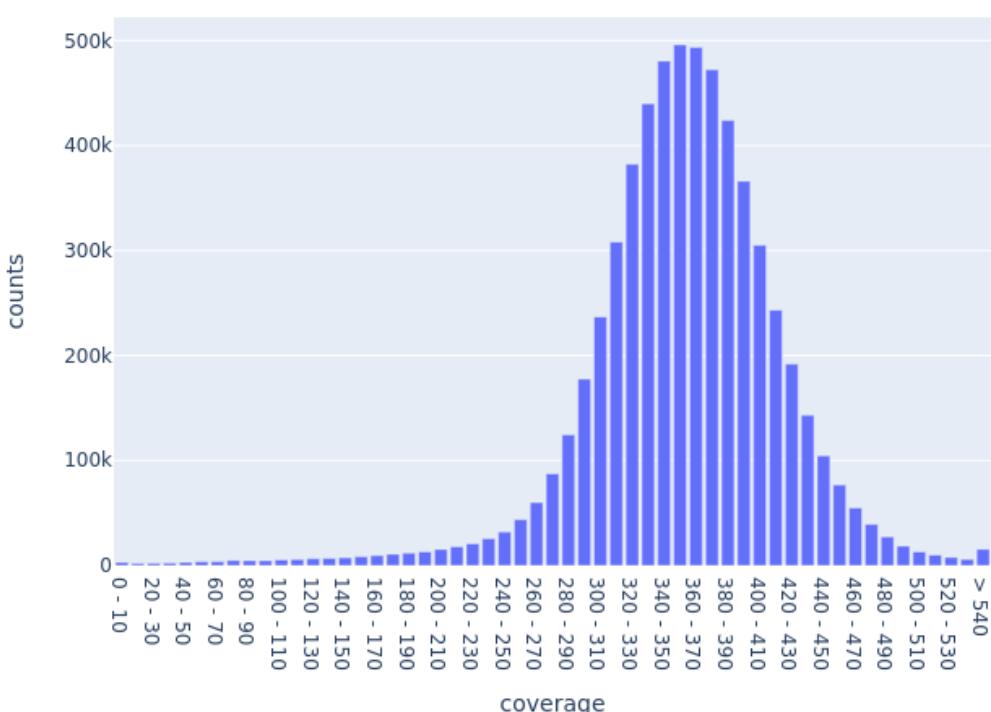
2278 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 356.629853012405

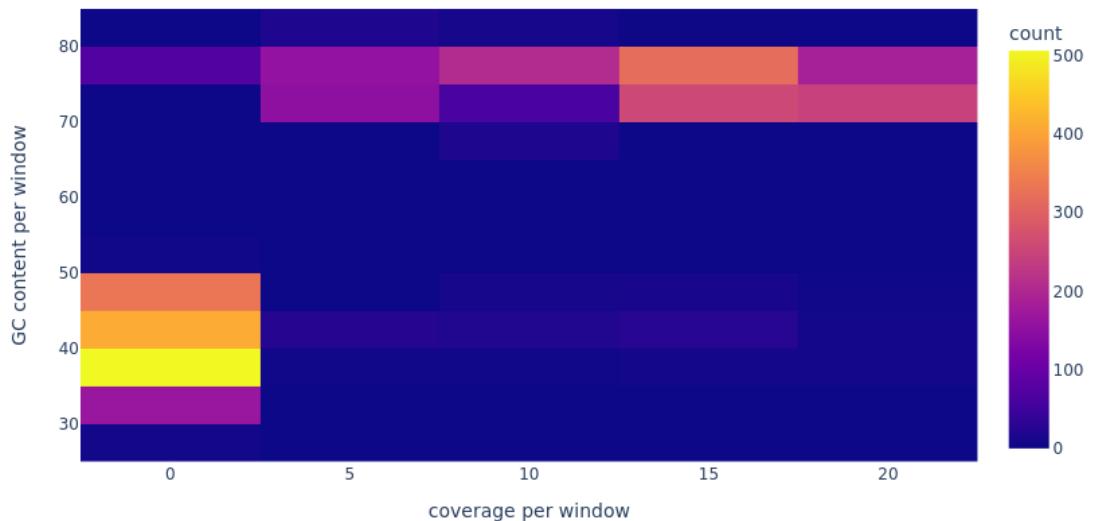
Comamonas testosterone in T44.2.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.2.1



# Report of *Comamonas testosteronei* in T44.2.2.rep

## Mapping stats of Illumina reads

13895161 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

9493 + 0 supplementary

0 + 0 duplicates

13886586 + 0 mapped (99.94% : N/A)

13885668 + 0 paired in sequencing

6942834 + 0 read1

6942834 + 0 read2

13827288 + 0 properly paired (99.58% : N/A)

13872058 + 0 with itself and mate mapped

5035 + 0 singletons (0.04% : N/A)

1726 + 0 with mate mapped to a different chr

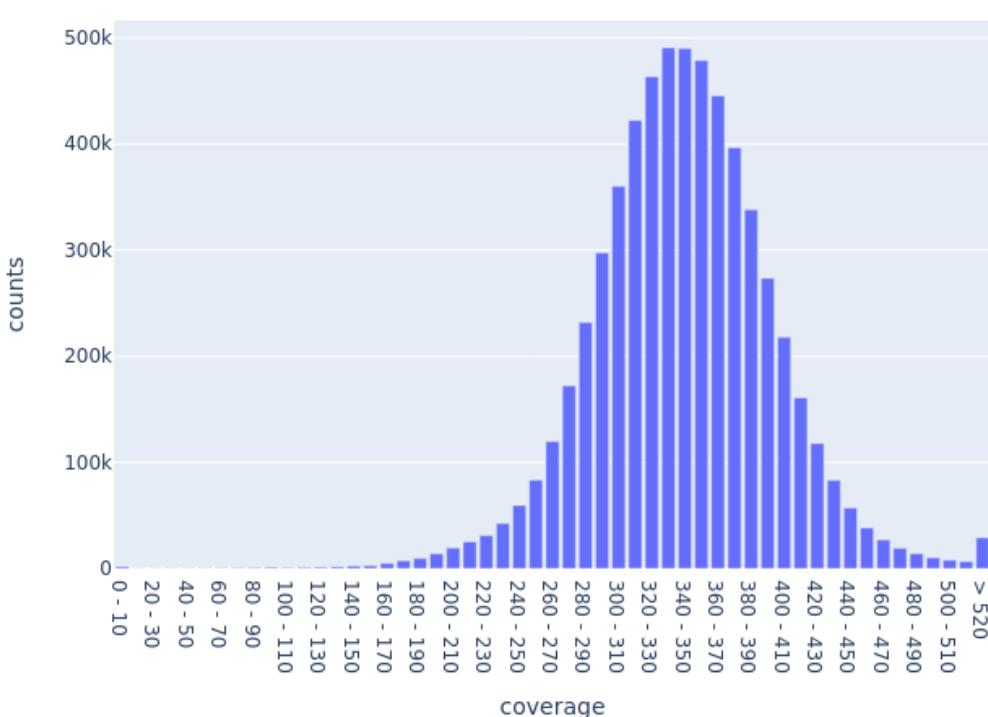
1471 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 343.3408183333385

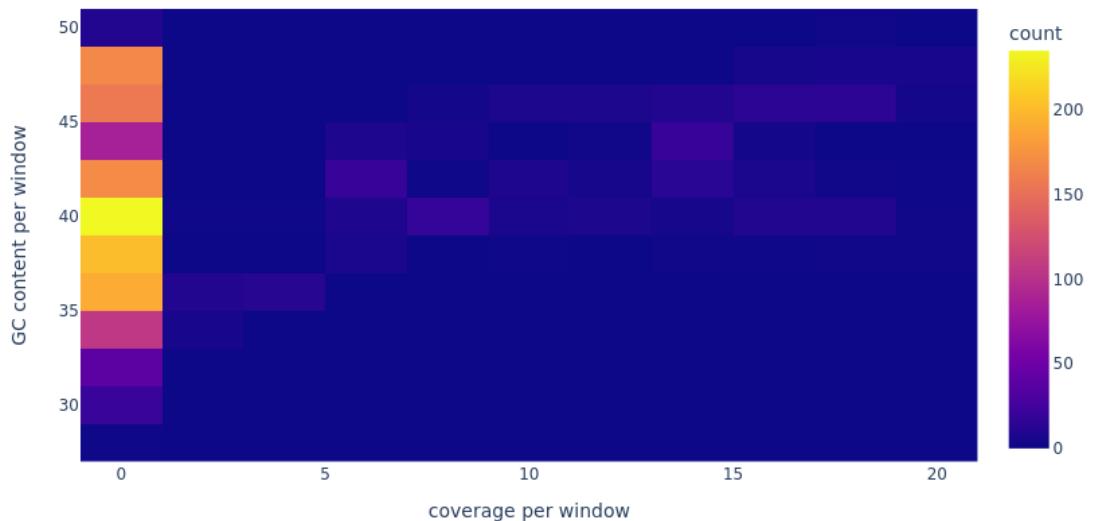
Comamonas testosteronei in T44.2.2.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.2.2.rep



# Report of *Comamonas testosteronei* in T44.2.3.rep

## Mapping stats of Illumina reads

15386397 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

15161 + 0 supplementary

0 + 0 duplicates

15378088 + 0 mapped (99.95% : N/A)

15371236 + 0 paired in sequencing

7685618 + 0 read1

7685618 + 0 read2

15275266 + 0 properly paired (99.38% : N/A)

15357494 + 0 with itself and mate mapped

5433 + 0 singletons (0.04% : N/A)

3006 + 0 with mate mapped to a different chr

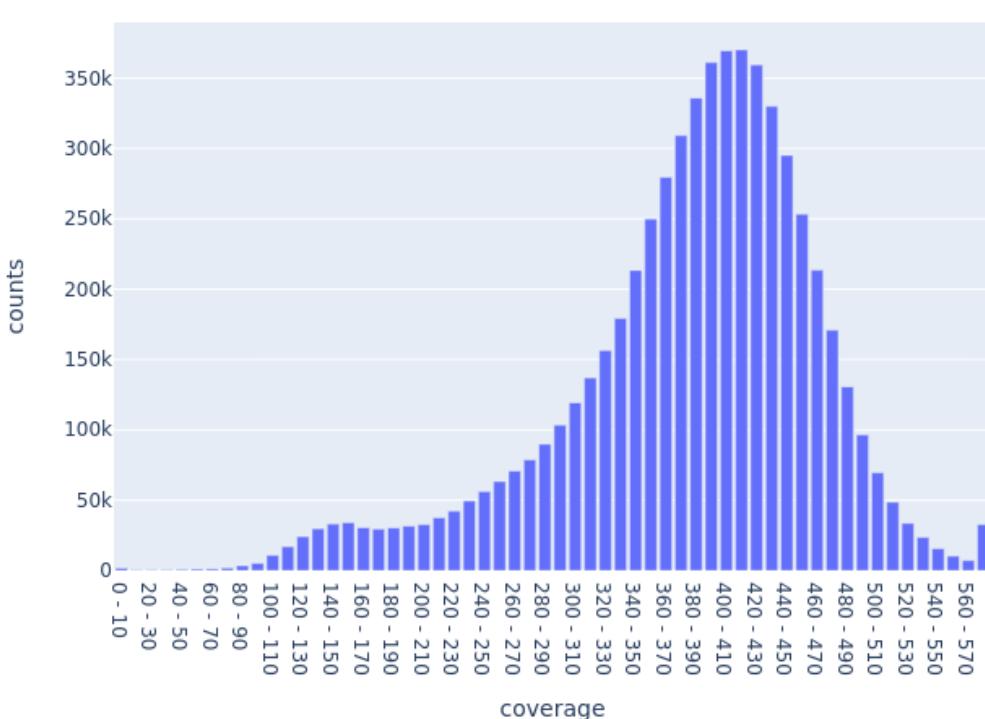
2834 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 380.1141402648186

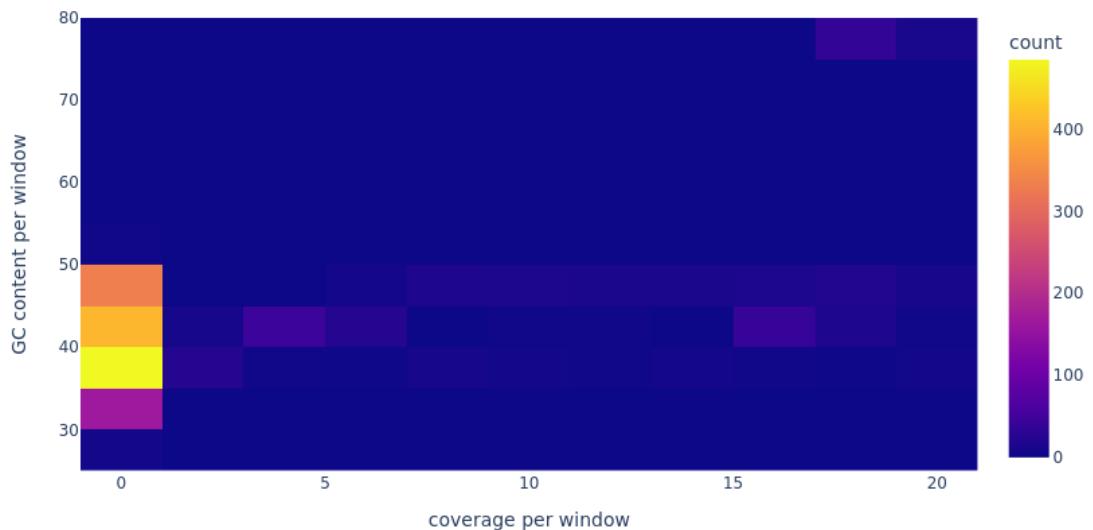
Comamonas testosteronei in T44.2.3.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.2.3.rep



# Report of *Comamonas testosteronei* in T44.2.4.rep

## Mapping stats of Illumina reads

14808491 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

7781 + 0 supplementary

0 + 0 duplicates

14799733 + 0 mapped (99.94% : N/A)

14800710 + 0 paired in sequencing

7400355 + 0 read1

7400355 + 0 read2

14684798 + 0 properly paired (99.22% : N/A)

14786510 + 0 with itself and mate mapped

5442 + 0 singletons (0.04% : N/A)

5724 + 0 with mate mapped to a different chr

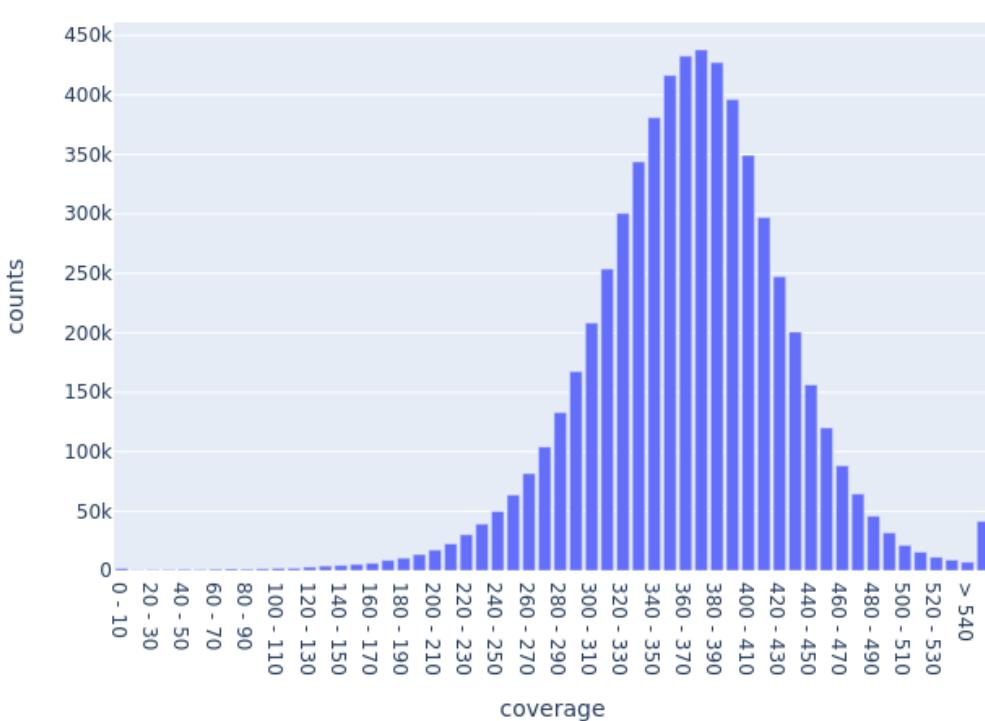
5473 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 365.94955929032176

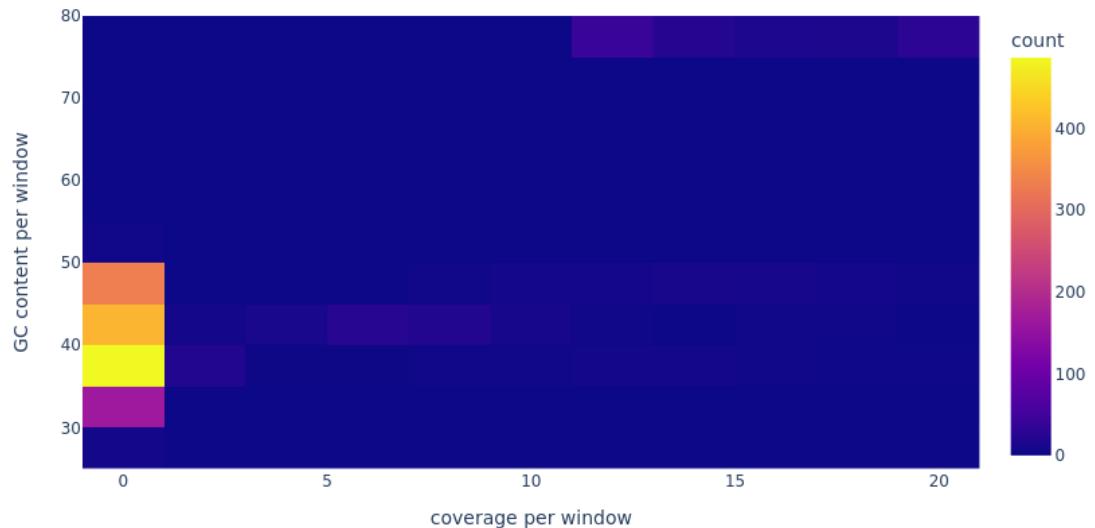
Comamonas testosteronei in T44.2.4.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteronei in T44.2.4.rep



# Report of *Comamonas testosteronei* in T44.2.5.rep

## Mapping stats of Illumina reads

15983720 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

29590 + 0 supplementary

0 + 0 duplicates

15973477 + 0 mapped (99.94% : N/A)

15954130 + 0 paired in sequencing

7977065 + 0 read1

7977065 + 0 read2

15794838 + 0 properly paired (99.00% : N/A)

15937392 + 0 with itself and mate mapped

6495 + 0 singletons (0.04% : N/A)

5258 + 0 with mate mapped to a different chr

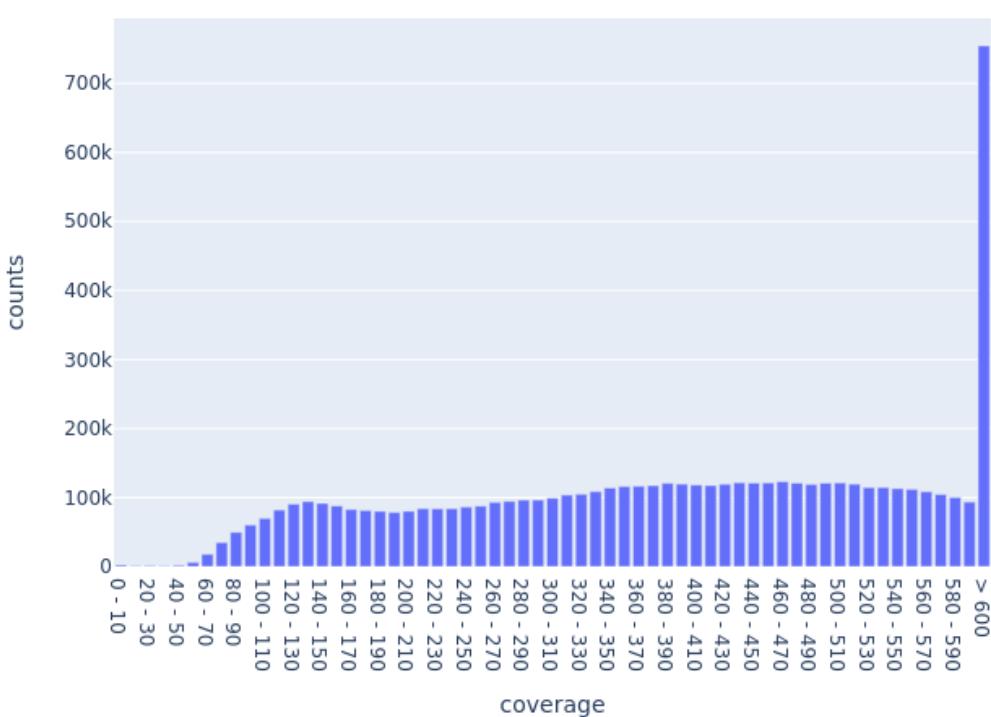
5075 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 394.3946958701372

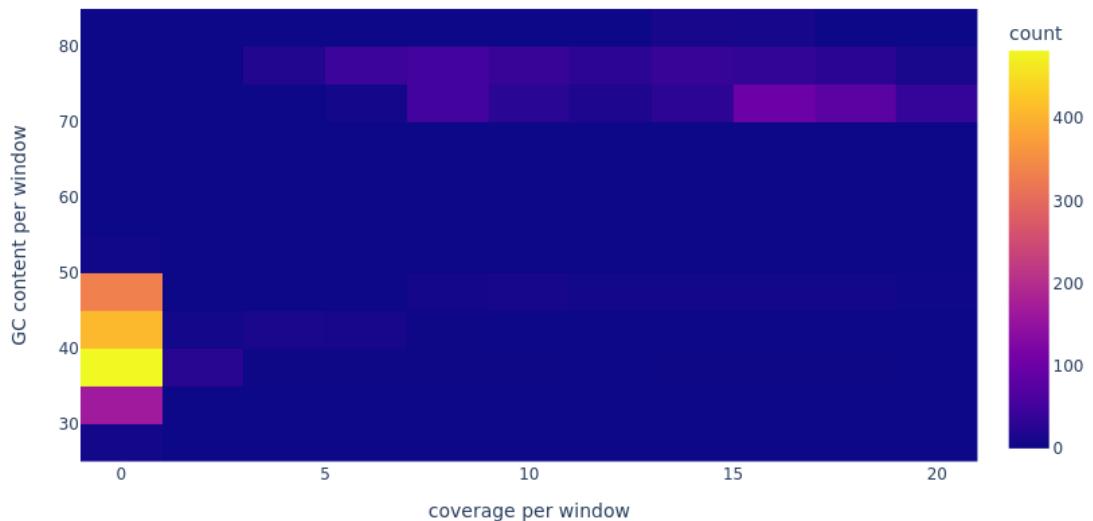
Comamonas testosteronei in T44.2.5.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.2.5.rep



# Report of *Agrobacterium tumefaciens* in T44.3.1

## Mapping stats of Illumina reads

165041224 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

153942 + 0 supplementary

0 + 0 duplicates

156826073 + 0 mapped (95.02% : N/A)

164887282 + 0 paired in sequencing

82443641 + 0 read1

82443641 + 0 read2

155372032 + 0 properly paired (94.23% : N/A)

156553538 + 0 with itself and mate mapped

118593 + 0 singletons (0.07% : N/A)

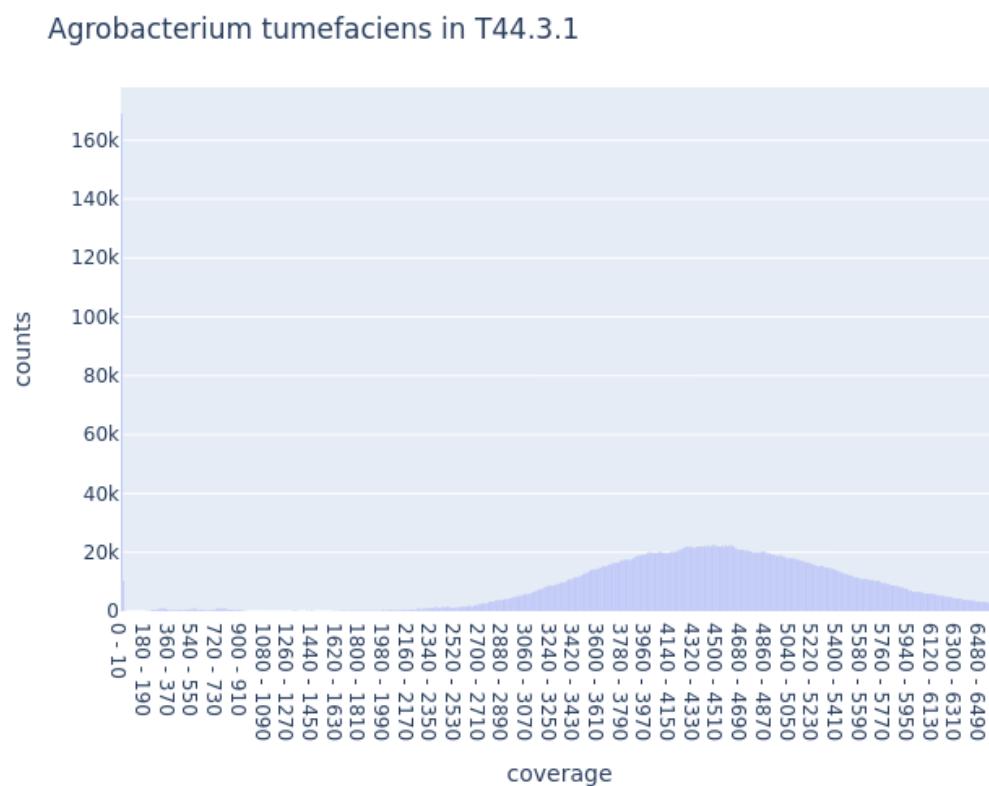
572854 + 0 with mate mapped to a different chr

546969 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

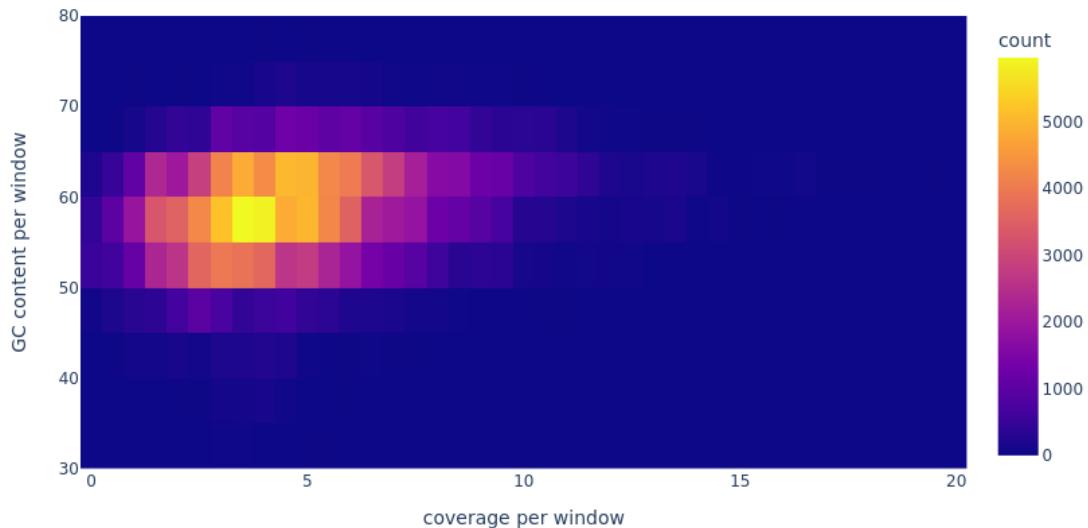
Average coverage: 4403.573100133551



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T44.3.1



# Report of Comamonas testosterone in T44.3.1

## Mapping stats of Illumina reads

164888412 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1130 + 0 supplementary

0 + 0 duplicates

7752310 + 0 mapped (4.70% : N/A)

164887282 + 0 paired in sequencing

82443641 + 0 read1

82443641 + 0 read2

7490980 + 0 properly paired (4.54% : N/A)

7498368 + 0 with itself and mate mapped

252812 + 0 singletons (0.15% : N/A)

190 + 0 with mate mapped to a different chr

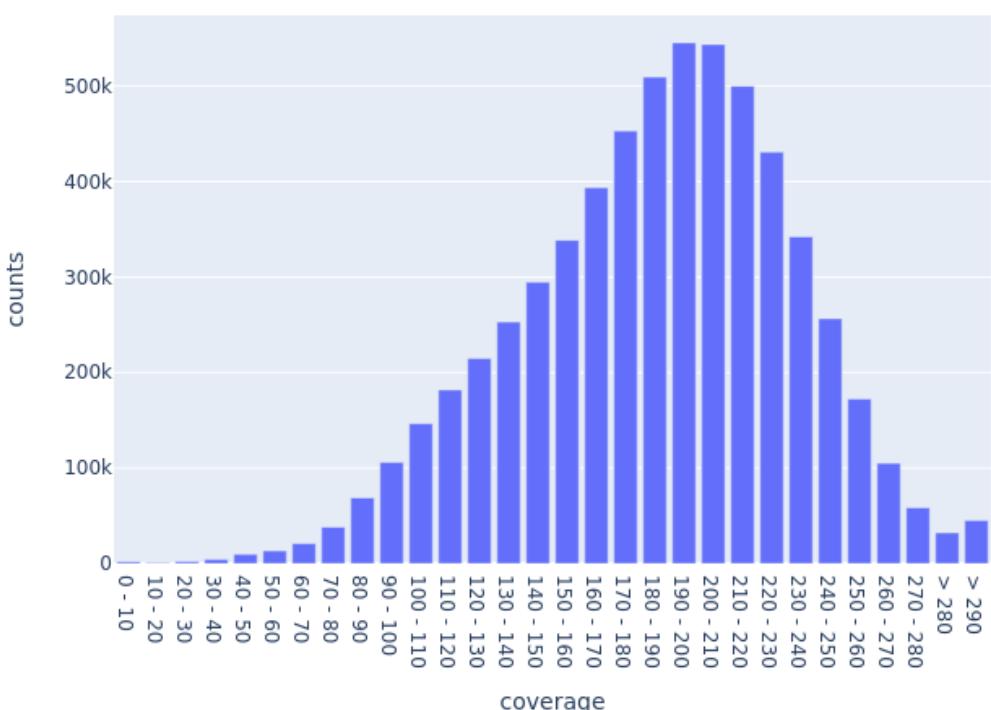
144 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 188.09339357053153

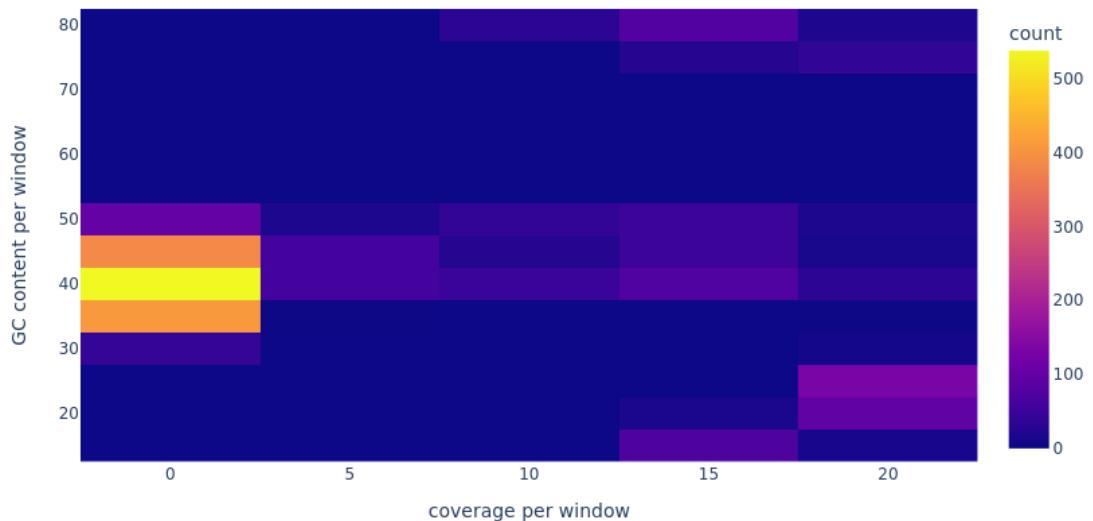
Comamonas testosterone in T44.3.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.3.1



# Report of *Microbacterium saperdae* in T44.3.1

## Mapping stats of Illumina reads

164887374 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

92 + 0 supplementary

0 + 0 duplicates

473032 + 0 mapped (0.29% : N/A)

164887282 + 0 paired in sequencing

82443641 + 0 read1

82443641 + 0 read2

390922 + 0 properly paired (0.24% : N/A)

392876 + 0 with itself and mate mapped

80064 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

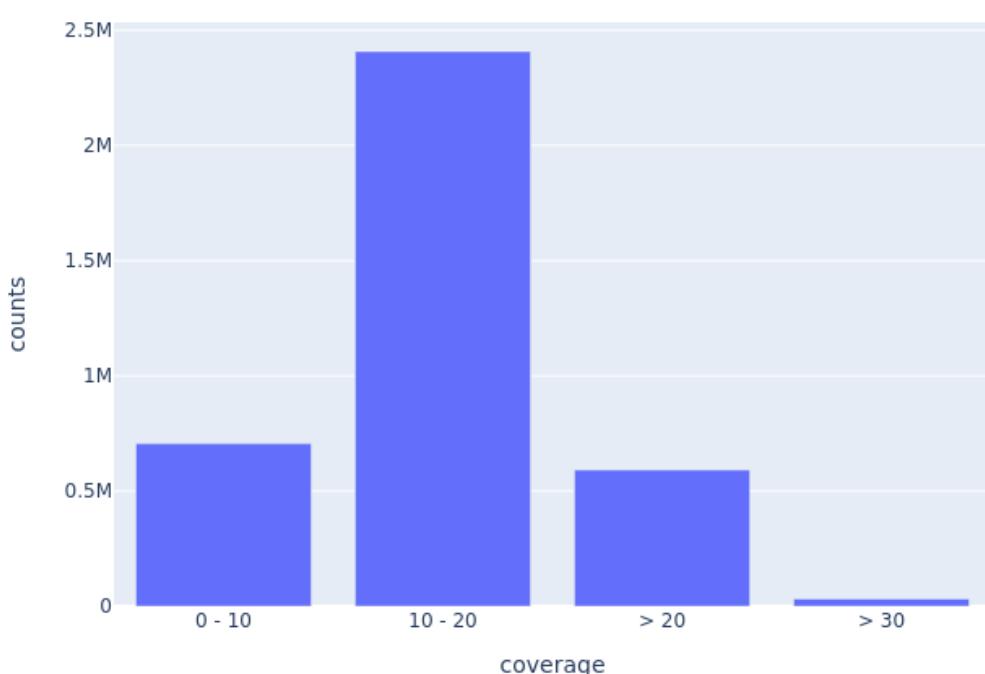
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 16.237247143600975

Microbacterium saperdae in T44.3.1

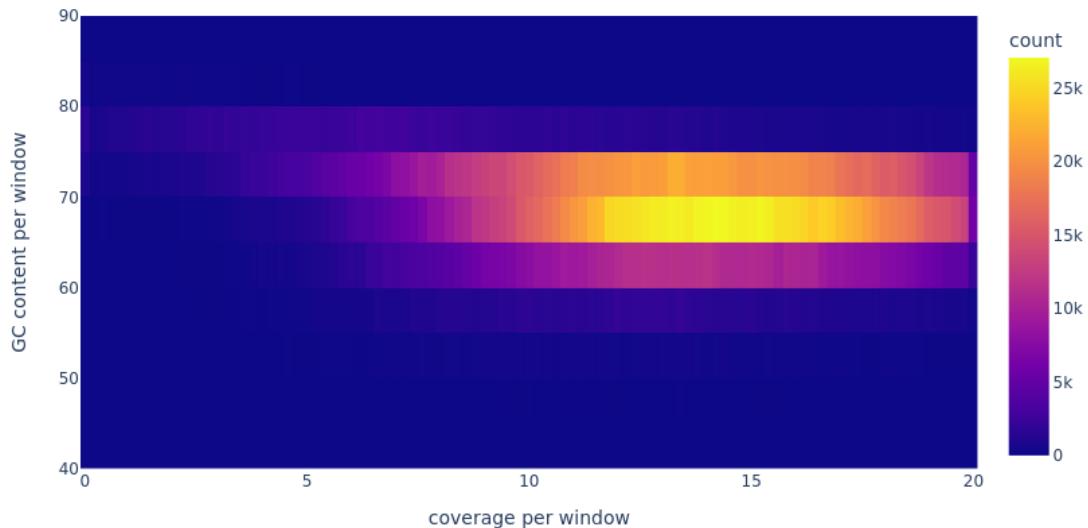


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T44.3.1



# Report of *Agrobacterium tumefaciens* in T44.3.2

## Mapping stats of Illumina reads

157419131 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

159631 + 0 supplementary

0 + 0 duplicates

153586762 + 0 mapped (97.57% : N/A)

157259500 + 0 paired in sequencing

78629750 + 0 read1

78629750 + 0 read2

152422960 + 0 properly paired (96.92% : N/A)

153351710 + 0 with itself and mate mapped

75421 + 0 singletons (0.05% : N/A)

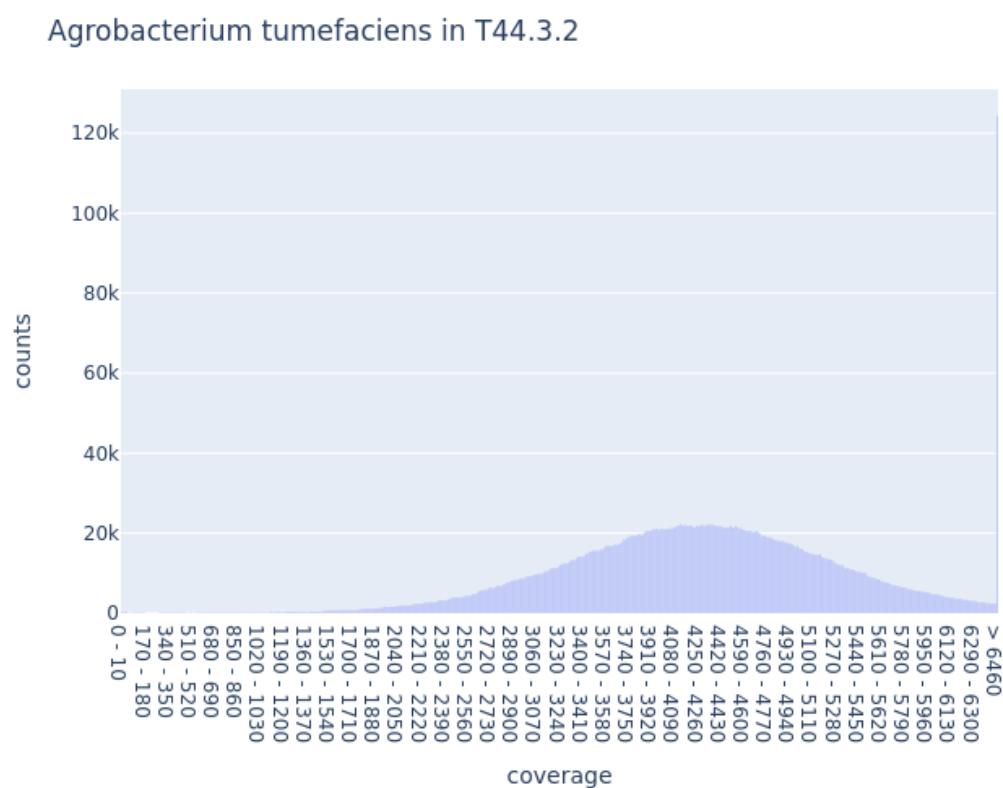
465052 + 0 with mate mapped to a different chr

447920 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

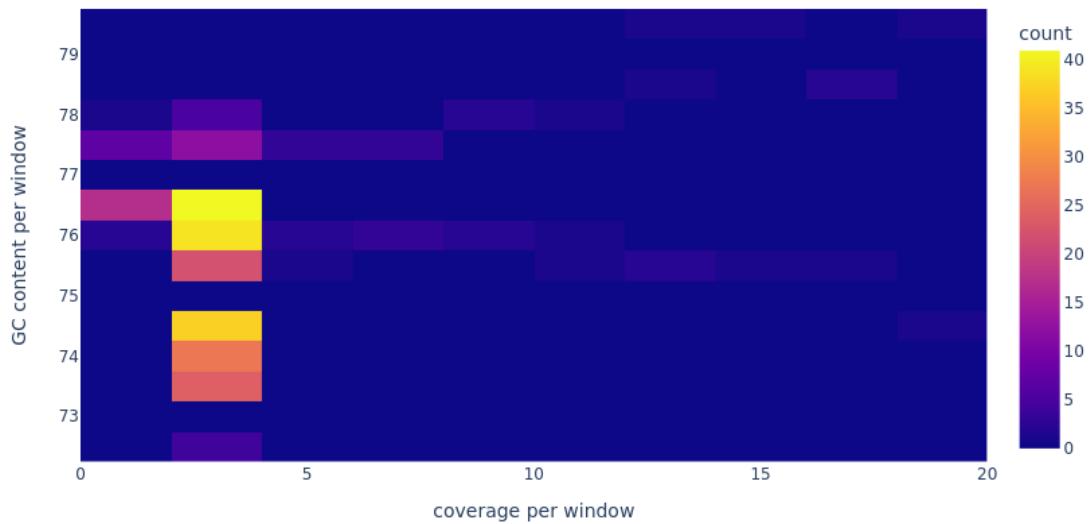
Average coverage: 4310.084908854686



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T44.3.2



# Report of Comamonas testosterone in T44.3.2

## Mapping stats of Illumina reads

157260010 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

510 + 0 supplementary

0 + 0 duplicates

3501858 + 0 mapped (2.23% : N/A)

157259500 + 0 paired in sequencing

78629750 + 0 read1

78629750 + 0 read2

3274388 + 0 properly paired (2.08% : N/A)

3276962 + 0 with itself and mate mapped

224386 + 0 singletons (0.14% : N/A)

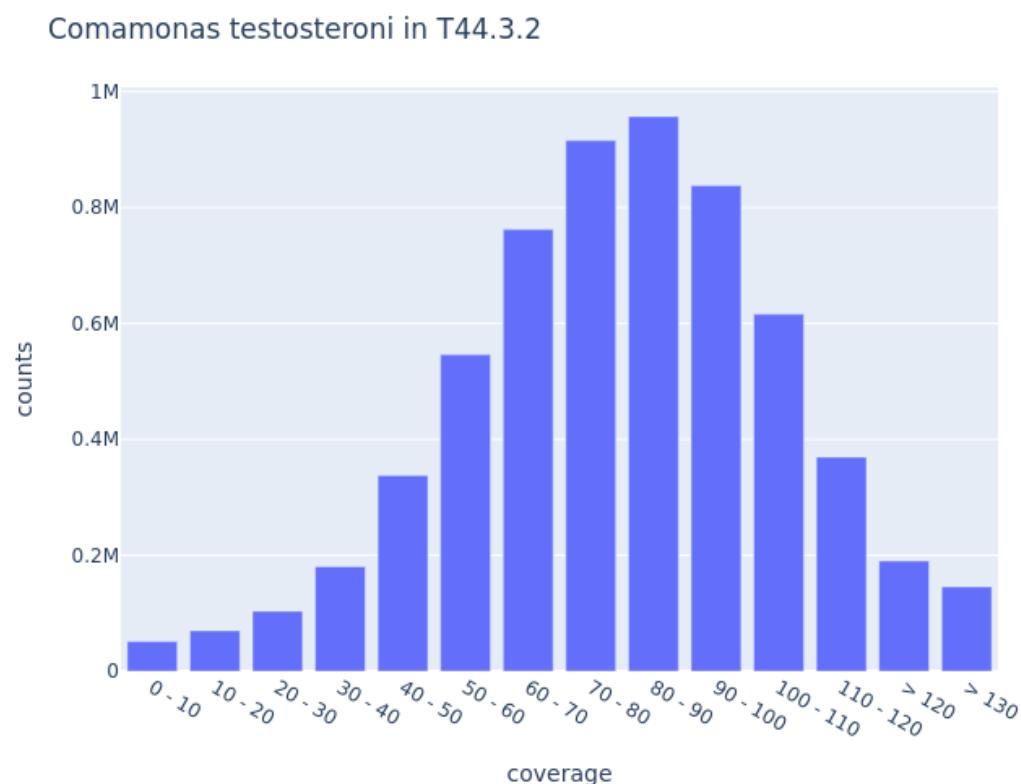
28 + 0 with mate mapped to a different chr

24 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 82.9289789232809

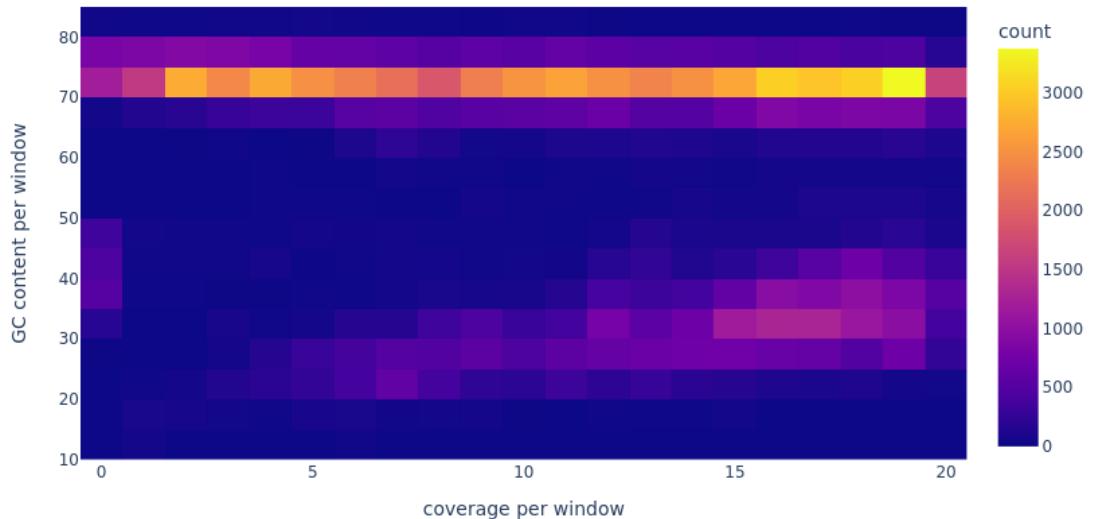


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.3.2



# Report of *Microbacterium saperdae* in T44.3.2

## Mapping stats of Illumina reads

157259595 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

95 + 0 supplementary

0 + 0 duplicates

469606 + 0 mapped (0.30% : N/A)

157259500 + 0 paired in sequencing

78629750 + 0 read1

78629750 + 0 read2

387906 + 0 properly paired (0.25% : N/A)

390068 + 0 with itself and mate mapped

79443 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

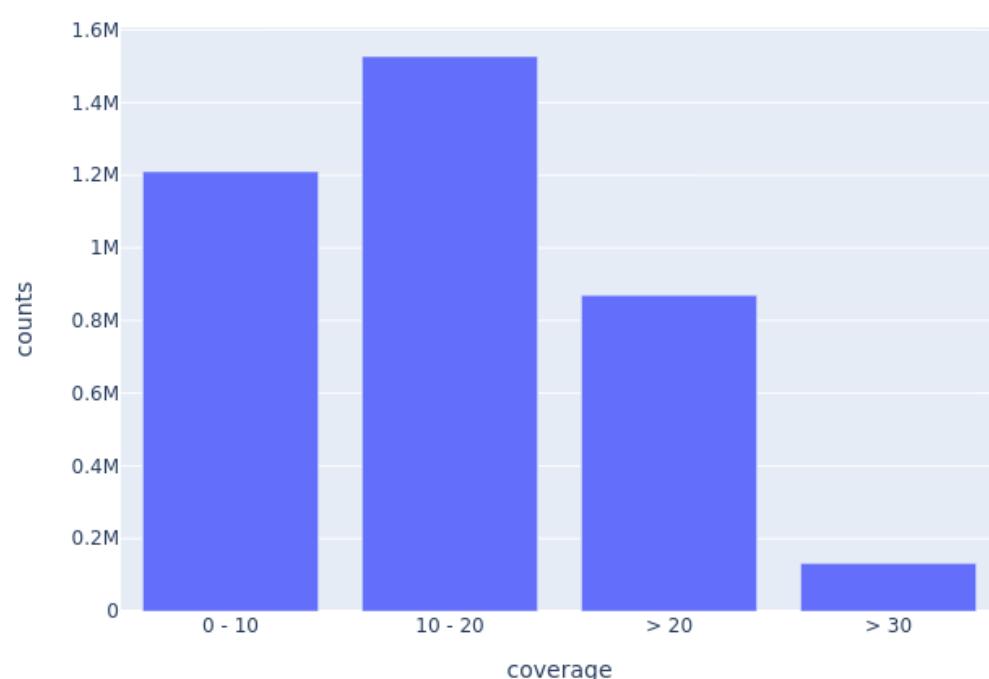
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 15.990927912949063

Microbacterium saperdae in T44.3.2

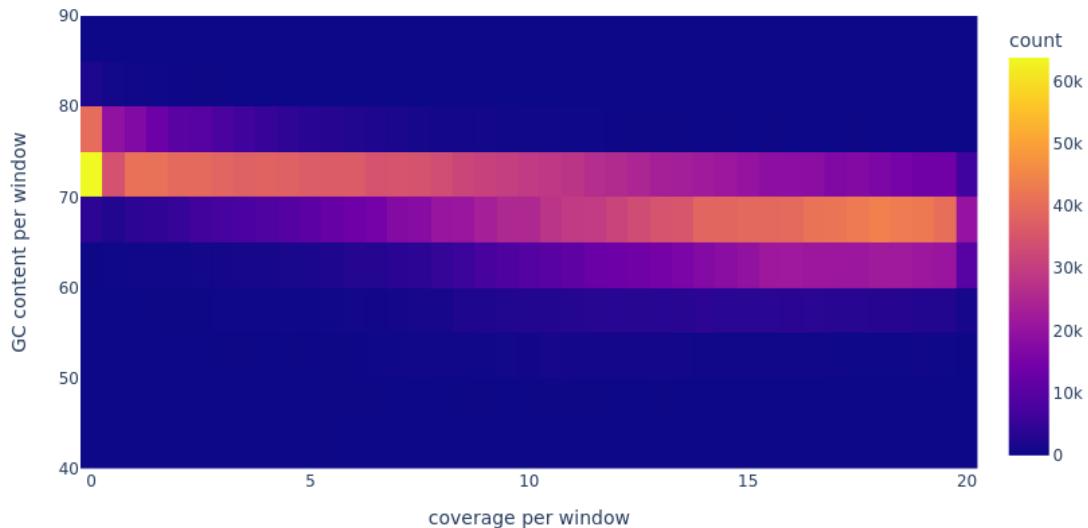


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T44.3.2



# Report of *Agrobacterium tumefaciens* in T44.3.rep

## Mapping stats of Illumina reads

192290734 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

464410 + 0 supplementary

0 + 0 duplicates

181726690 + 0 mapped (94.51% : N/A)

191826324 + 0 paired in sequencing

95913162 + 0 read1

95913162 + 0 read2

179131764 + 0 properly paired (93.38% : N/A)

181094790 + 0 with itself and mate mapped

167490 + 0 singletons (0.09% : N/A)

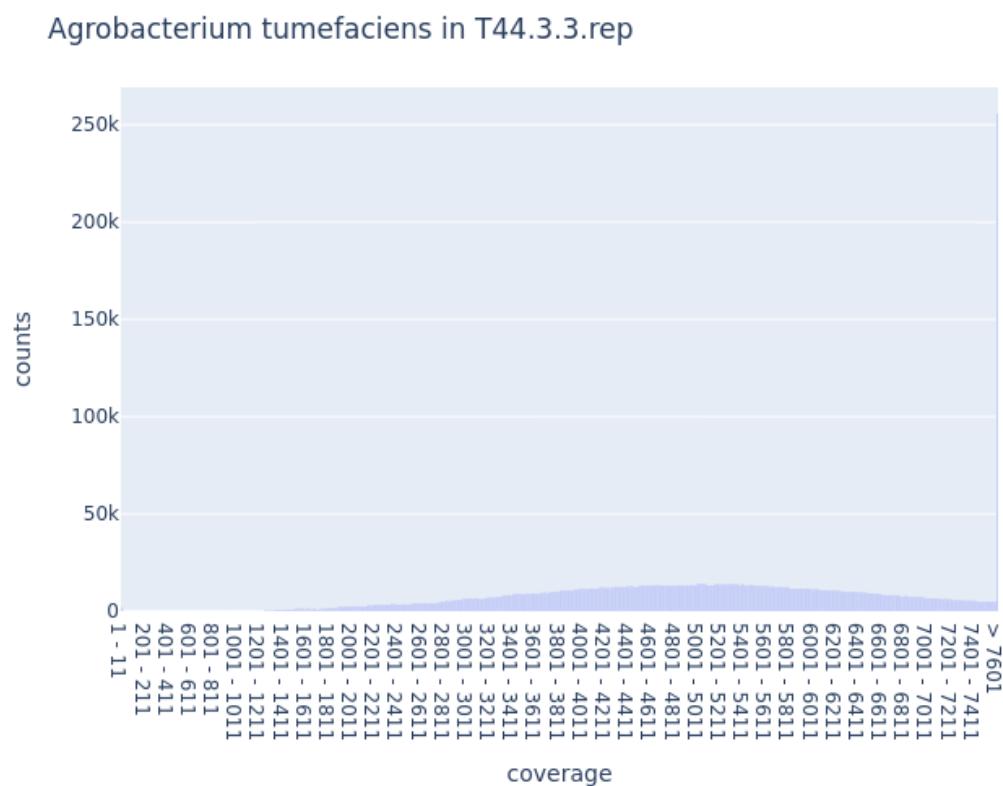
963676 + 0 with mate mapped to a different chr

932094 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

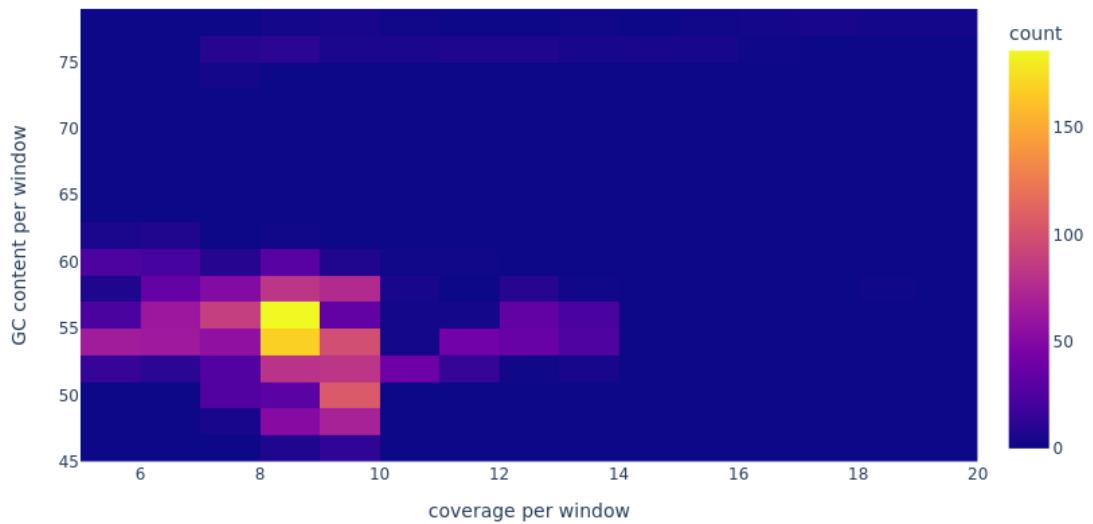
Average coverage: 5070.958349061904



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T44.3.3.rep



# Report of *Comamonas testosteronei* in T44.3.3.rep

## Mapping stats of Illumina reads

191828768 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

2444 + 0 supplementary

0 + 0 duplicates

9468760 + 0 mapped (4.94% : N/A)

191826324 + 0 paired in sequencing

95913162 + 0 read1

95913162 + 0 read2

9155984 + 0 properly paired (4.77% : N/A)

9167990 + 0 with itself and mate mapped

298326 + 0 singletons (0.16% : N/A)

146 + 0 with mate mapped to a different chr

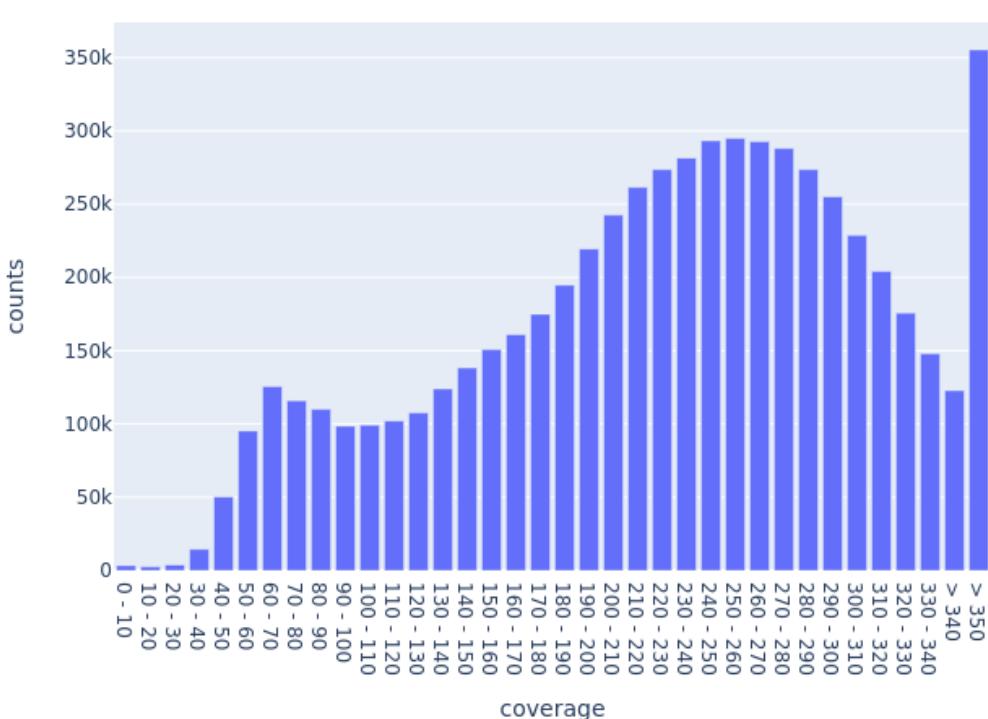
114 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 229.93267592434478

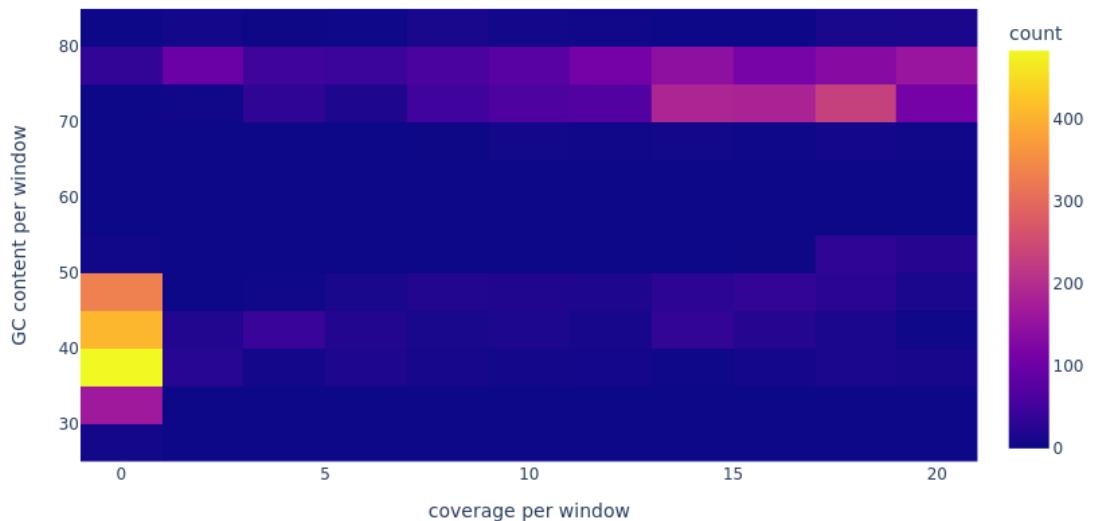
Comamonas testosteronei in T44.3.3.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.3.3.rep



# Report of *Microbacterium saperdae* in T44.3.3.rep

## Mapping stats of Illumina reads

191826498 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

174 + 0 supplementary

0 + 0 duplicates

975958 + 0 mapped (0.51% : N/A)

191826324 + 0 paired in sequencing

95913162 + 0 read1

95913162 + 0 read2

887164 + 0 properly paired (0.46% : N/A)

889778 + 0 with itself and mate mapped

86006 + 0 singletons (0.04% : N/A)

0 + 0 with mate mapped to a different chr

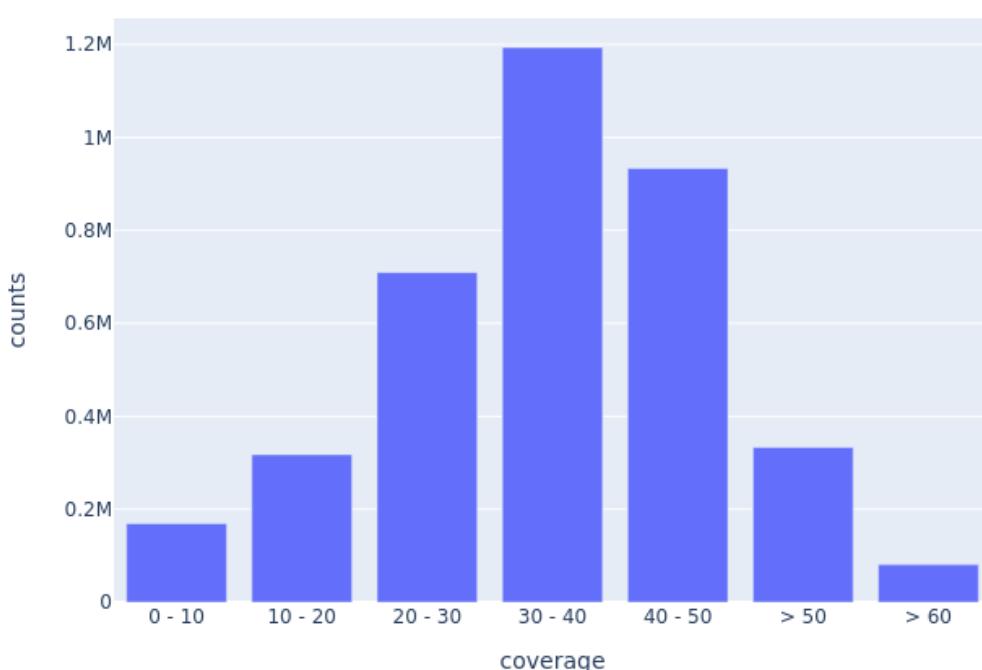
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 36.35619487140519

Microbacterium saperdae in T44.3.3.rep

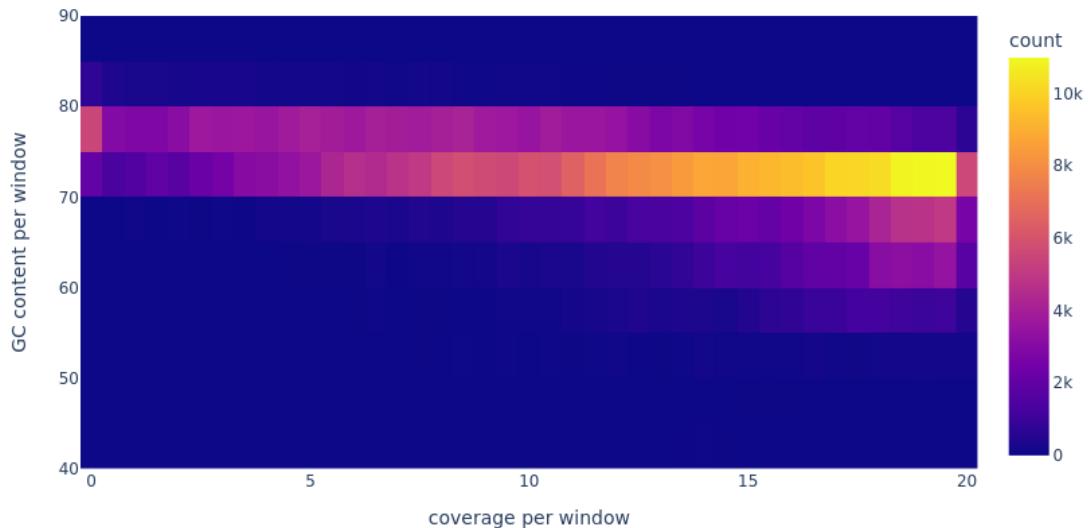


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T44.3.3.rep



# Report of *Agrobacterium tumefaciens* in T44.3.4

## Mapping stats of Illumina reads

199813744 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

145382 + 0 supplementary

0 + 0 duplicates

191111841 + 0 mapped (95.64% : N/A)

199668362 + 0 paired in sequencing

99834181 + 0 read1

99834181 + 0 read2

189916476 + 0 properly paired (95.12% : N/A)

190852056 + 0 with itself and mate mapped

114403 + 0 singletons (0.06% : N/A)

430556 + 0 with mate mapped to a different chr

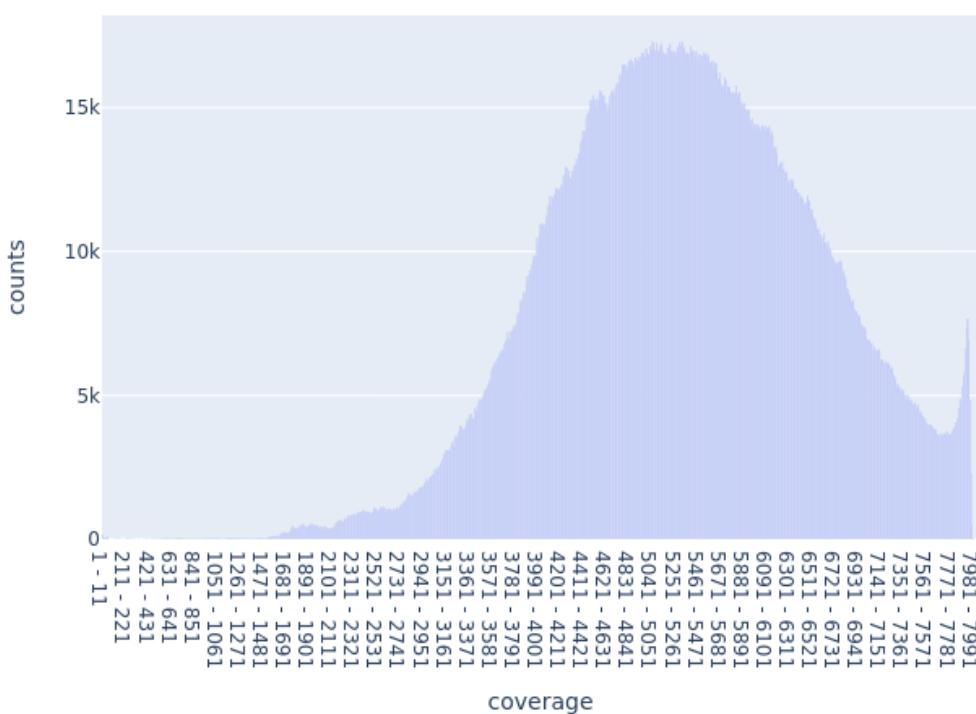
410002 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

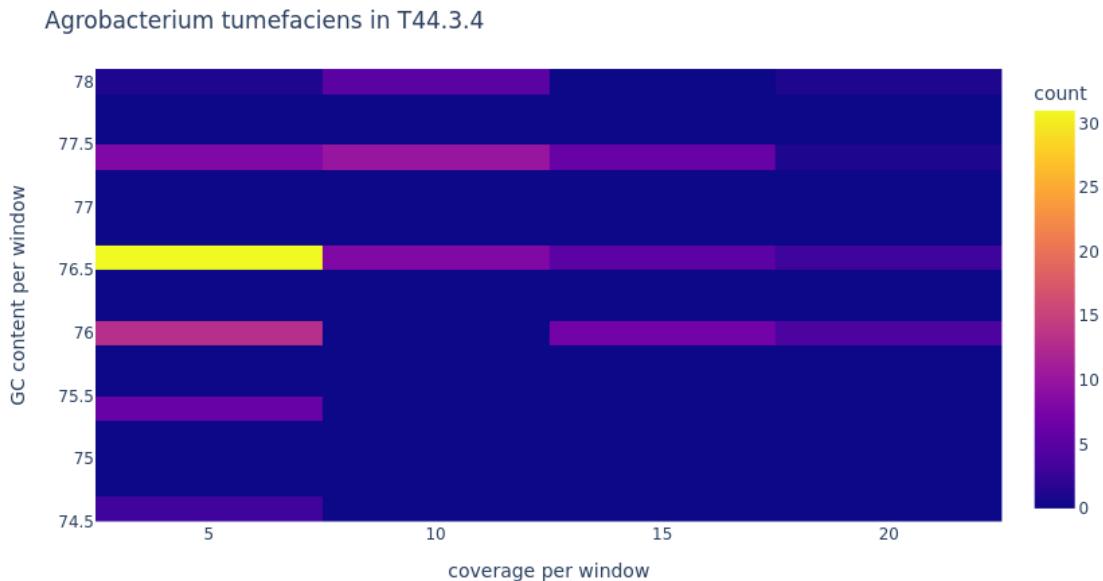
Average coverage: 5359.061823145613

Agrobacterium tumefaciens in T44.3.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.



# Report of Comamonas testosterone in T44.3.4

## Mapping stats of Illumina reads

199669259 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

897 + 0 supplementary

0 + 0 duplicates

8027741 + 0 mapped (4.02% : N/A)

199668362 + 0 paired in sequencing

99834181 + 0 read1

99834181 + 0 read2

7730794 + 0 properly paired (3.87% : N/A)

7737500 + 0 with itself and mate mapped

289344 + 0 singletons (0.14% : N/A)

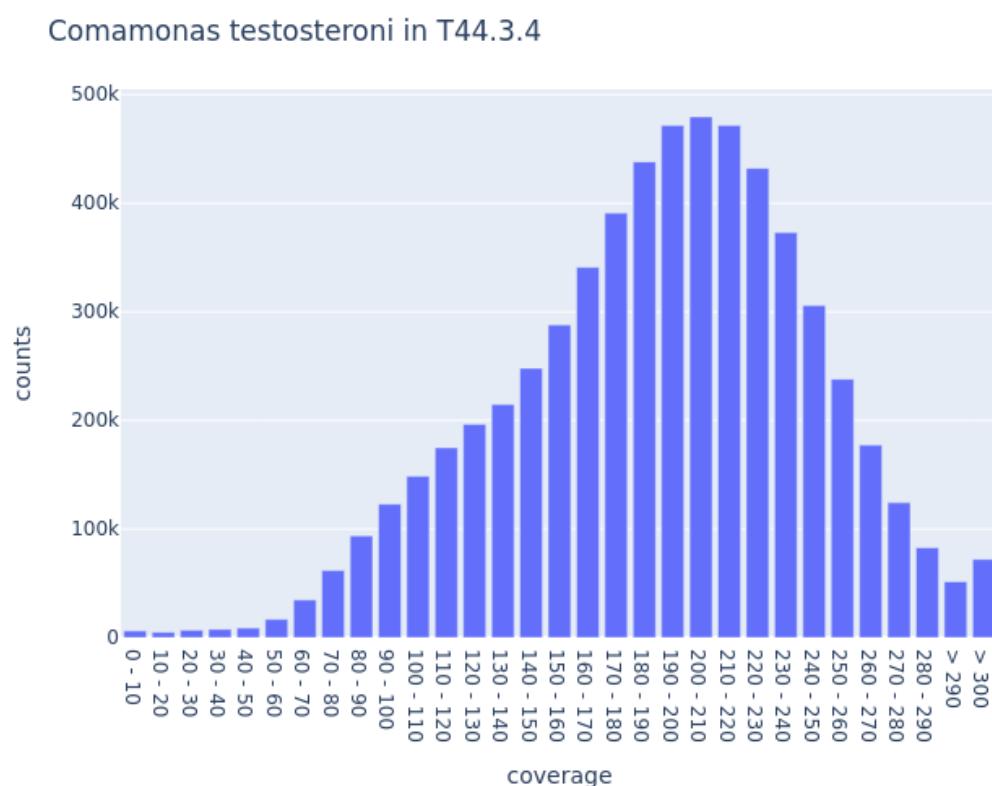
124 + 0 with mate mapped to a different chr

86 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

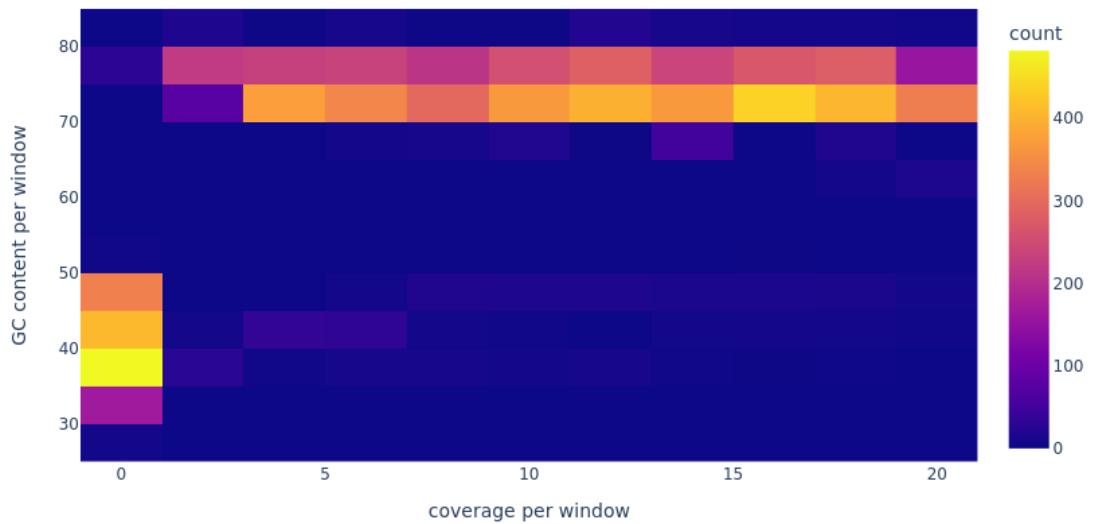
Average coverage: 194.00946356011636



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.3.4



# Report of *Microbacterium saperdae* in T44.3.4

## Mapping stats of Illumina reads

199668409 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

47 + 0 supplementary

0 + 0 duplicates

645564 + 0 mapped (0.32% : N/A)

199668362 + 0 paired in sequencing

99834181 + 0 read1

99834181 + 0 read2

547728 + 0 properly paired (0.27% : N/A)

550180 + 0 with itself and mate mapped

95337 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

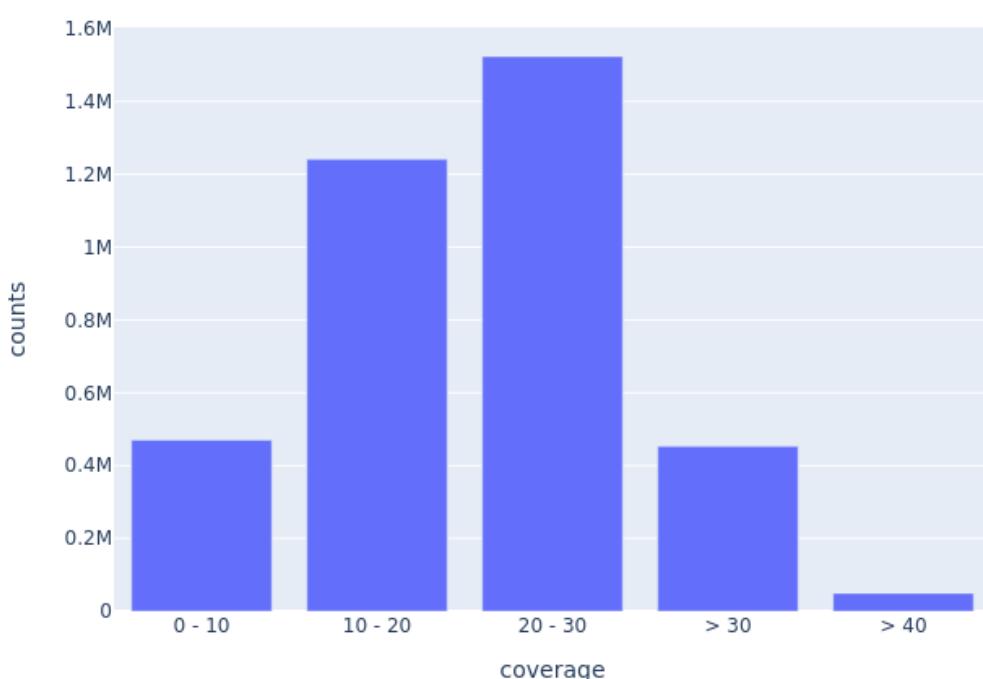
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 22.482845284339533

Microbacterium saperdae in T44.3.4

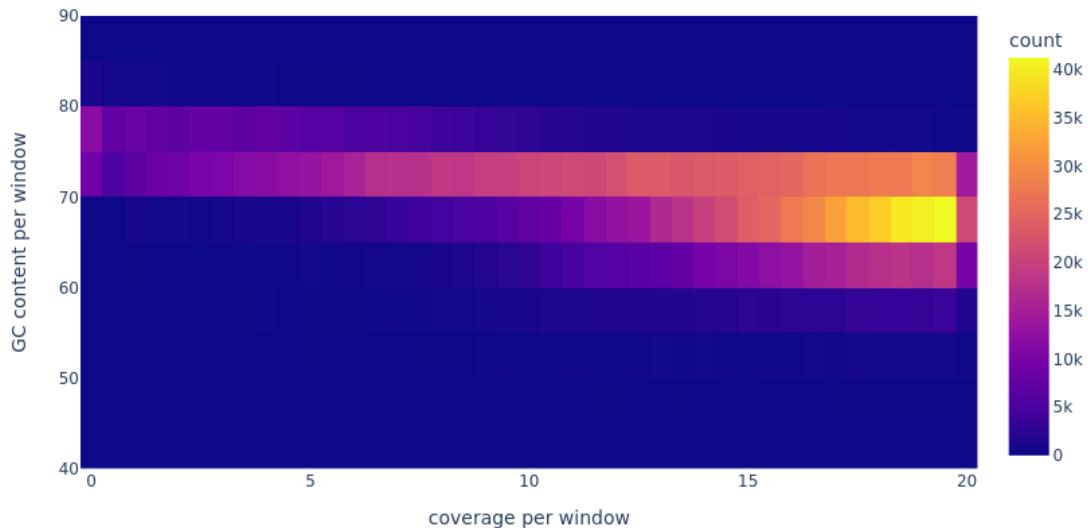


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T44.3.4



# Report of *Agrobacterium tumefaciens* in T44.3.5

## Mapping stats of Illumina reads

175059727 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

85687 + 0 supplementary

0 + 0 duplicates

167375120 + 0 mapped (95.61% : N/A)

174974040 + 0 paired in sequencing

87487020 + 0 read1

87487020 + 0 read2

166444150 + 0 properly paired (95.13% : N/A)

167180026 + 0 with itself and mate mapped

109407 + 0 singletons (0.06% : N/A)

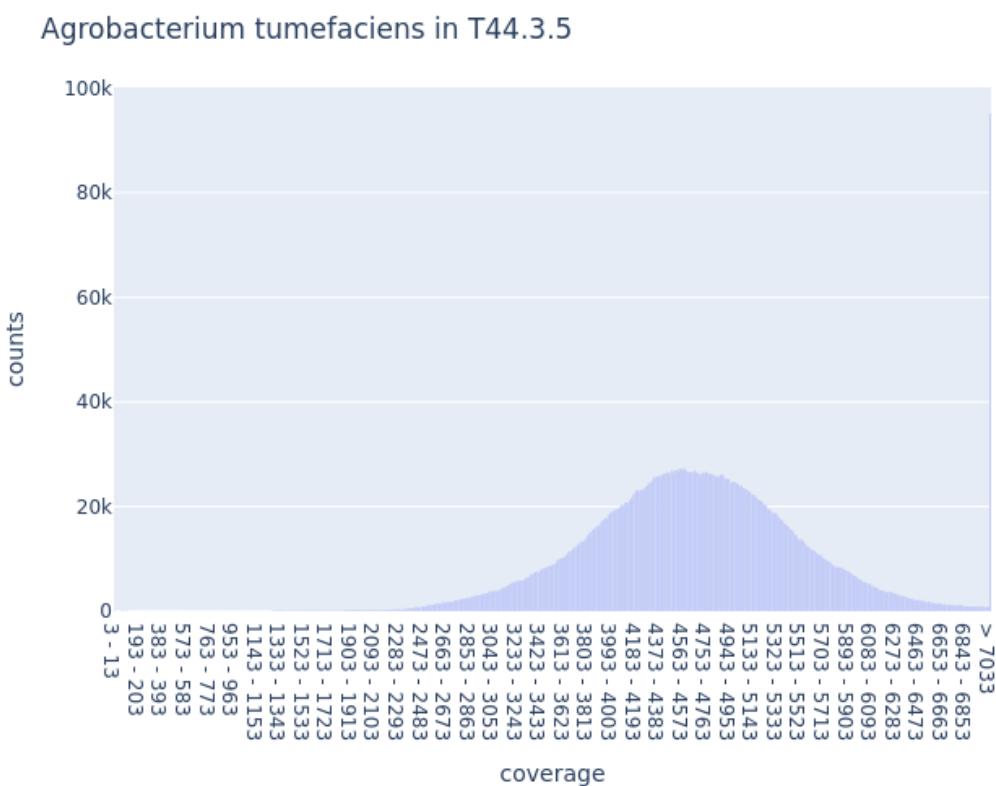
342140 + 0 with mate mapped to a different chr

330231 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 4694.553141628932

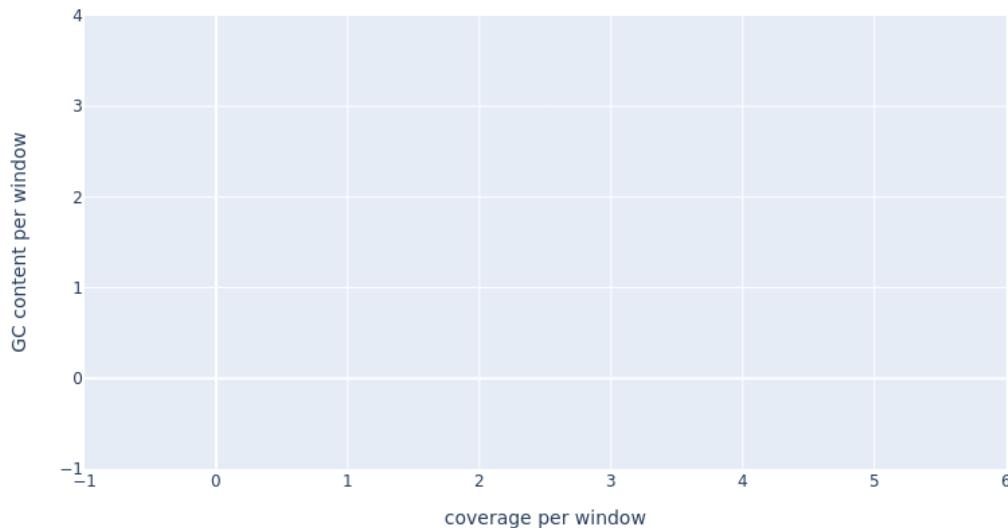


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T44.3.5



# Report of Comamonas testosterone in T44.3.5

## Mapping stats of Illumina reads

174974728 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

688 + 0 supplementary

0 + 0 duplicates

6360125 + 0 mapped (3.63% : N/A)

174974040 + 0 paired in sequencing

87487020 + 0 read1

87487020 + 0 read2

6103260 + 0 properly paired (3.49% : N/A)

6107972 + 0 with itself and mate mapped

251465 + 0 singletons (0.14% : N/A)

40 + 0 with mate mapped to a different chr

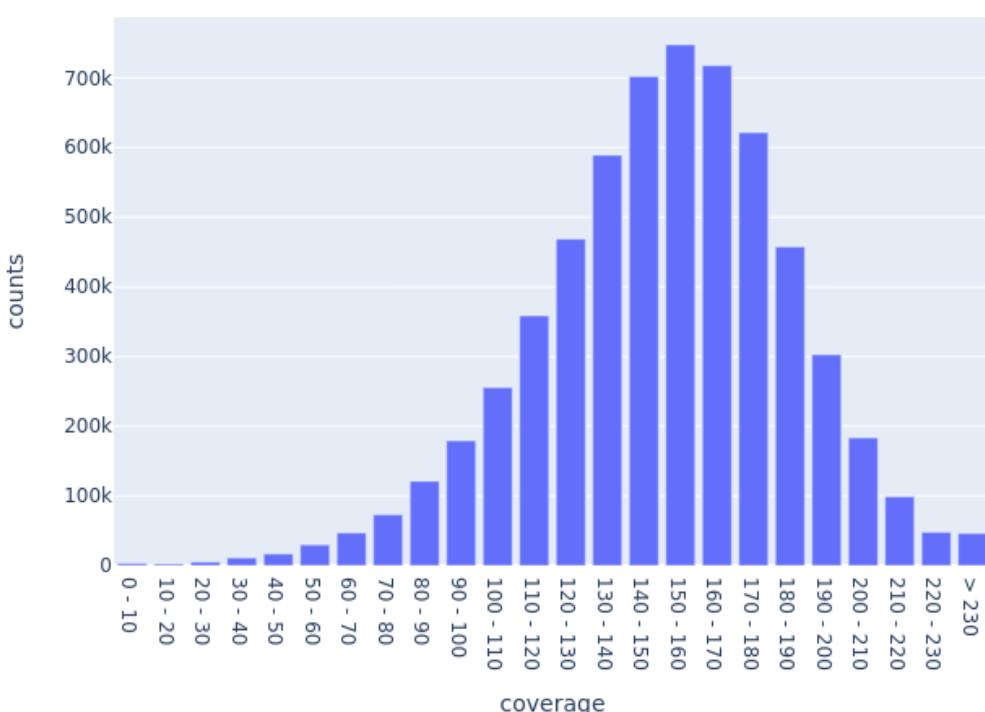
37 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 153.38563415796256

Comamonas testosterone in T44.3.5

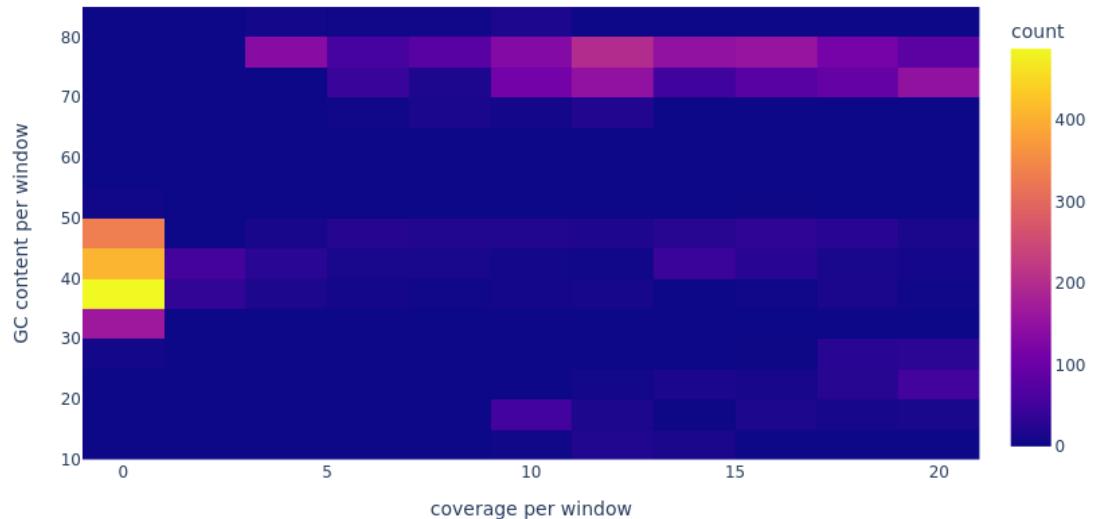


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.3.5



# Report of *Microbacterium saperdae* in T44.3.5

## Mapping stats of Illumina reads

174974178 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

138 + 0 supplementary

0 + 0 duplicates

1057210 + 0 mapped (0.60% : N/A)

174974040 + 0 paired in sequencing

87487020 + 0 read1

87487020 + 0 read2

967558 + 0 properly paired (0.55% : N/A)

970170 + 0 with itself and mate mapped

86902 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

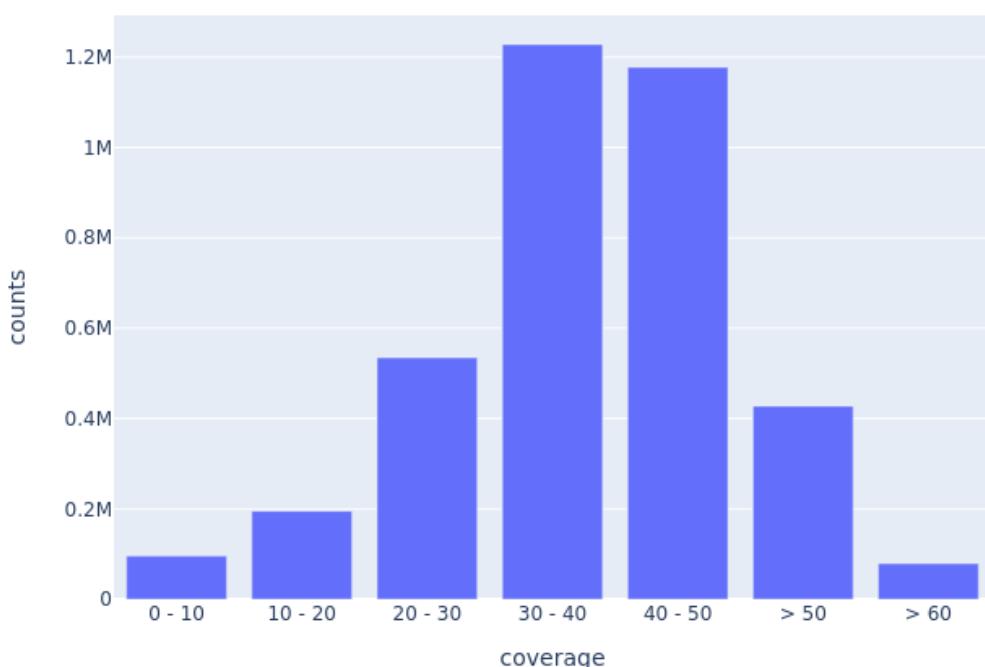
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 39.47370068694851

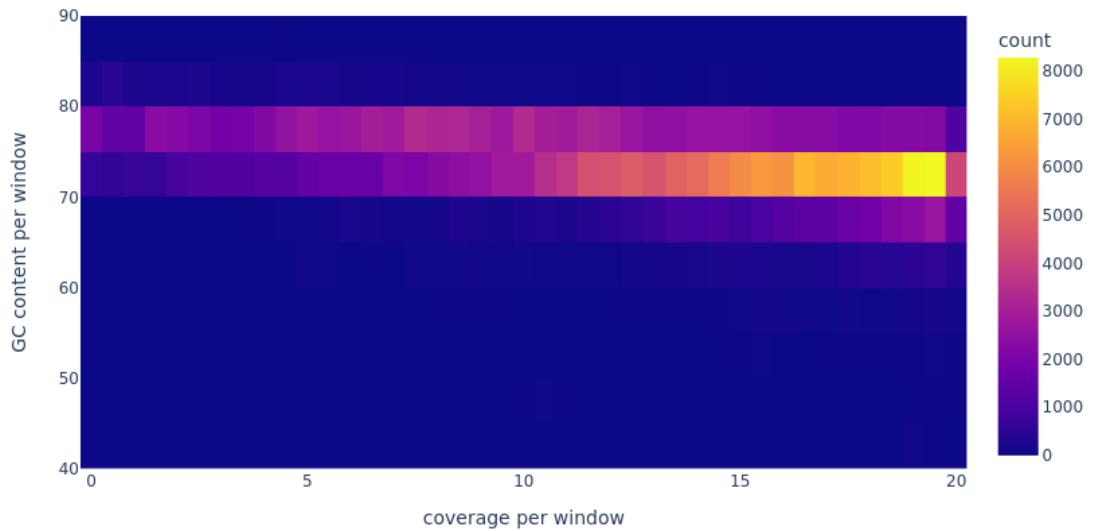
Microbacterium saperdae in T44.3.5



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T44.3.5



# Report of *Agrobacterium tumefaciens* in T44.4.1

## Mapping stats of Illumina reads

181182611 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

374635 + 0 supplementary

0 + 0 duplicates

169835301 + 0 mapped (93.74% : N/A)

180807976 + 0 paired in sequencing

90403988 + 0 read1

90403988 + 0 read2

168277240 + 0 properly paired (93.07% : N/A)

169323066 + 0 with itself and mate mapped

137600 + 0 singletons (0.08% : N/A)

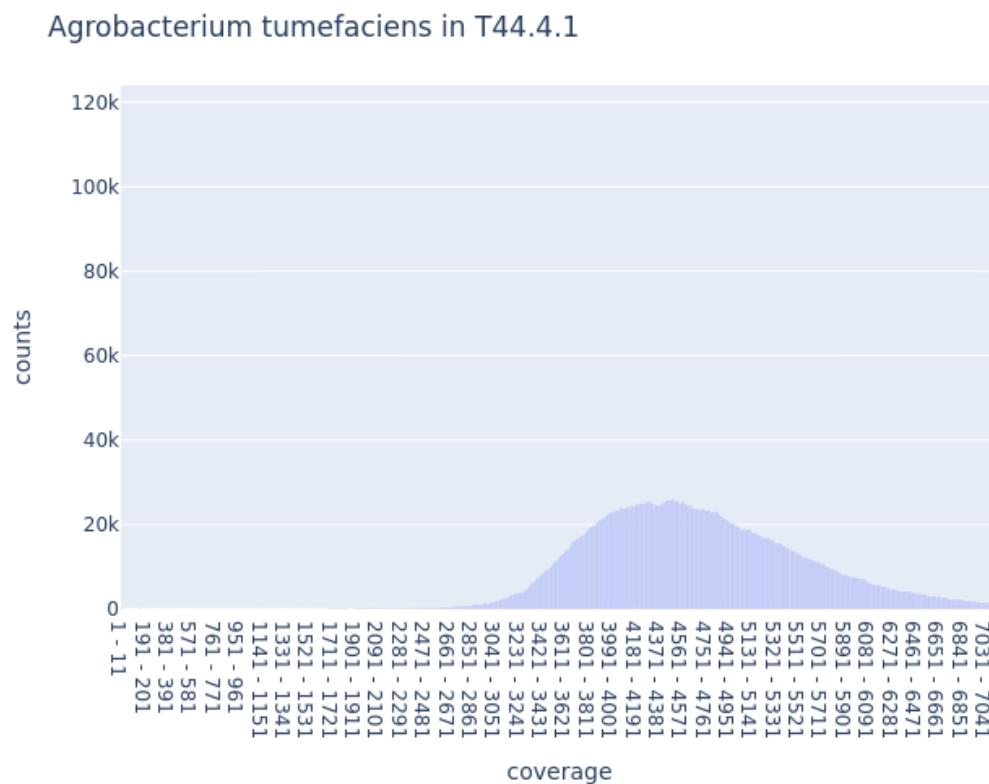
390616 + 0 with mate mapped to a different chr

373962 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

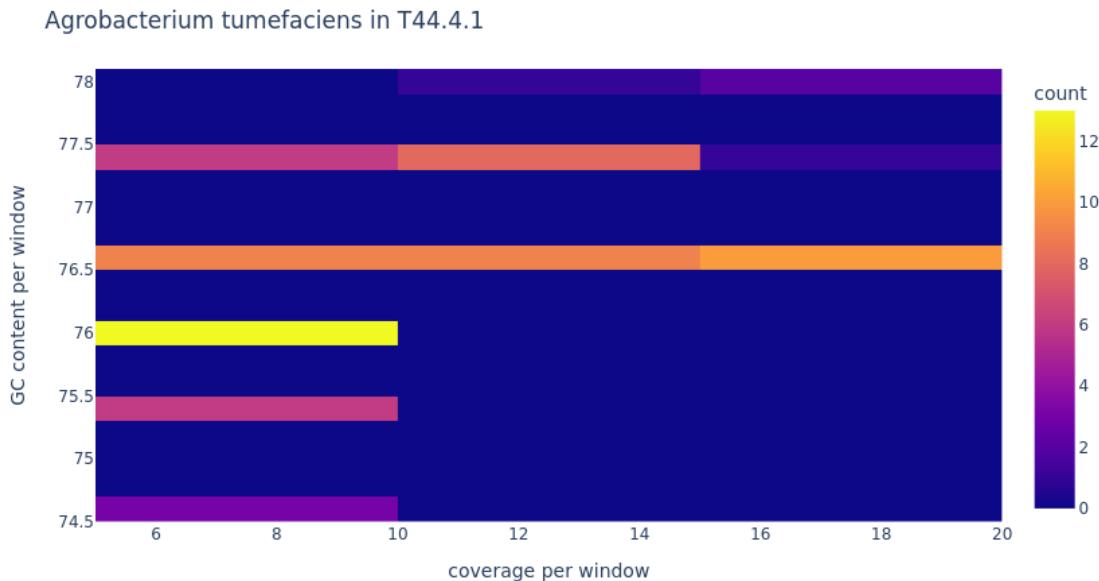
This plots shows the coverage per position in the genome.

Average coverage: 4753.510819293539



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.



# Report of Comamonas testosterone in T44.4.1

## Mapping stats of Illumina reads

180810270 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

2294 + 0 supplementary

0 + 0 duplicates

8691974 + 0 mapped (4.81% : N/A)

180807976 + 0 paired in sequencing

90403988 + 0 read1

90403988 + 0 read2

8440012 + 0 properly paired (4.67% : N/A)

8458632 + 0 with itself and mate mapped

231048 + 0 singletons (0.13% : N/A)

136 + 0 with mate mapped to a different chr

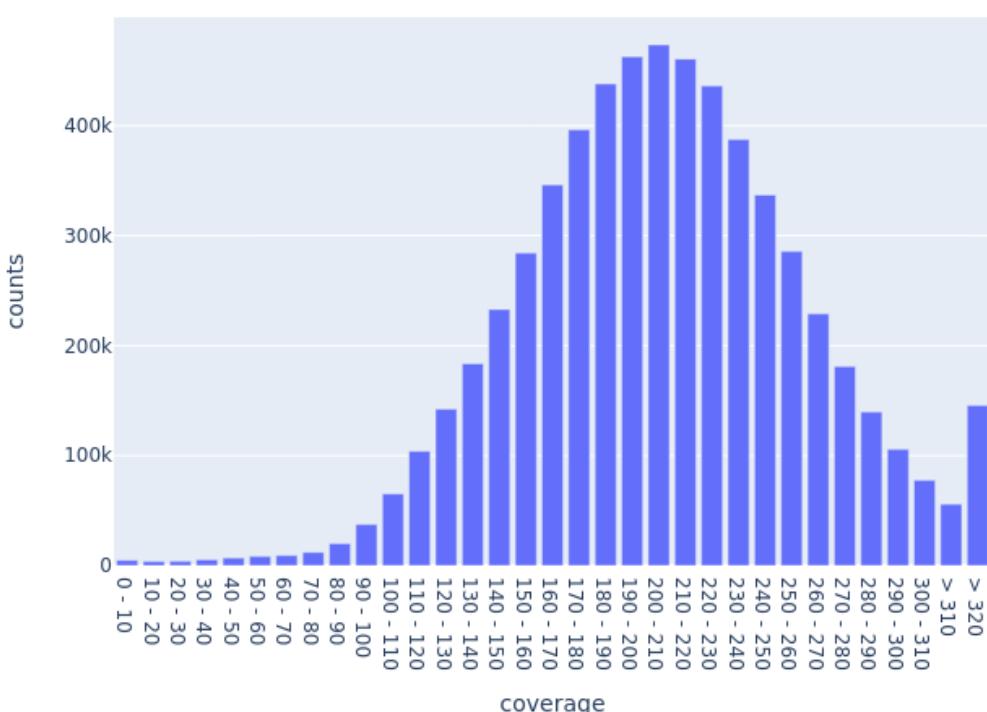
111 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 210.48596383762975

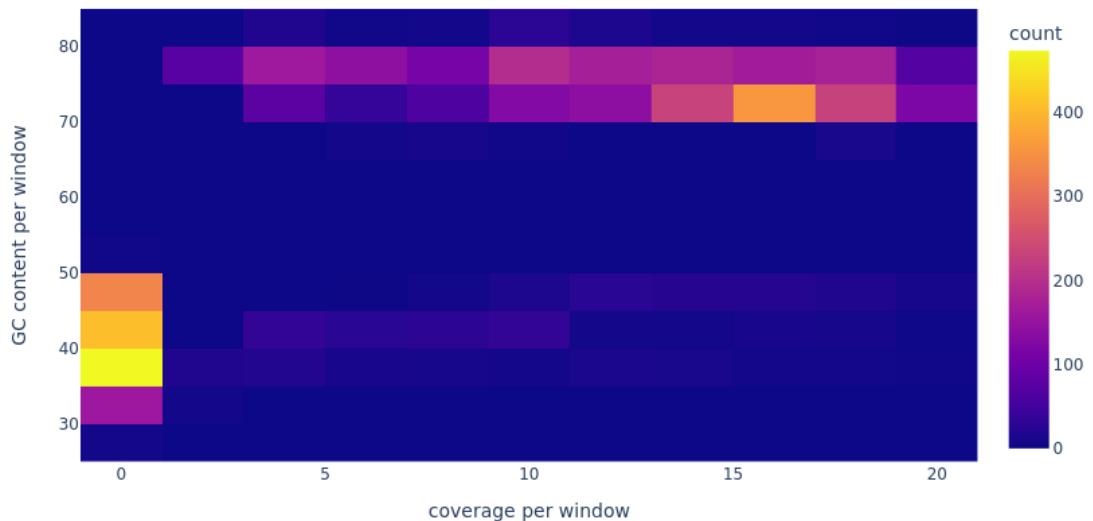
Comamonas testosterone in T44.4.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.4.1



# Report of *Microbacterium saperdae* in T44.4.1

## Mapping stats of Illumina reads

180808007 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

31 + 0 supplementary

0 + 0 duplicates

158005 + 0 mapped (0.09% : N/A)

180807976 + 0 paired in sequencing

90403988 + 0 read1

90403988 + 0 read2

84852 + 0 properly paired (0.05% : N/A)

87210 + 0 with itself and mate mapped

70764 + 0 singletons (0.04% : N/A)

0 + 0 with mate mapped to a different chr

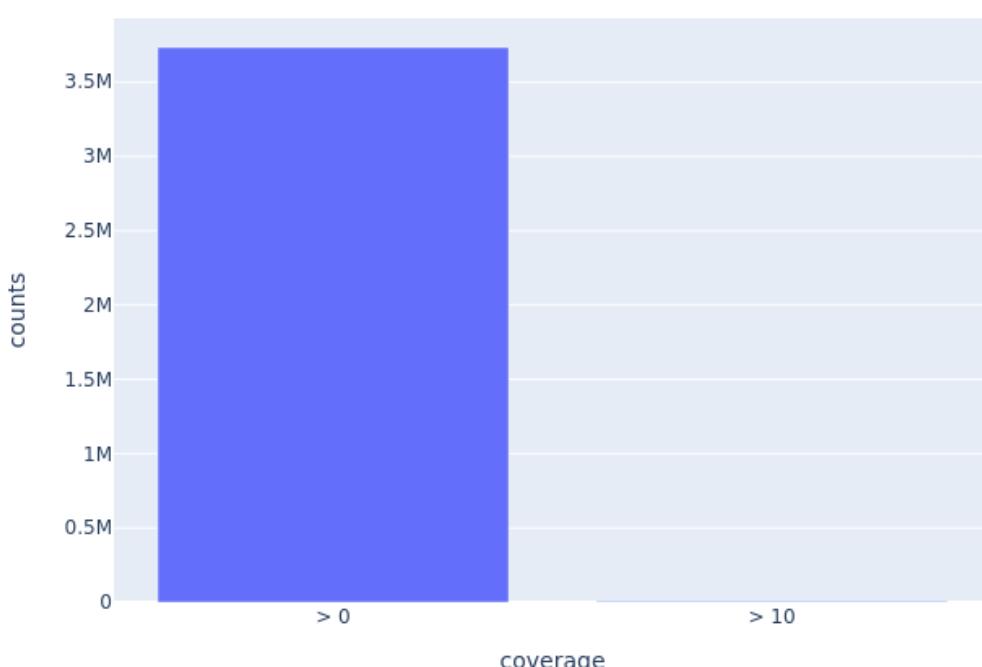
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 2.8821583893393212

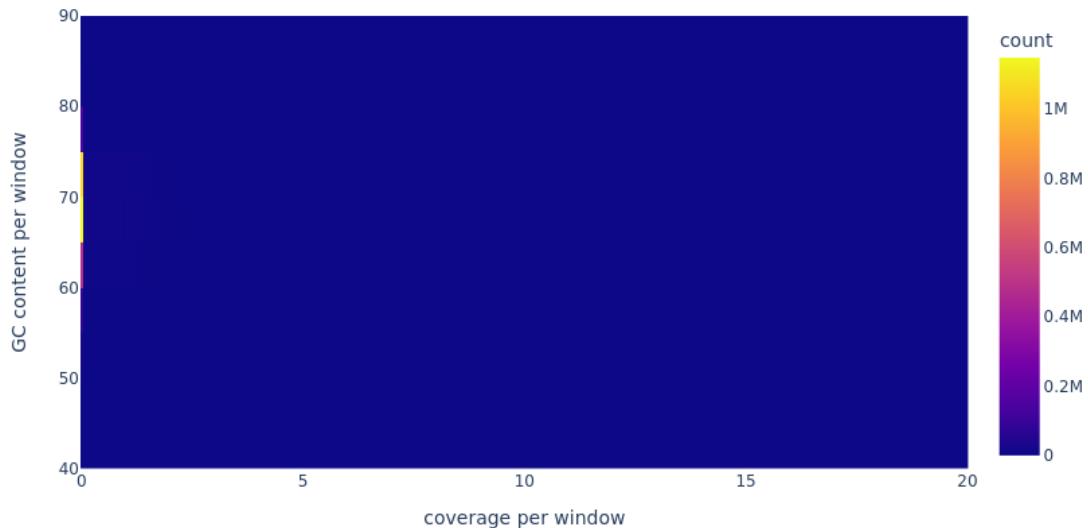
Microbacterium saperdae in T44.4.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T44.4.1



# Report of *Ochrobactrum anthropi* in T44.4.1

## Mapping stats of Illumina reads

180812822 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

4846 + 0 supplementary

0 + 0 duplicates

5282904 + 0 mapped (2.92% : N/A)

180807976 + 0 paired in sequencing

90403988 + 0 read1

90403988 + 0 read2

3969044 + 0 properly paired (2.20% : N/A)

4028214 + 0 with itself and mate mapped

1249844 + 0 singletons (0.69% : N/A)

28988 + 0 with mate mapped to a different chr

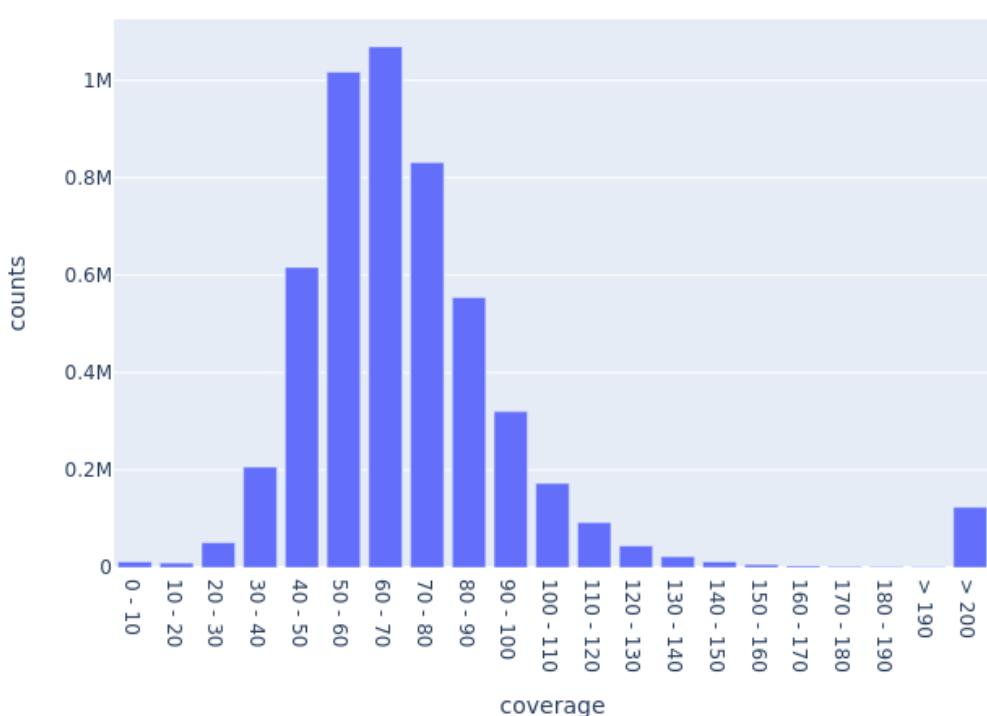
19769 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 127.3990720635415

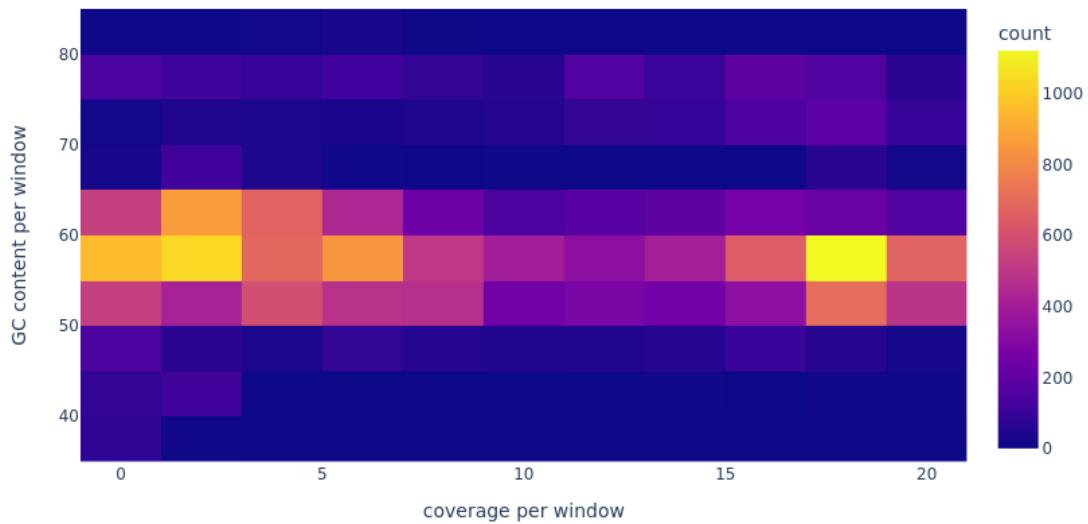
Ochrobactrum anthropi in T44.4.1



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T44.4.1



# Report of *Agrobacterium tumefaciens* in T44.4.2

## Mapping stats of Illumina reads

181332486 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

138362 + 0 supplementary

0 + 0 duplicates

175505041 + 0 mapped (96.79% : N/A)

181194124 + 0 paired in sequencing

90597062 + 0 read1

90597062 + 0 read2

174373092 + 0 properly paired (96.24% : N/A)

175249802 + 0 with itself and mate mapped

116877 + 0 singletons (0.06% : N/A)

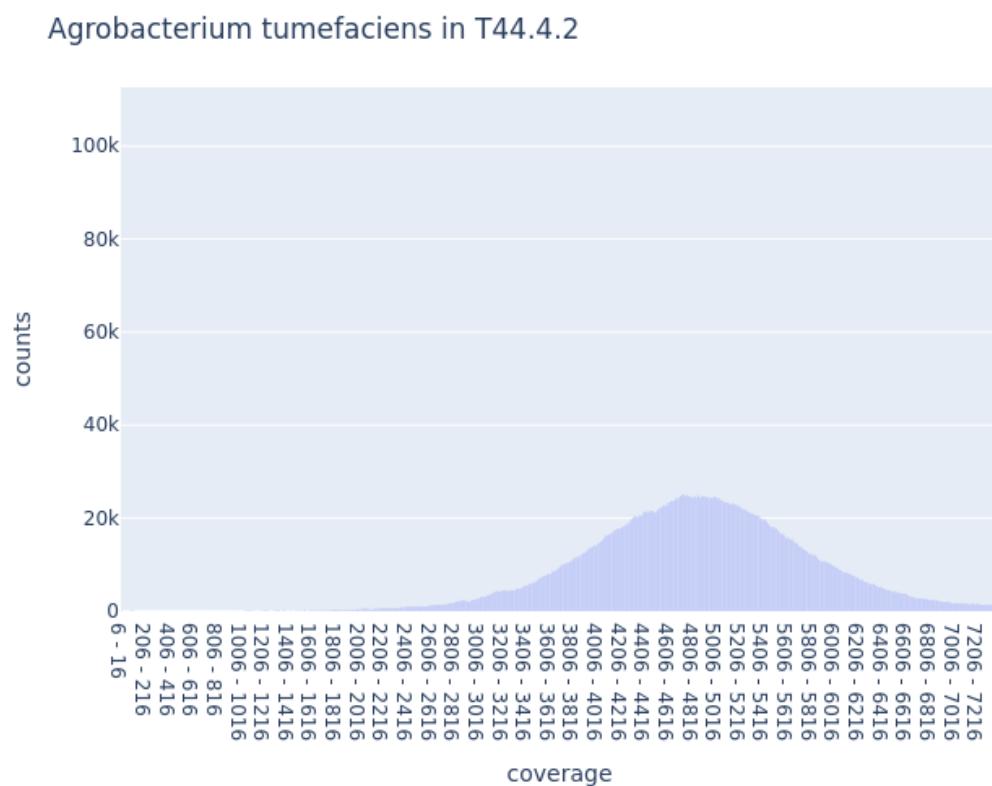
434788 + 0 with mate mapped to a different chr

418202 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 4913.771897676135

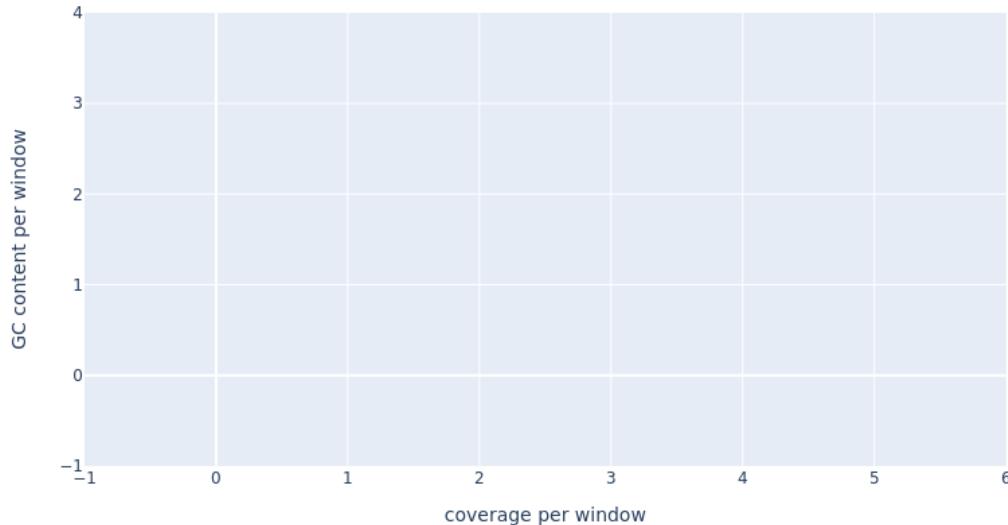


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T44.4.2



# Report of Comamonas testosterone in T44.4.2

## Mapping stats of Illumina reads

181194791 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

667 + 0 supplementary

0 + 0 duplicates

4352732 + 0 mapped (2.40% : N/A)

181194124 + 0 paired in sequencing

90597062 + 0 read1

90597062 + 0 read2

4100254 + 0 properly paired (2.26% : N/A)

4103358 + 0 with itself and mate mapped

248707 + 0 singletons (0.14% : N/A)

58 + 0 with mate mapped to a different chr

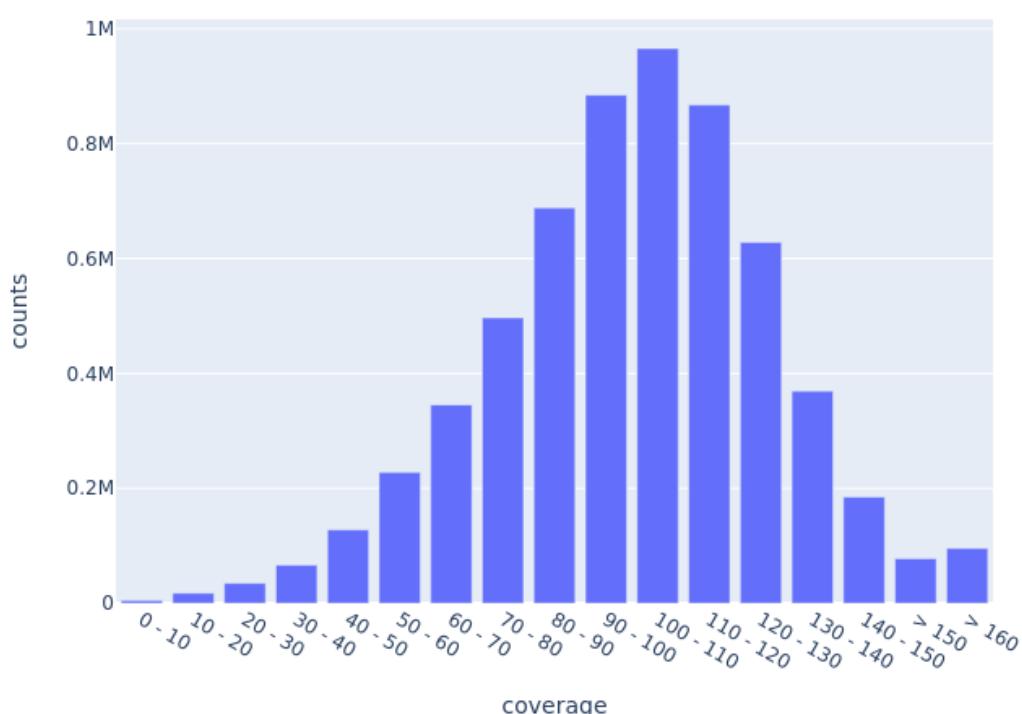
48 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 103.62697992288793

Comamonas testosterone in T44.4.2

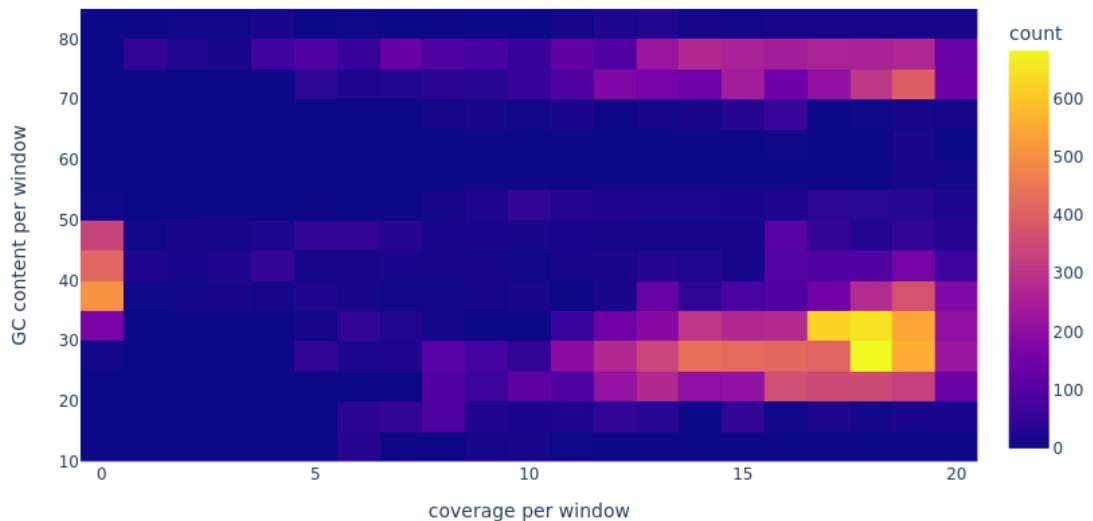


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.4.2



# Report of *Microbacterium saperdae* in T44.4.2

## Mapping stats of Illumina reads

181194191 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

67 + 0 supplementary

0 + 0 duplicates

414175 + 0 mapped (0.23% : N/A)

181194124 + 0 paired in sequencing

90597062 + 0 read1

90597062 + 0 read2

328676 + 0 properly paired (0.18% : N/A)

330744 + 0 with itself and mate mapped

83364 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

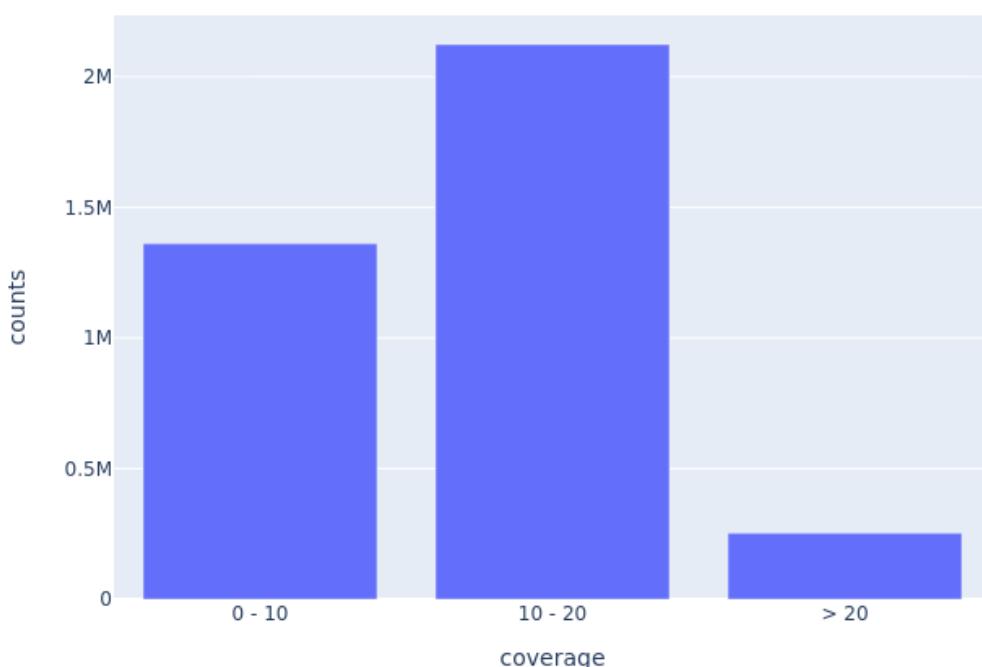
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 13.61470841478483

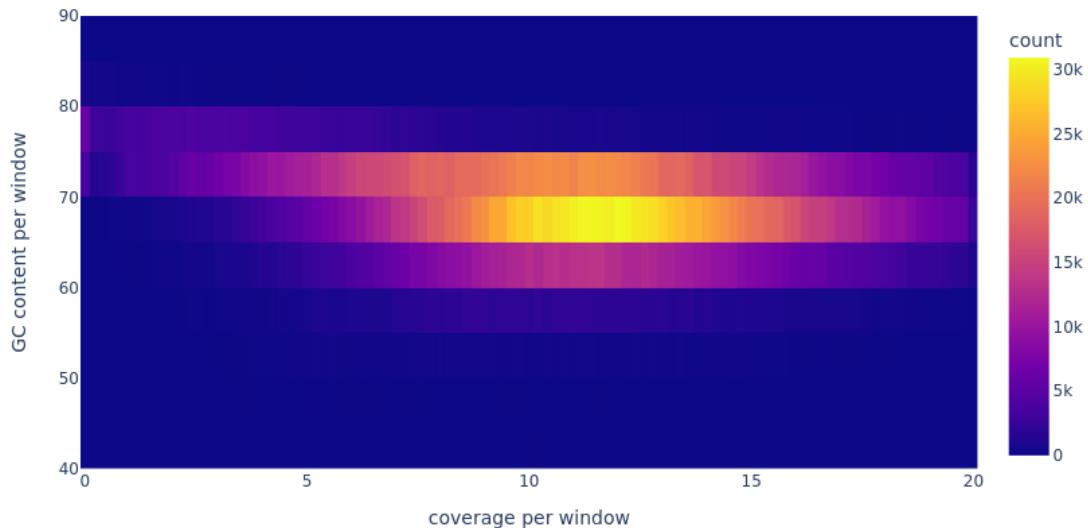
Microbacterium saperdae in T44.4.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T44.4.2



# Report of *Ochrobactrum anthropi* in T44.4.2

## Mapping stats of Illumina reads

181197855 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

3731 + 0 supplementary

0 + 0 duplicates

4054926 + 0 mapped (2.24% : N/A)

181194124 + 0 paired in sequencing

90597062 + 0 read1

90597062 + 0 read2

2486780 + 0 properly paired (1.37% : N/A)

2525736 + 0 with itself and mate mapped

1525459 + 0 singletons (0.84% : N/A)

25036 + 0 with mate mapped to a different chr

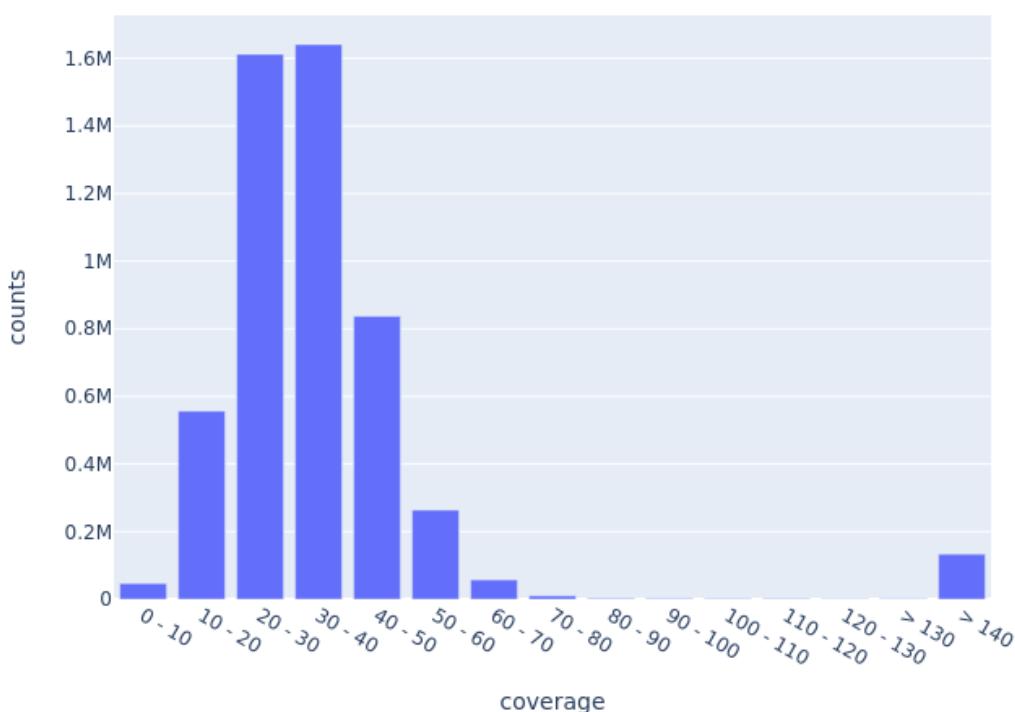
16897 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 91.74495926616224

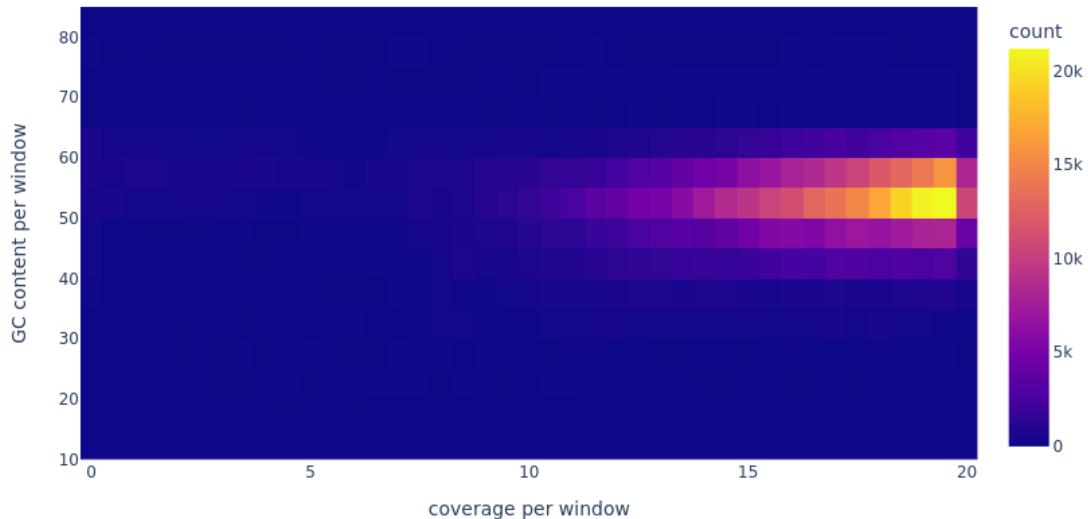
Ochrobactrum anthropi in T44.4.2



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T44.4.2



# Report of *Agrobacterium tumefaciens* in T44.4.3

## Mapping stats of Illumina reads

176305958 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

210374 + 0 supplementary

0 + 0 duplicates

169413654 + 0 mapped (96.09% : N/A)

176095584 + 0 paired in sequencing

88047792 + 0 read1

88047792 + 0 read2

167929388 + 0 properly paired (95.36% : N/A)

169091882 + 0 with itself and mate mapped

111398 + 0 singletons (0.06% : N/A)

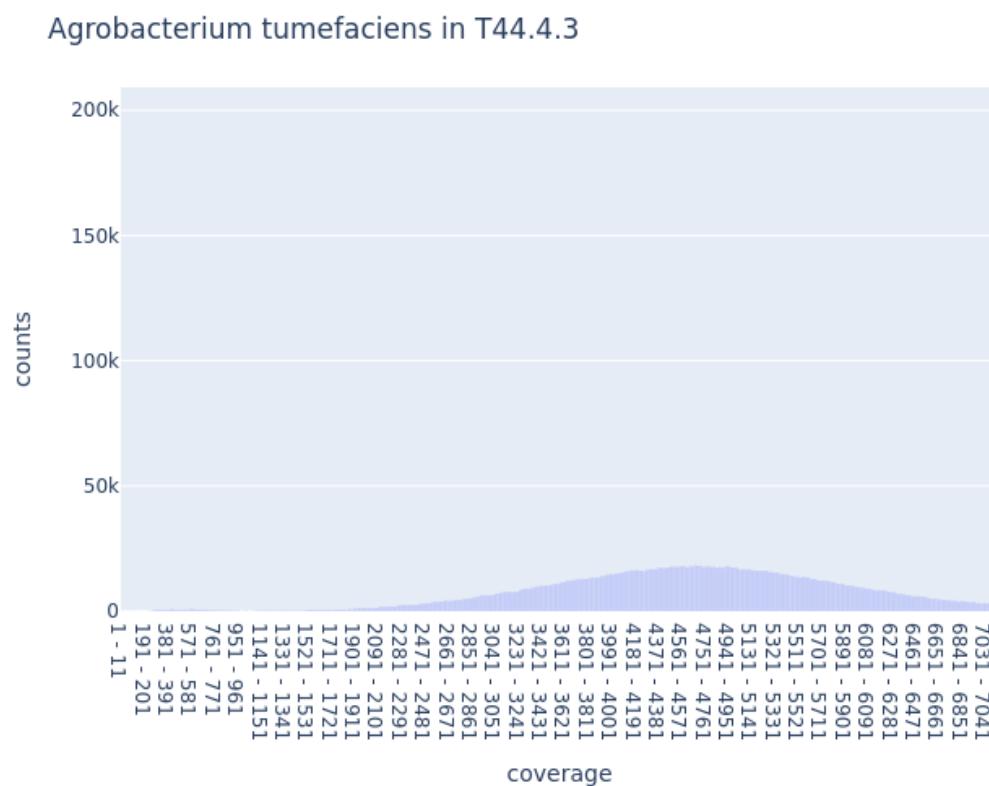
571798 + 0 with mate mapped to a different chr

549061 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

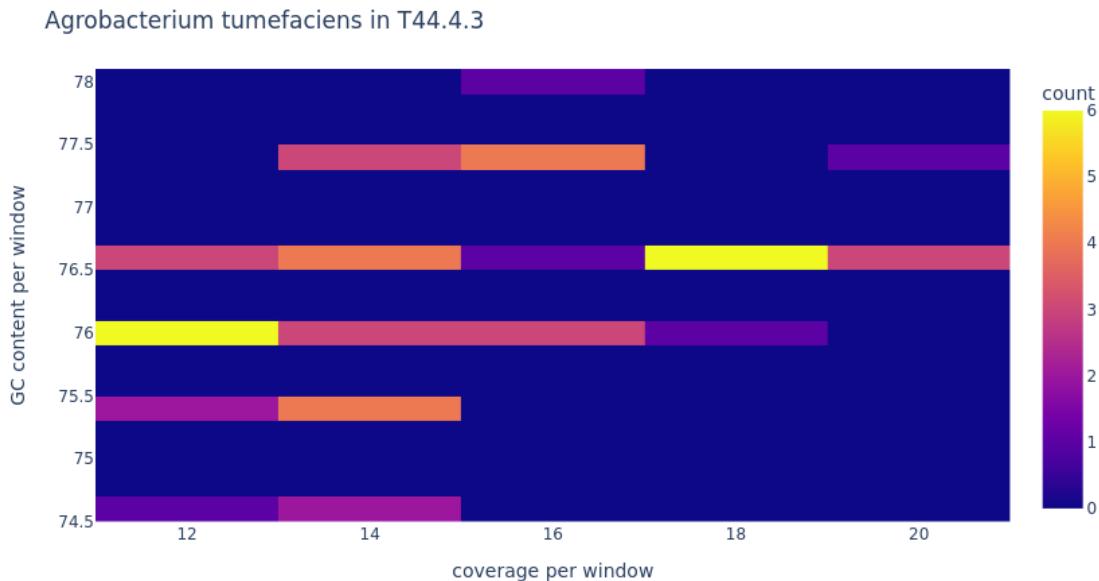
This plots shows the coverage per position in the genome.

Average coverage: 4750.392582508857



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.



# Report of Comamonas testosterone in T44.4.3

## Mapping stats of Illumina reads

176096229 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

645 + 0 supplementary

0 + 0 duplicates

4873800 + 0 mapped (2.77% : N/A)

176095584 + 0 paired in sequencing

88047792 + 0 read1

88047792 + 0 read2

4616364 + 0 properly paired (2.62% : N/A)

4620676 + 0 with itself and mate mapped

252479 + 0 singletons (0.14% : N/A)

54 + 0 with mate mapped to a different chr

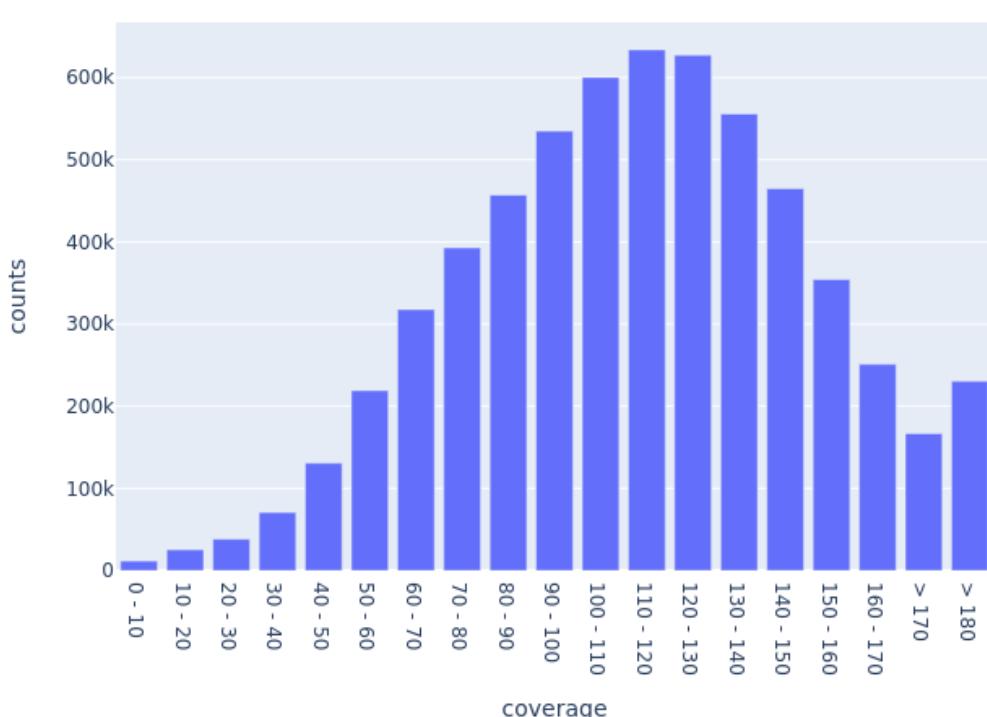
41 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 116.49030872604999

Comamonas testosterone in T44.4.3

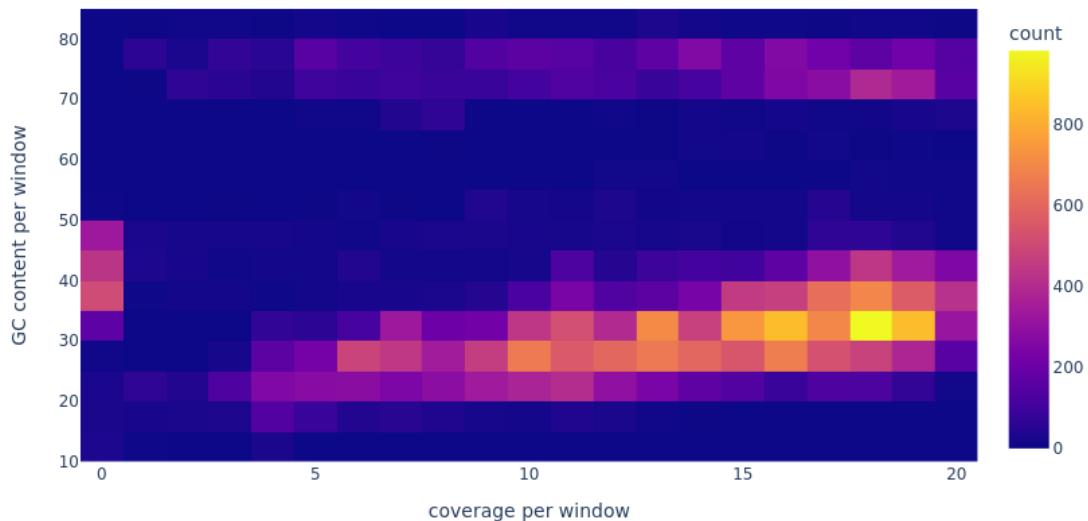


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.4.3



# Report of *Microbacterium saperdae* in T44.4.3

## Mapping stats of Illumina reads

176095691 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

107 + 0 supplementary

0 + 0 duplicates

626255 + 0 mapped (0.36% : N/A)

176095584 + 0 paired in sequencing

88047792 + 0 read1

88047792 + 0 read2

537268 + 0 properly paired (0.31% : N/A)

539530 + 0 with itself and mate mapped

86618 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

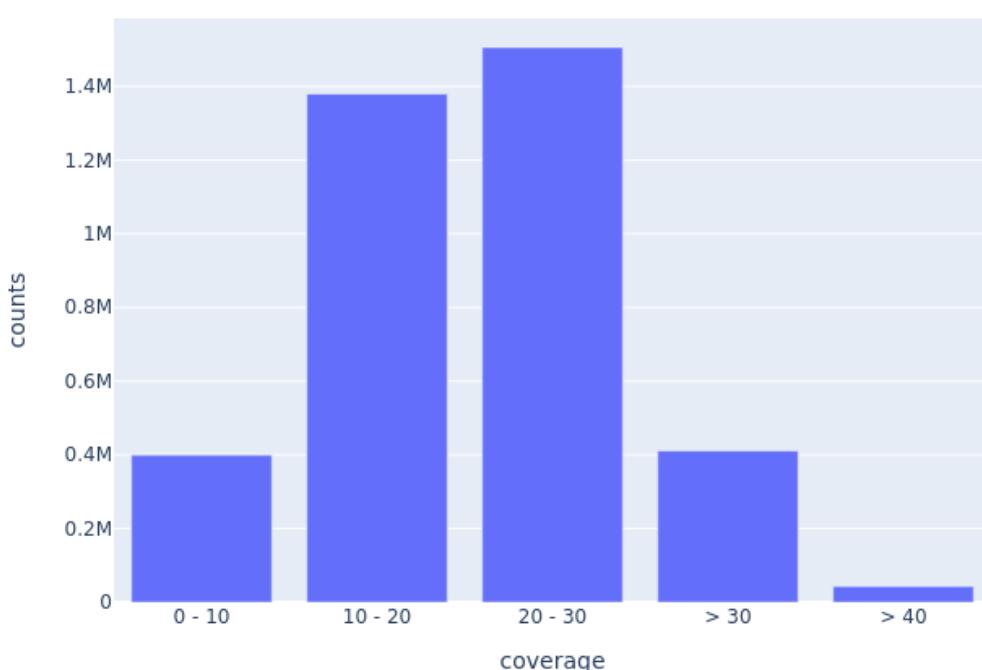
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 22.06032967321115

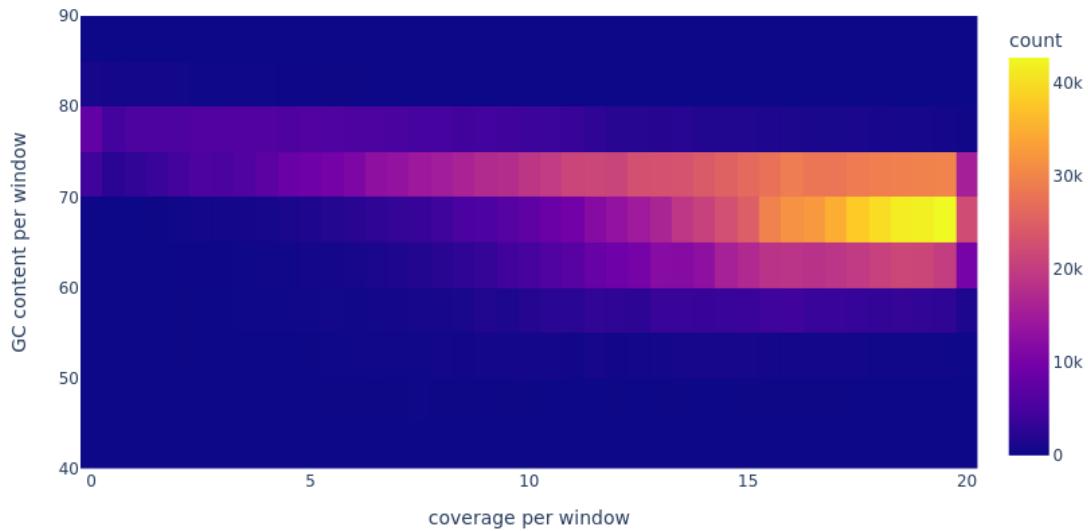
Microbacterium saperdae in T44.4.3



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T44.4.3



# Report of *Ochrobactrum anthropi* in T44.4.3

## Mapping stats of Illumina reads

176098949 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

3365 + 0 supplementary

0 + 0 duplicates

4635803 + 0 mapped (2.63% : N/A)

176095584 + 0 paired in sequencing

88047792 + 0 read1

88047792 + 0 read2

3067926 + 0 properly paired (1.74% : N/A)

3109878 + 0 with itself and mate mapped

1522560 + 0 singletons (0.86% : N/A)

26510 + 0 with mate mapped to a different chr

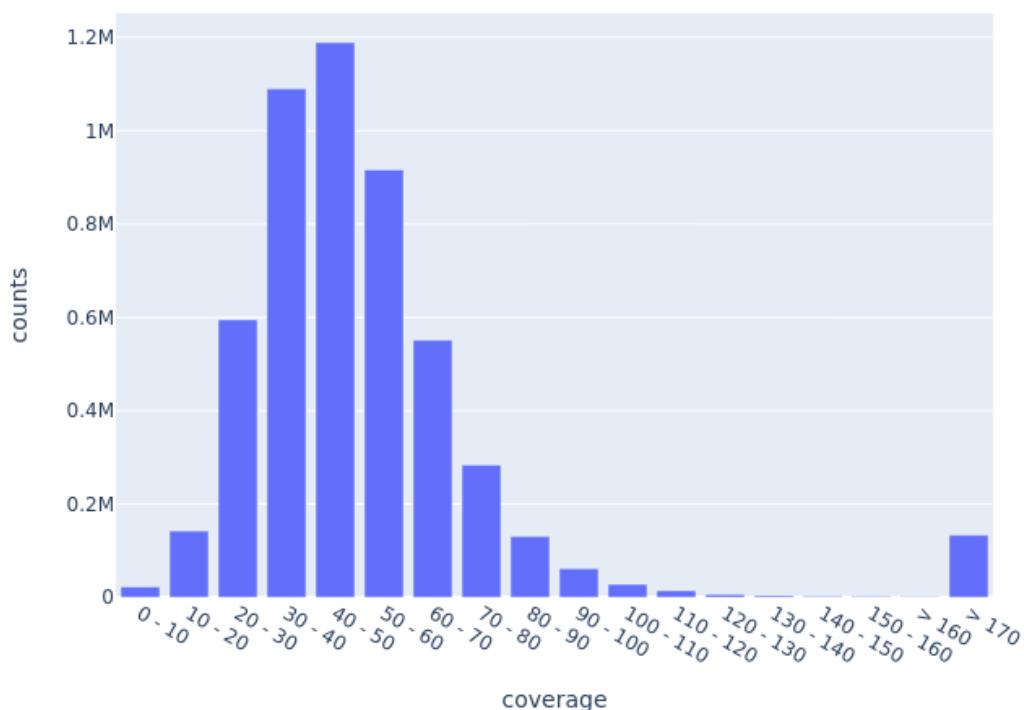
18539 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 108.49335211000603

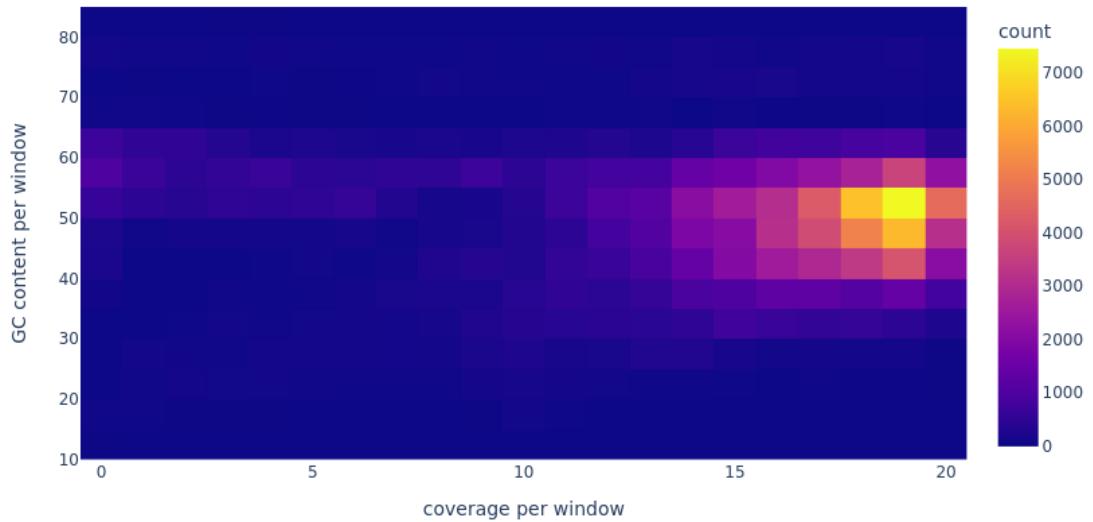
Ochrobactrum anthropi in T44.4.3



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T44.4.3



# Report of *Agrobacterium tumefaciens* in T44.4.4

## Mapping stats of Illumina reads

186322431 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

44817 + 0 supplementary

0 + 0 duplicates

177853034 + 0 mapped (95.45% : N/A)

186277614 + 0 paired in sequencing

93138807 + 0 read1

93138807 + 0 read2

177363336 + 0 properly paired (95.21% : N/A)

177714174 + 0 with itself and mate mapped

94043 + 0 singletons (0.05% : N/A)

138720 + 0 with mate mapped to a different chr

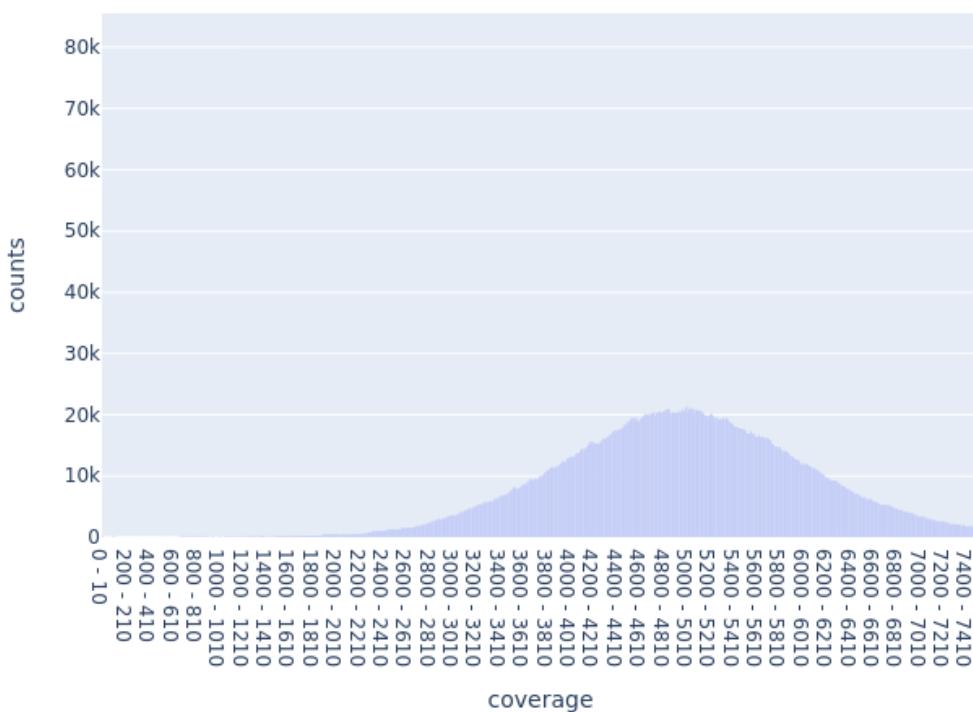
131694 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

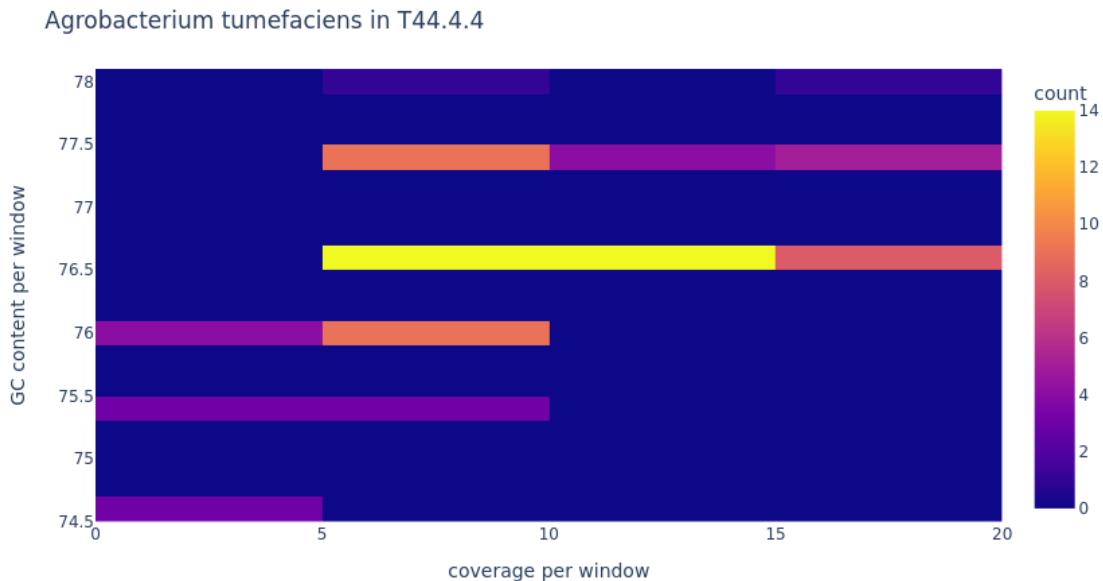
Average coverage: 4995.527800167036

Agrobacterium tumefaciens in T44.4.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.



# Report of Comamonas testosterone in T44.4.4

## Mapping stats of Illumina reads

186279717 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

2103 + 0 supplementary

0 + 0 duplicates

7057178 + 0 mapped (3.79% : N/A)

186277614 + 0 paired in sequencing

93138807 + 0 read1

93138807 + 0 read2

6810800 + 0 properly paired (3.66% : N/A)

6818284 + 0 with itself and mate mapped

236791 + 0 singletons (0.13% : N/A)

388 + 0 with mate mapped to a different chr

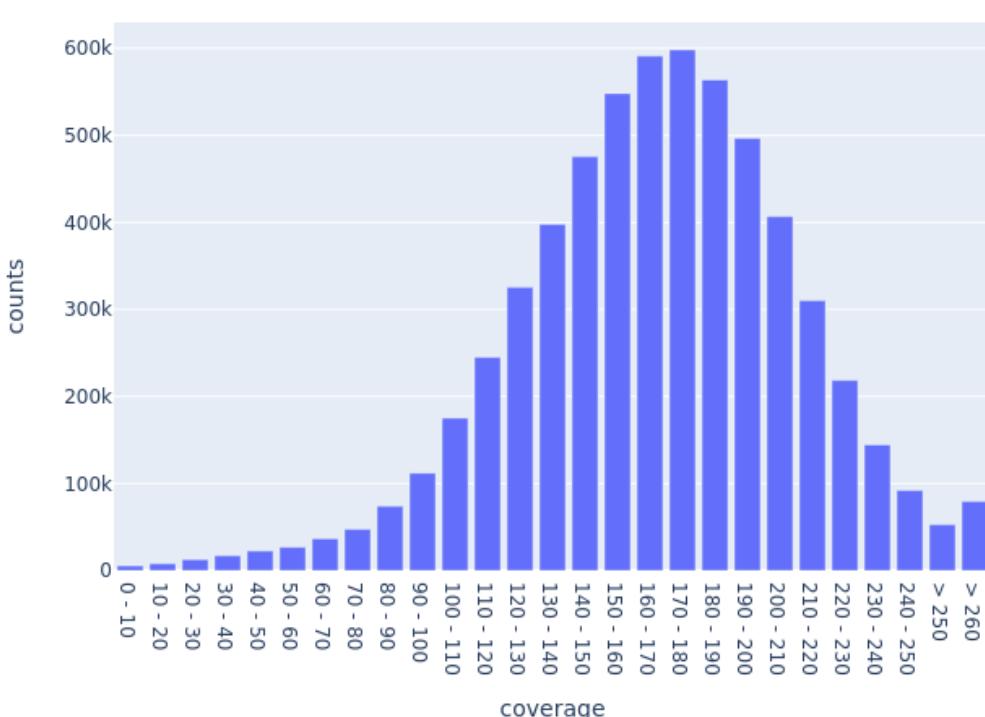
215 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 170.3652266923674

Comamonas testosterone in T44.4.4

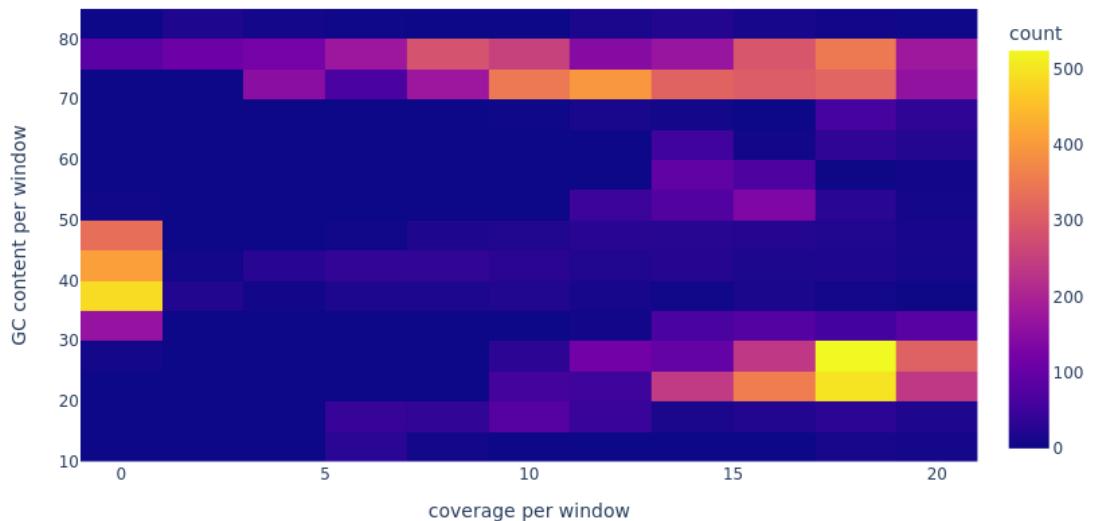


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteroni in T44.4.4



# Report of *Microbacterium saperdae* in T44.4.4

## Mapping stats of Illumina reads

186277623 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

9 + 0 supplementary

0 + 0 duplicates

145644 + 0 mapped (0.08% : N/A)

186277614 + 0 paired in sequencing

93138807 + 0 read1

93138807 + 0 read2

59664 + 0 properly paired (0.03% : N/A)

61990 + 0 with itself and mate mapped

83645 + 0 singletons (0.04% : N/A)

0 + 0 with mate mapped to a different chr

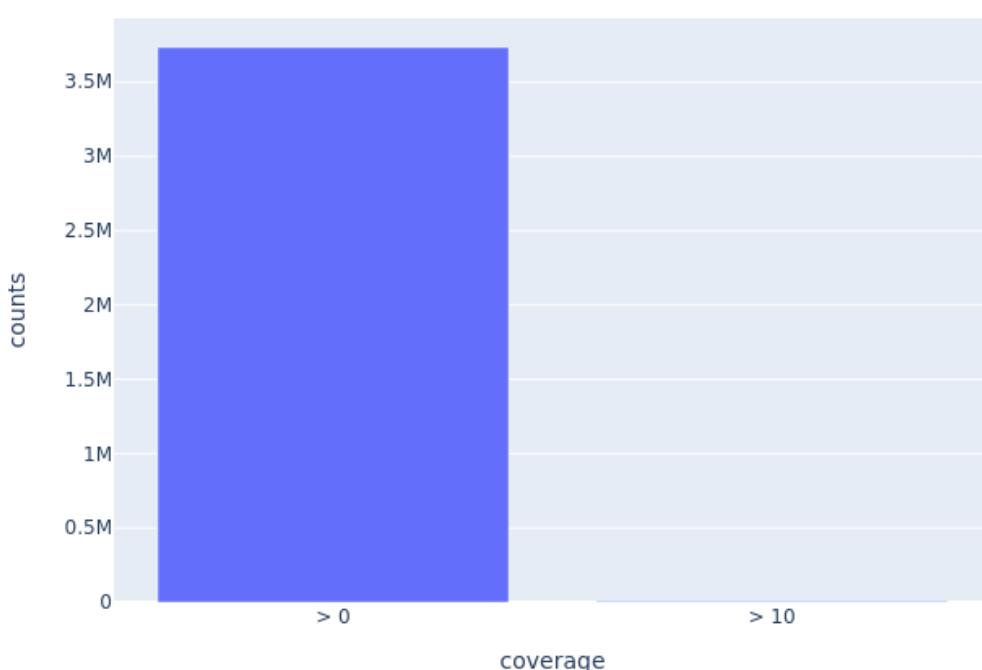
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 2.4711267036585345

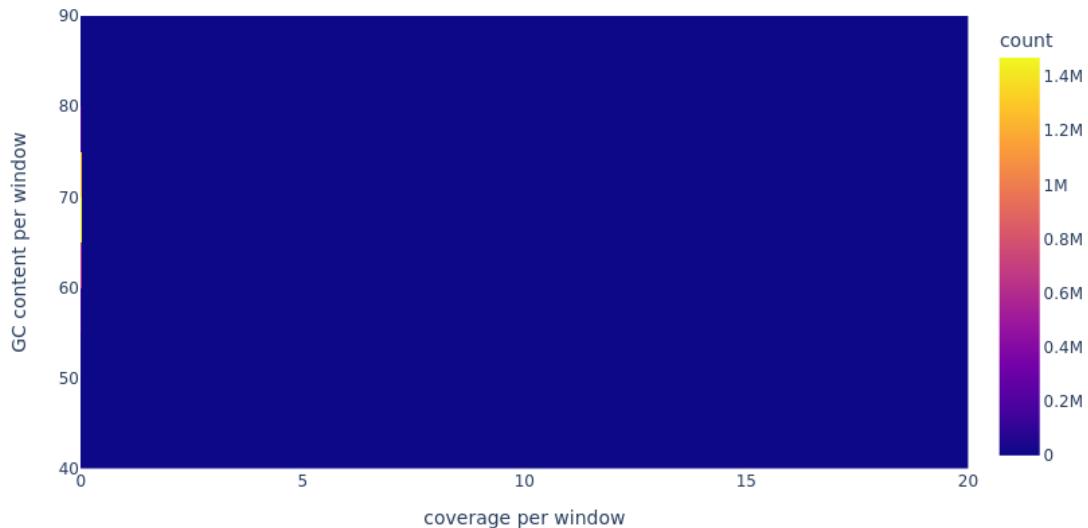
Microbacterium saperdae in T44.4.4



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T44.4.4



# Report of *Ochrobactrum anthropi* in T44.4.4

## Mapping stats of Illumina reads

186281365 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

3751 + 0 supplementary

0 + 0 duplicates

4444508 + 0 mapped (2.39% : N/A)

186277614 + 0 paired in sequencing

93138807 + 0 read1

93138807 + 0 read2

2911414 + 0 properly paired (1.56% : N/A)

2955220 + 0 with itself and mate mapped

1485537 + 0 singletons (0.80% : N/A)

25144 + 0 with mate mapped to a different chr

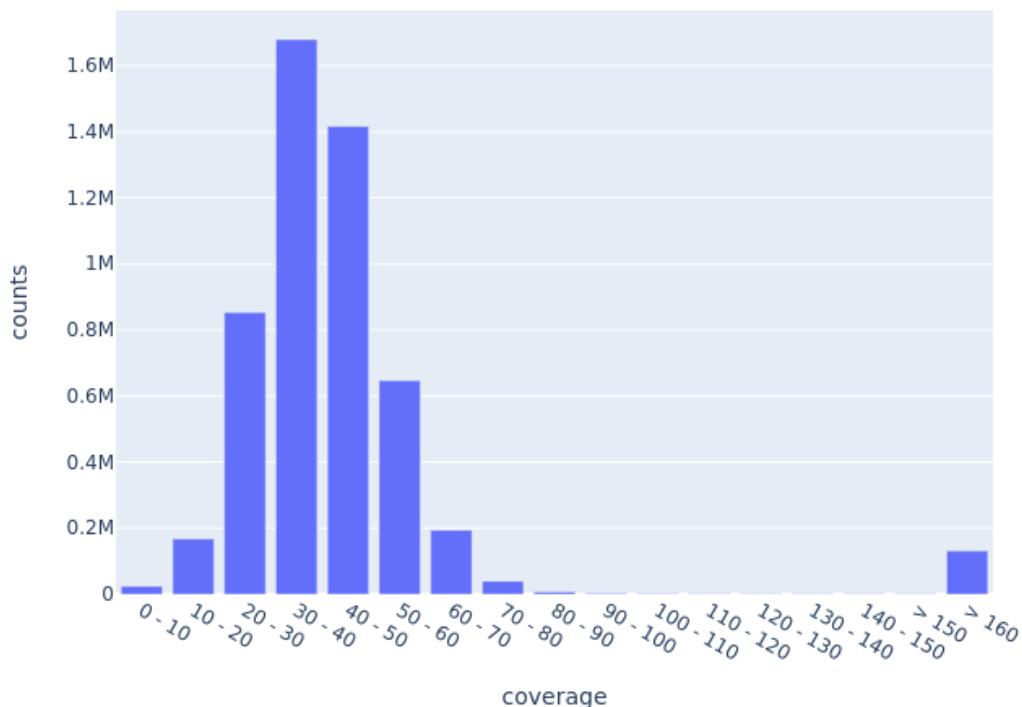
17649 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 102.21543736525625

Ochrobactrum anthropi in T44.4.4

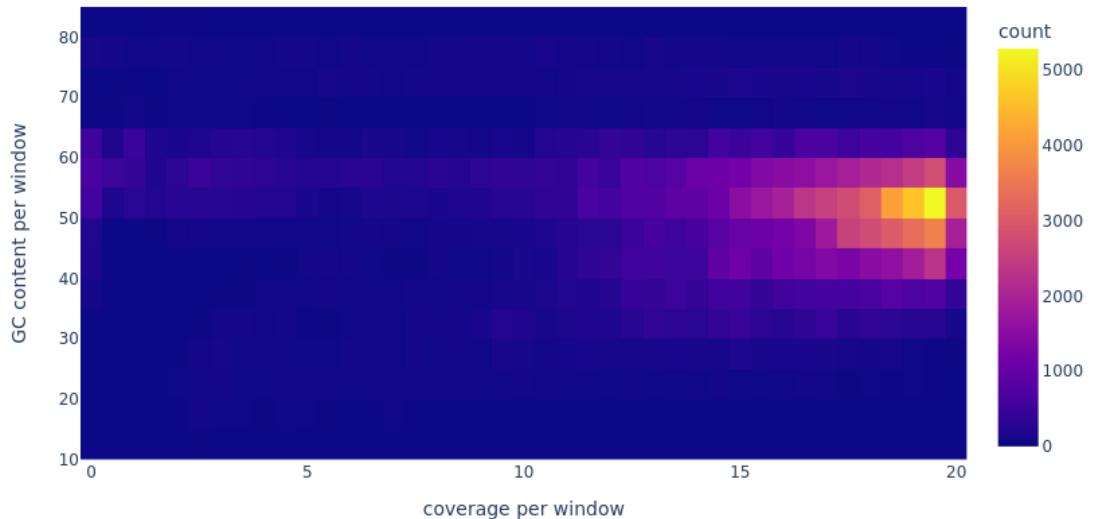


## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T44.4.4



# Report of *Agrobacterium tumefaciens* in T44.4.5.rep

## Mapping stats of Illumina reads

190097303 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

49249 + 0 supplementary

0 + 0 duplicates

178768658 + 0 mapped (94.04% : N/A)

190048054 + 0 paired in sequencing

95024027 + 0 read1

95024027 + 0 read2

177898584 + 0 properly paired (93.61% : N/A)

178576904 + 0 with itself and mate mapped

142505 + 0 singletons (0.07% : N/A)

327450 + 0 with mate mapped to a different chr

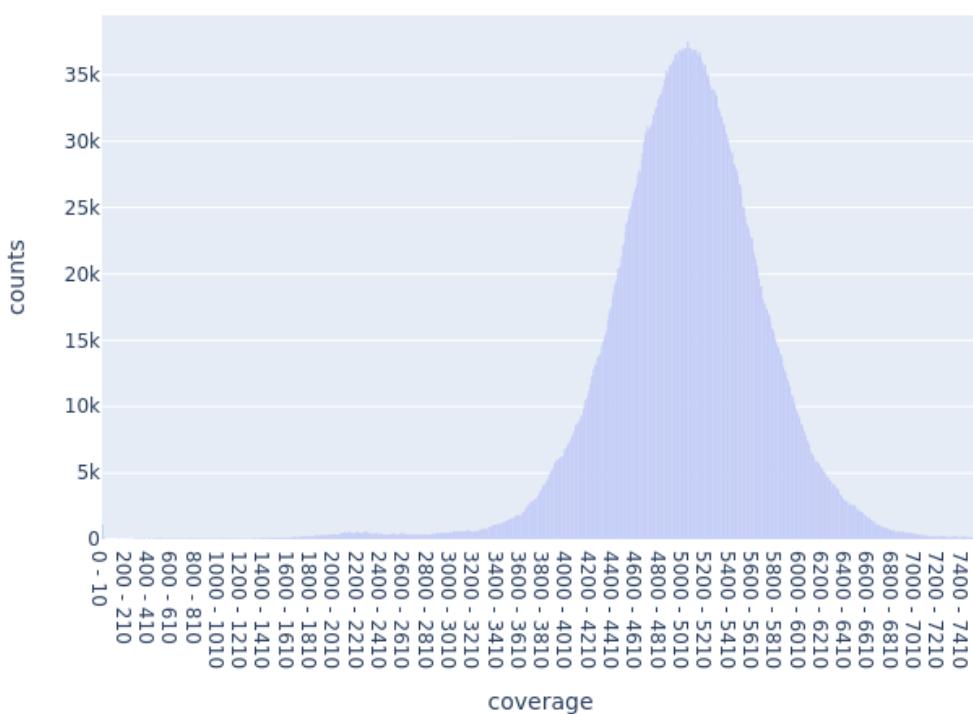
313658 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 5025.911538404729

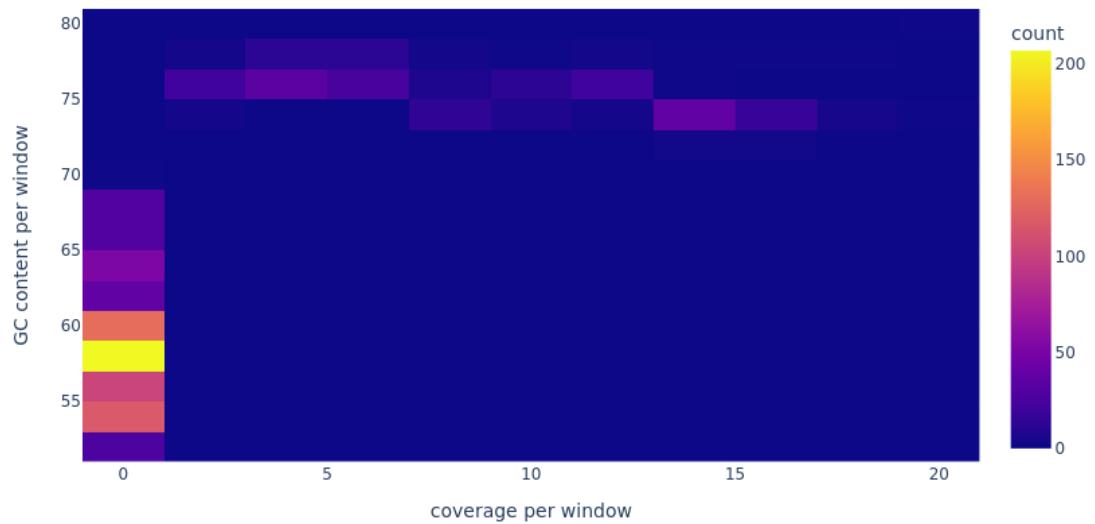
Agrobacterium tumefaciens in T44.4.5.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Agrobacterium tumefaciens in T44.4.5.rep



# Report of *Comamonas testosteronei* in T44.4.5.rep

## Mapping stats of Illumina reads

190049191 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

1137 + 0 supplementary

0 + 0 duplicates

8496546 + 0 mapped (4.47% : N/A)

190048054 + 0 paired in sequencing

95024027 + 0 read1

95024027 + 0 read2

8203582 + 0 properly paired (4.32% : N/A)

8209560 + 0 with itself and mate mapped

285849 + 0 singletons (0.15% : N/A)

274 + 0 with mate mapped to a different chr

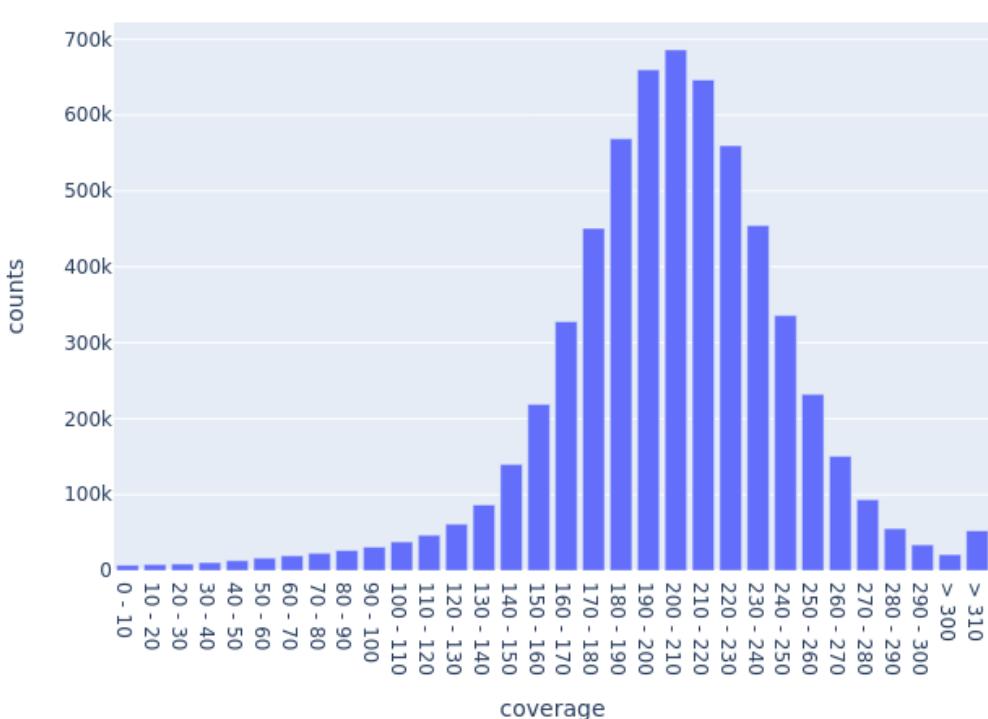
161 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 205.75931773615469

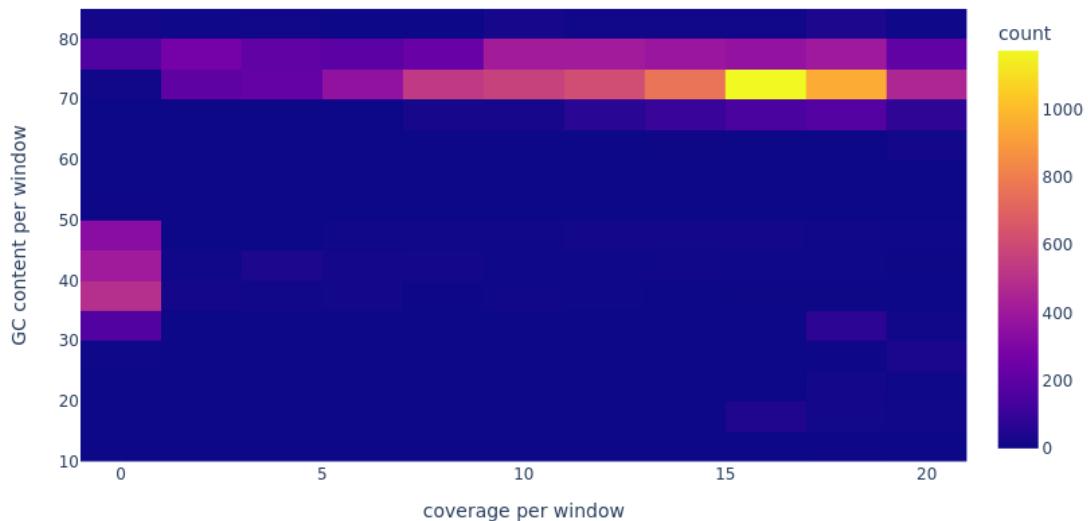
Comamonas testosteronei in T44.4.5.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Comamonas testosteronei in T44.4.5.rep



# Report of *Microbacterium saperdae* in T44.4.5.rep

## Mapping stats of Illumina reads

190048130 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

76 + 0 supplementary

0 + 0 duplicates

1059144 + 0 mapped (0.56% : N/A)

190048054 + 0 paired in sequencing

95024027 + 0 read1

95024027 + 0 read2

958108 + 0 properly paired (0.50% : N/A)

960436 + 0 with itself and mate mapped

98632 + 0 singletons (0.05% : N/A)

0 + 0 with mate mapped to a different chr

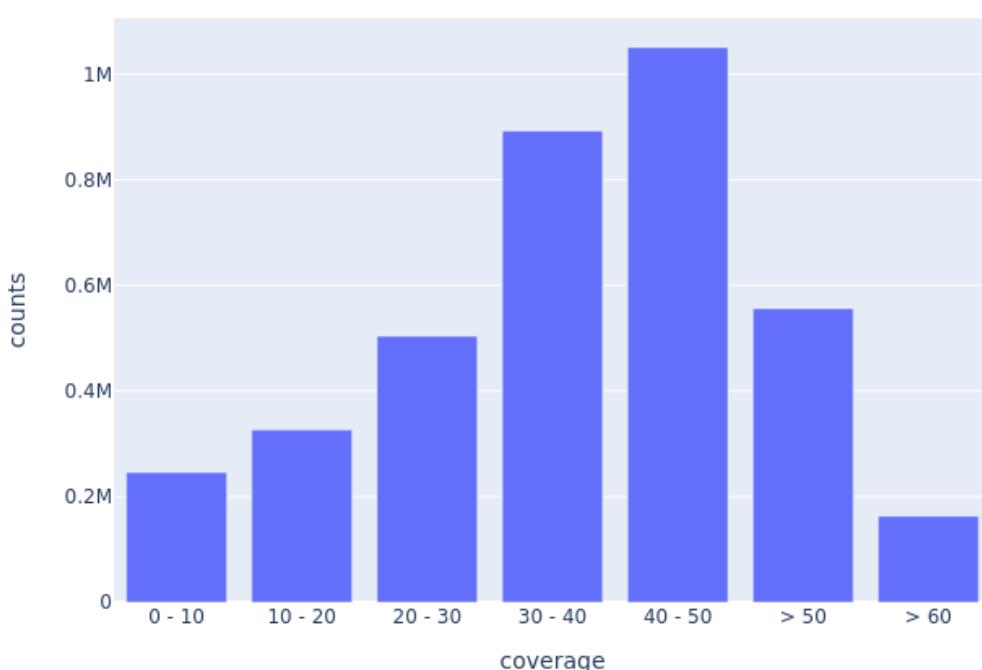
0 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 39.02066196856744

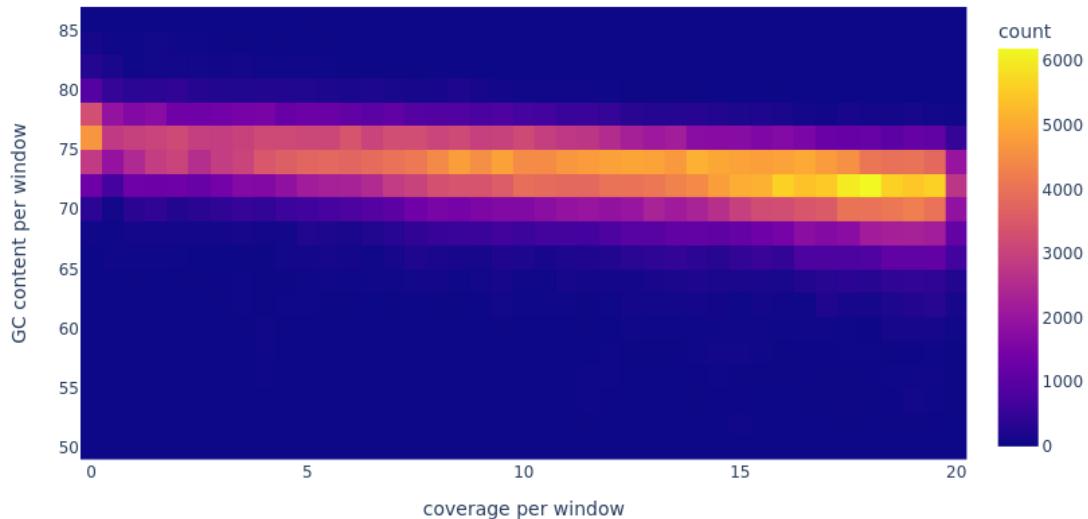
Microbacterium saperdae in T44.4.5.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram. There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Microbacterium saperdae in T44.4.5.rep



# Report of *Ochrobactrum anthropi* in T44.4.5.rep

## Mapping stats of Illumina reads

190051873 + 0 in total (QC-passed reads + QC-failed reads)

0 + 0 secondary

3819 + 0 supplementary

0 + 0 duplicates

5059279 + 0 mapped (2.66% : N/A)

190048054 + 0 paired in sequencing

95024027 + 0 read1

95024027 + 0 read2

3399494 + 0 properly paired (1.79% : N/A)

3433742 + 0 with itself and mate mapped

1621718 + 0 singletons (0.85% : N/A)

21646 + 0 with mate mapped to a different chr

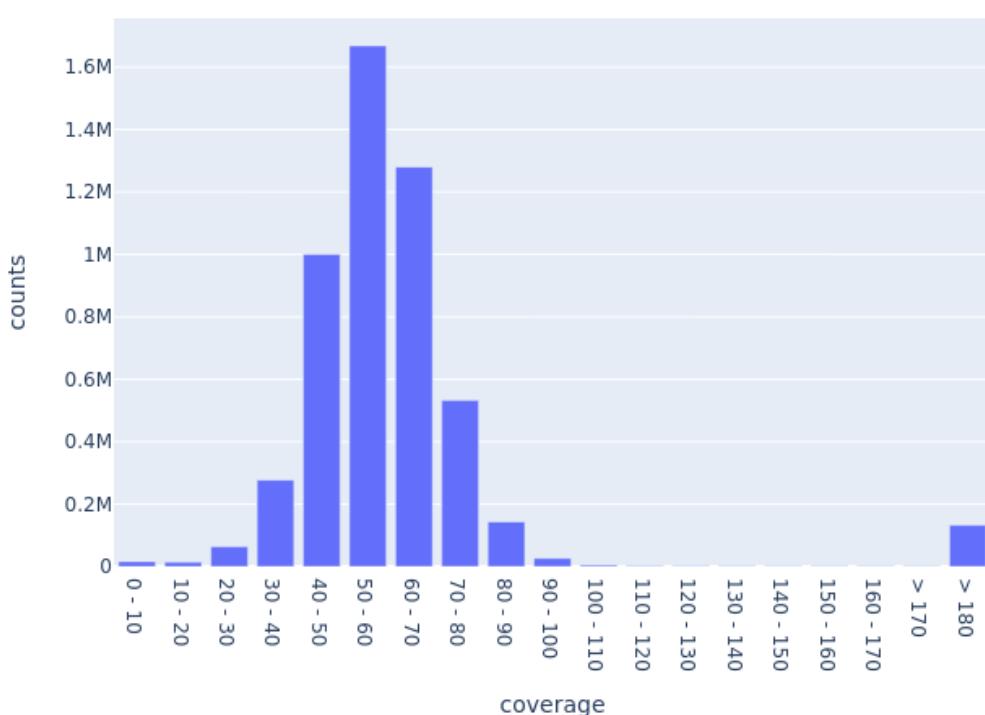
14697 + 0 with mate mapped to a different chr (mapQ>=5)

## Coverage plot

This plots shows the coverage per position in the genome.

Average coverage: 119.60460176785726

Ochrobactrum anthropi in T44.4.5.rep



## Sequence bias of Illumina reads

The reference sequence was split into 150 BP windows using a k-mer approach. Of every window the GC content and the coverage was calculated. Those values were visualized using a 2d histogram.

There is a cut off for the coverage at 20 because we want to inspect low coverage areas using this plot. Therefore if the plot is empty, check the average coverage and the coverage histogram because maybe the coverage over the entire genome is > 20.

Ochrobactrum anthropi in T44.4.5.rep

