

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 22:09:37*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819091.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1819091 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819091.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 22:09:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819091.sorted.bam

## 2. Summary

### 2.1. Globals

Reference size	3,095,693,983
Number of reads	3,361,107
Mapped reads	3,087,492 / 91.86%
Unmapped reads	273,615 / 8.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,538 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	195,830 / 5.83%
Duplication rate	4.73%
Clipped reads	3,093,465 / 92.04%

### 2.2. ACGT Content

Number/percentage of A's	45,885,764 / 25.49%
Number/percentage of C's	33,965,932 / 18.87%
Number/percentage of T's	57,595,874 / 31.99%
Number/percentage of G's	42,595,396 / 23.66%
Number/percentage of N's	2,627 / 0%
GC Percentage	42.52%

### 2.3. Coverage

Mean	0.0582

Standard Deviation	0.4918
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## 2.4. Mapping Quality

Mean Mapping Quality	44.86
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## 2.5. Mismatches and indels

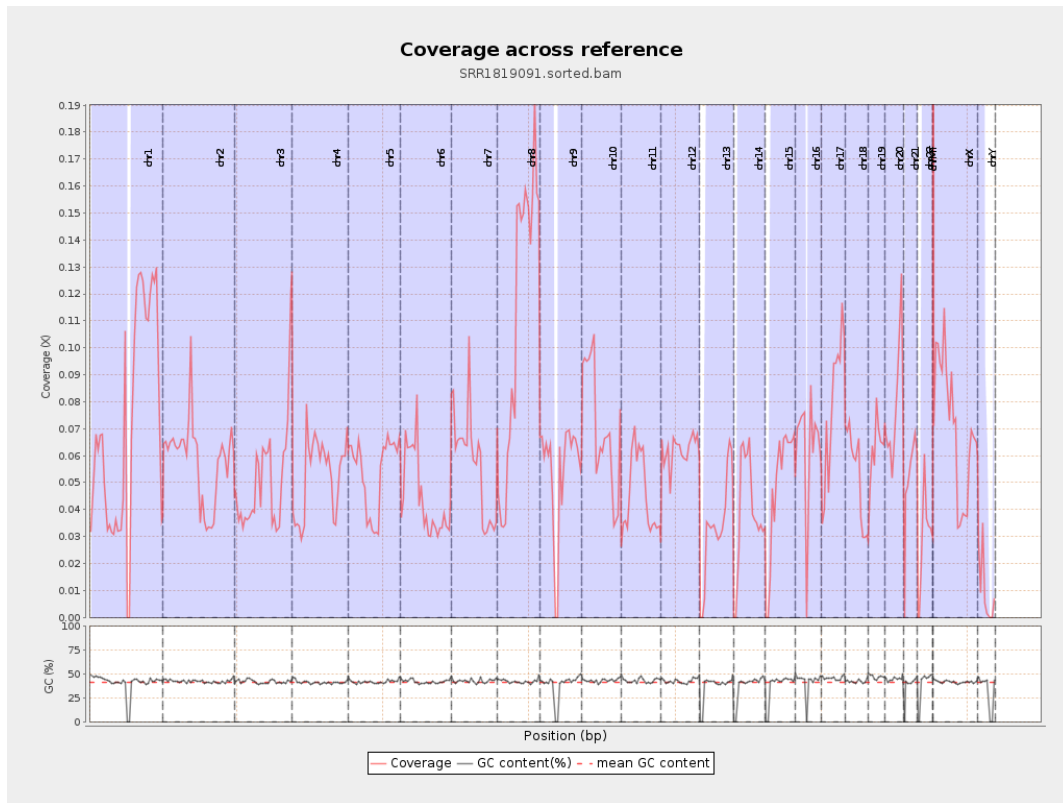
General error rate	0.52%
Mismatches	909,950
Insertions	12,777
Mapped reads with at least one insertion	0.41%
Deletions	33,456
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.4%

## 2.6. Chromosome stats

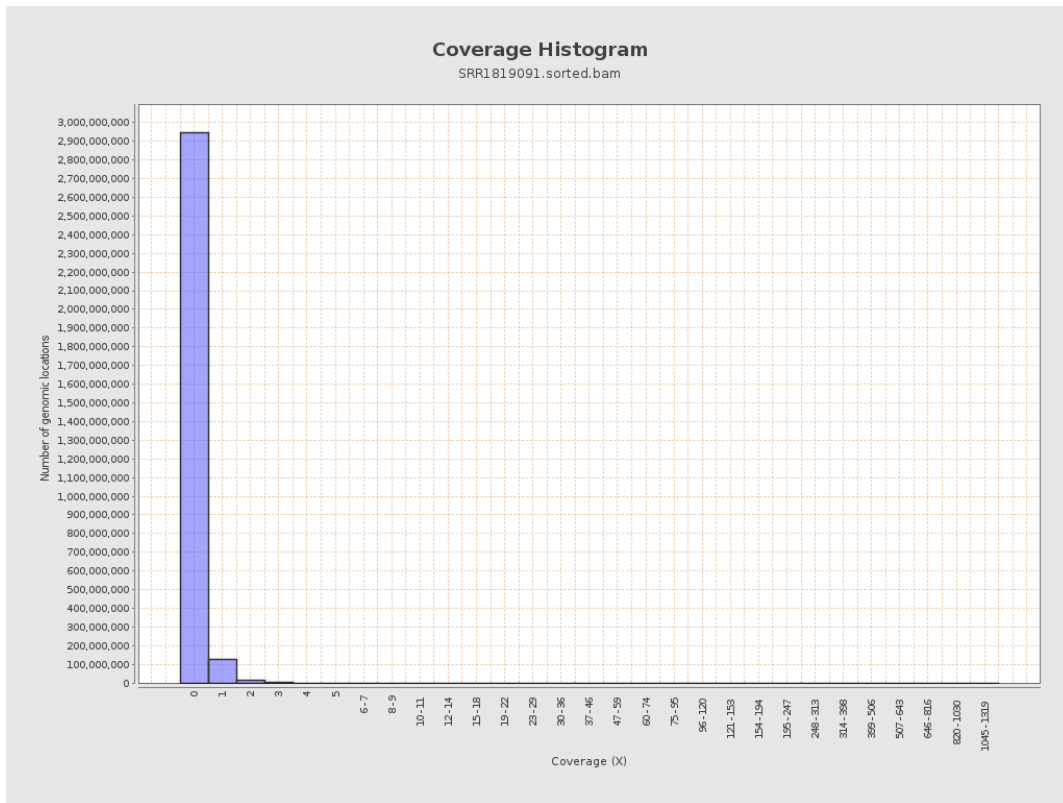
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17734454	0.0712	0.99
chr2	243199373	14159957	0.0582	0.5692
chr3	198022430	10082901	0.0509	0.2702
chr4	191154276	10083227	0.0527	0.3264
chr5	180915260	9758363	0.0539	0.2755
chr6	171115067	7619329	0.0445	0.3567
chr7	159138663	9033741	0.0568	0.6567

chr8	146364022	16491973	0.1127	0.5087
chr9	141213431	7676010	0.0544	0.4069
chr10	135534747	9429755	0.0696	0.472
chr11	135006516	6106657	0.0452	0.4527
chr12	133851895	8358994	0.0624	0.2968
chr13	115169878	3940021	0.0342	0.217
chr14	107349540	4282865	0.0399	0.2453
chr15	102531392	4854128	0.0473	0.2723
chr16	90354753	5601758	0.062	0.3245
chr17	81195210	6361749	0.0784	0.3669
chr18	78077248	4157162	0.0532	0.7951
chr19	59128983	3721146	0.0629	0.6588
chr20	63025520	5065335	0.0804	0.3409
chr21	48129895	2498687	0.0519	0.3079
chr22	51304566	1487595	0.029	0.1974
chrMT	16571	14852	0.8963	1.2418
chrX	155270560	10986551	0.0708	0.3744
chrY	59373566	594089	0.01	0.2658

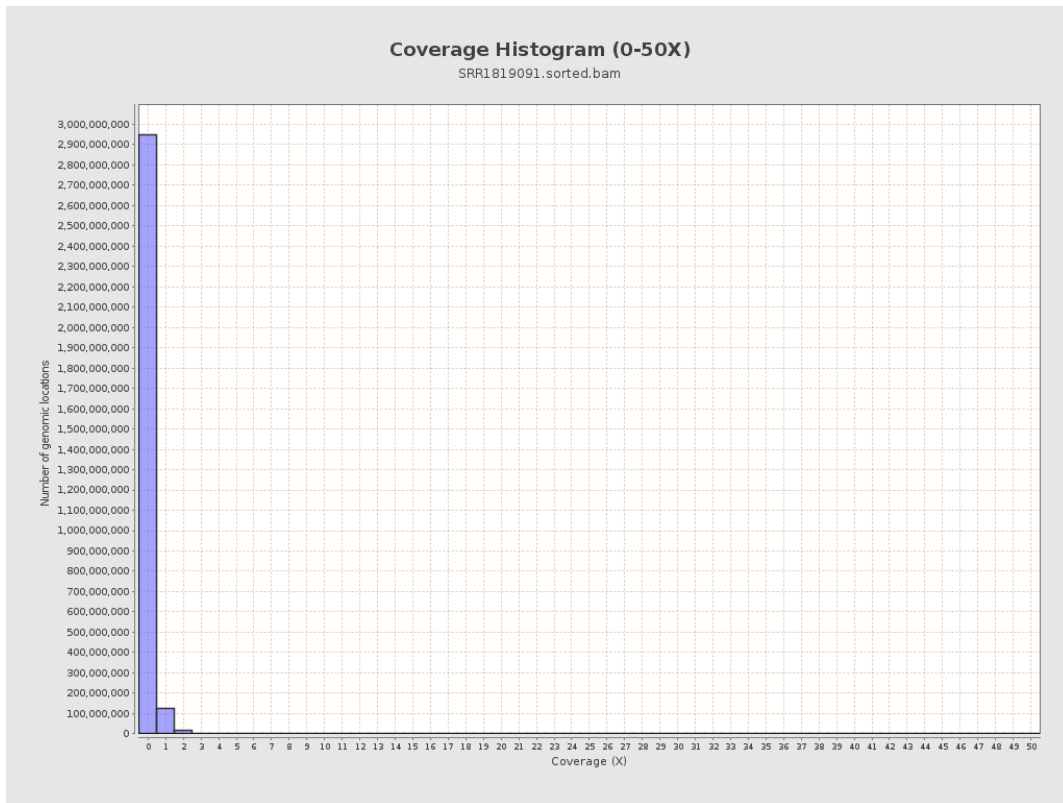
### 3. Results : Coverage across reference



# 4. Results : Coverage Histogram

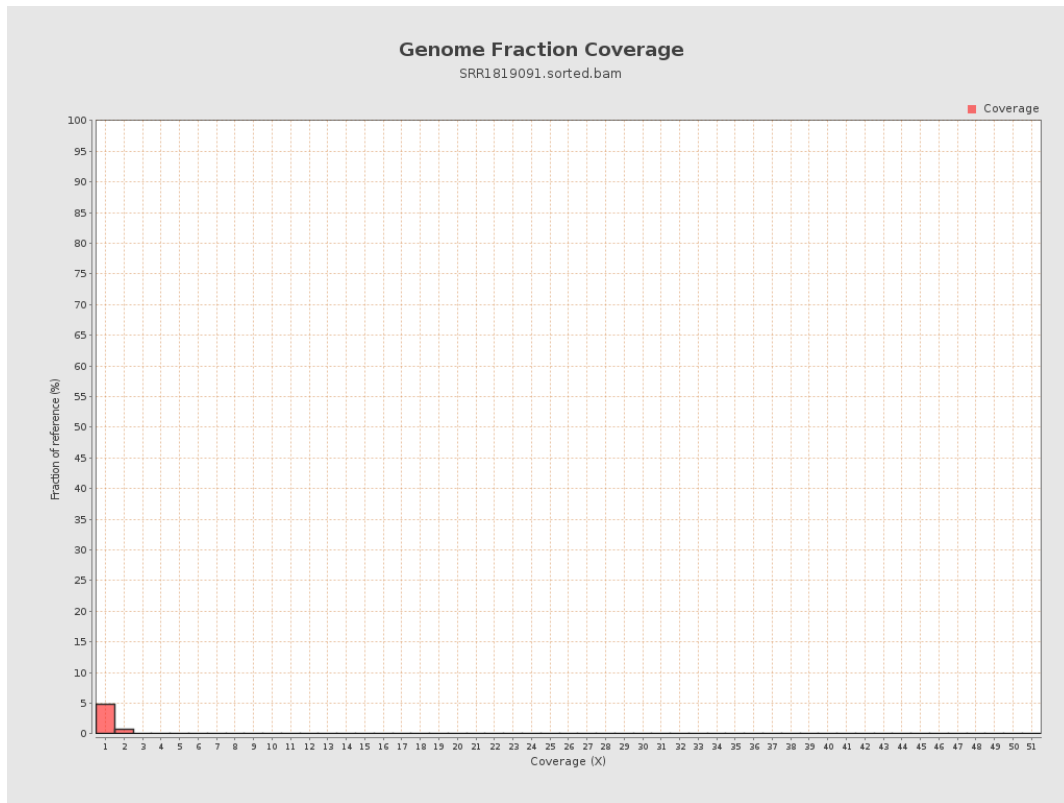


# 5. Results : Coverage Histogram (0-50X)

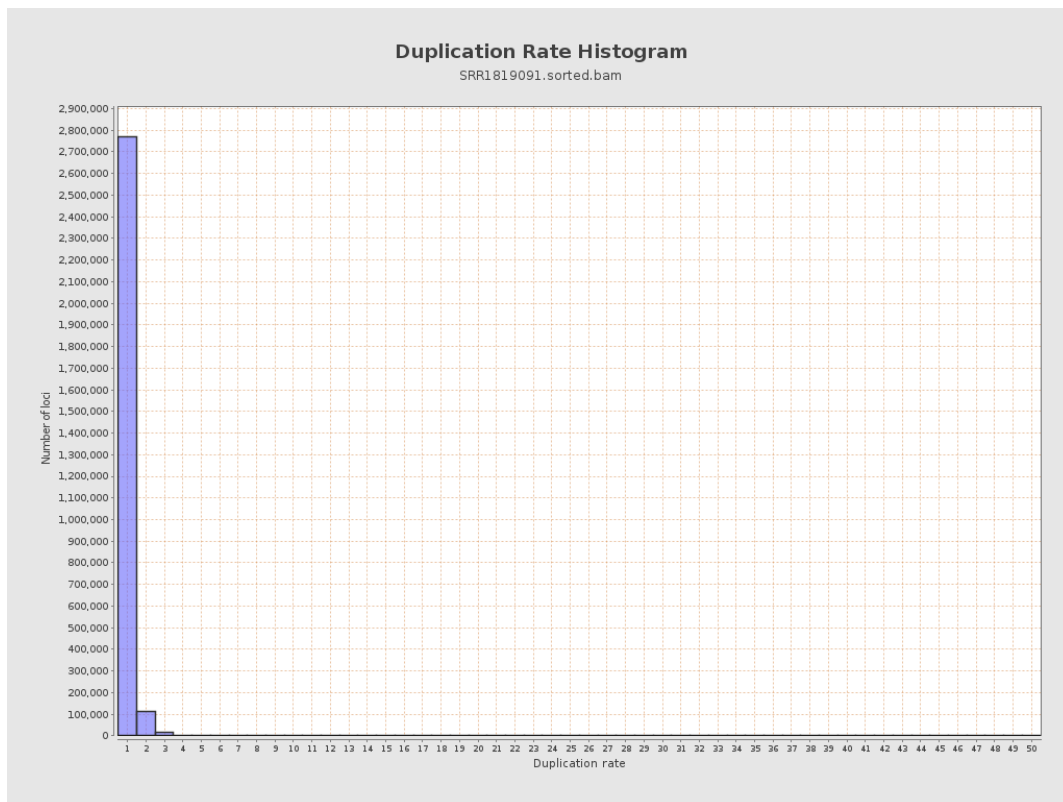




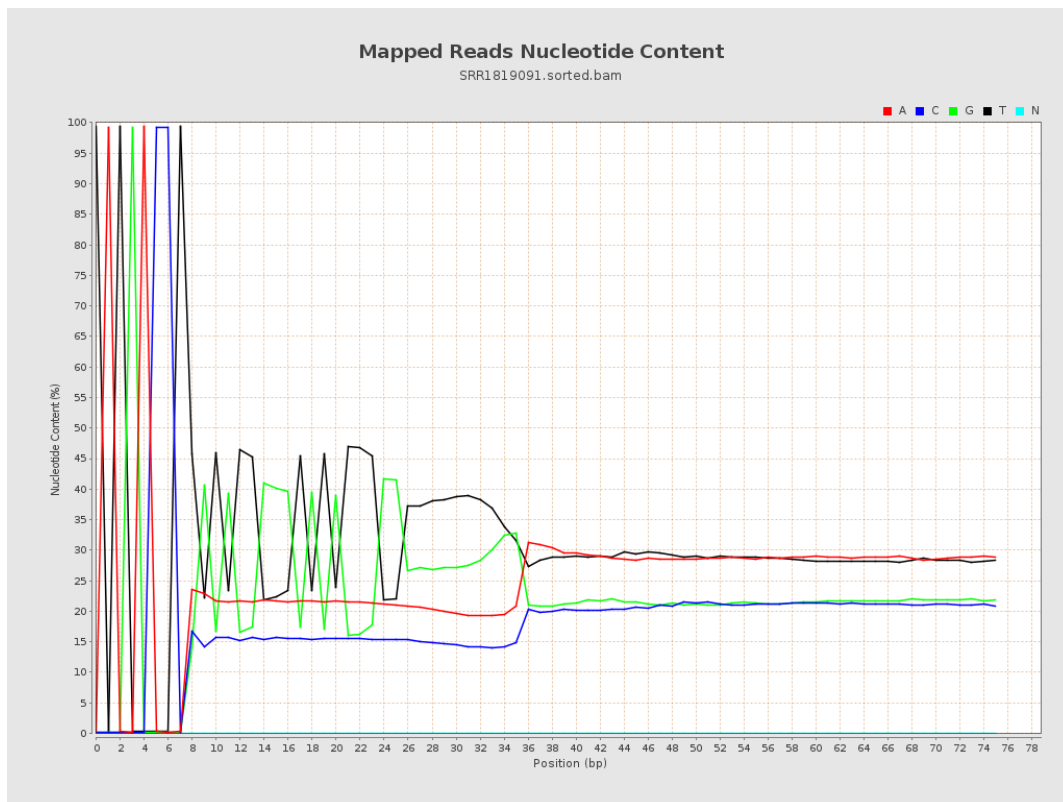
## 6. Results : Genome Fraction Coverage



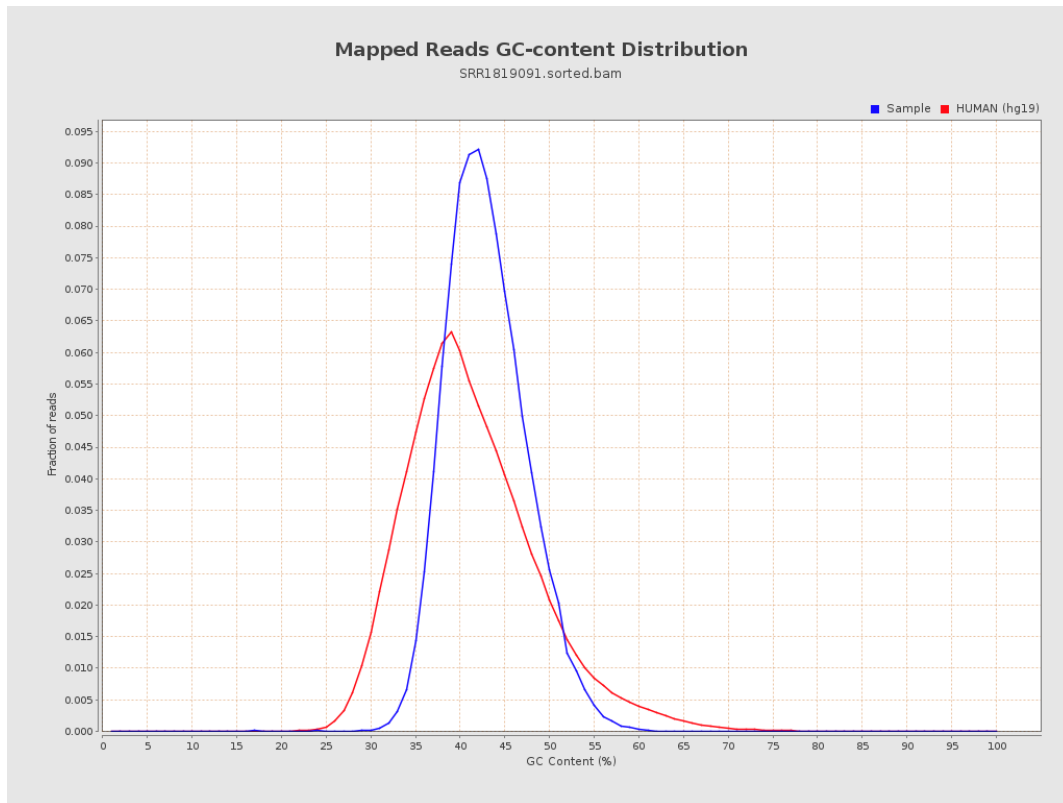
# 7. Results : Duplication Rate Histogram



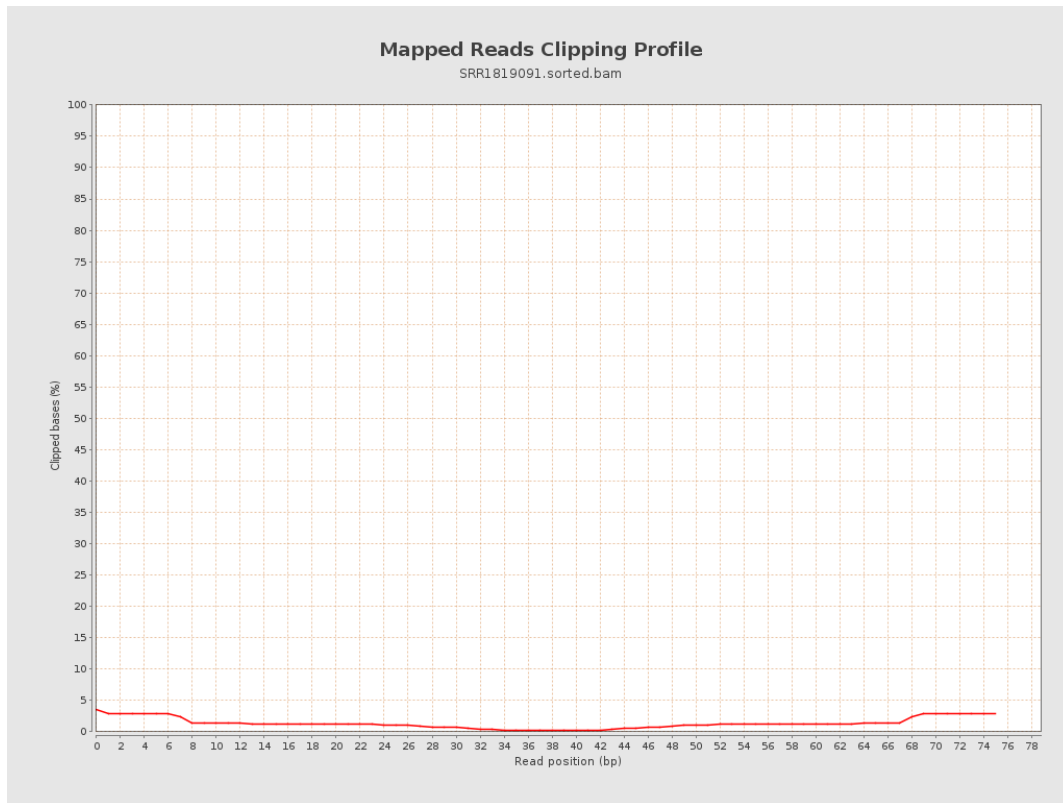
# 8. Results : Mapped Reads Nucleotide Content



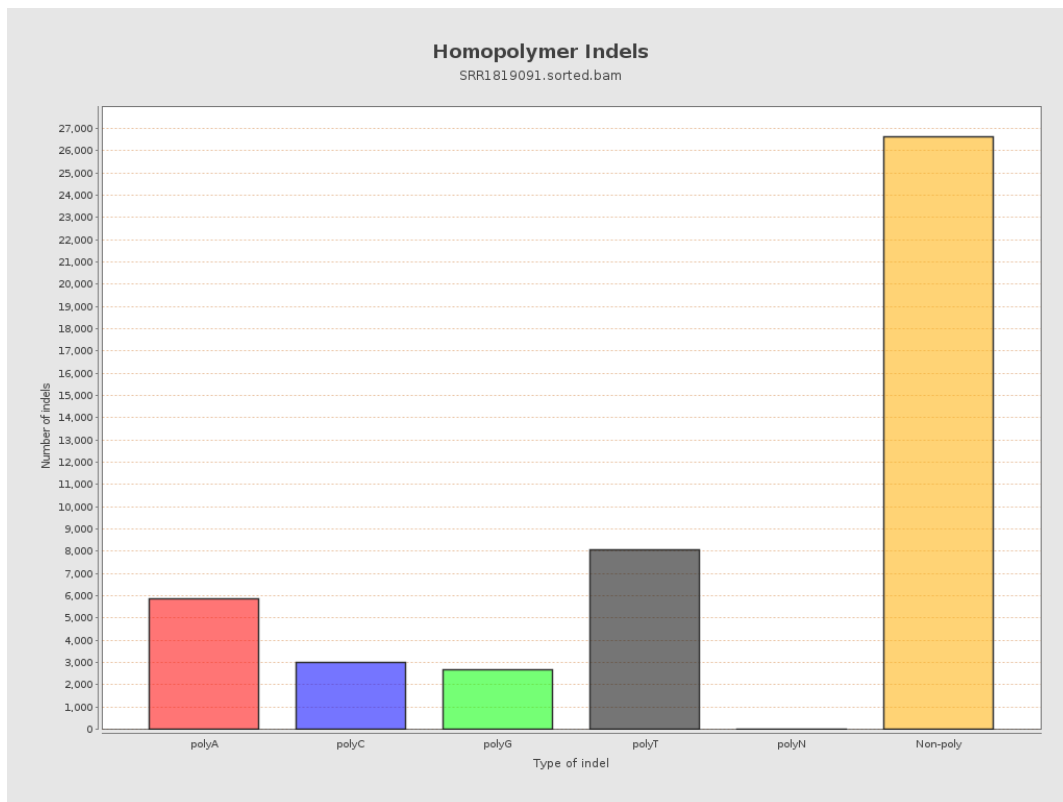
## 9. Results : Mapped Reads GC-content Distribution



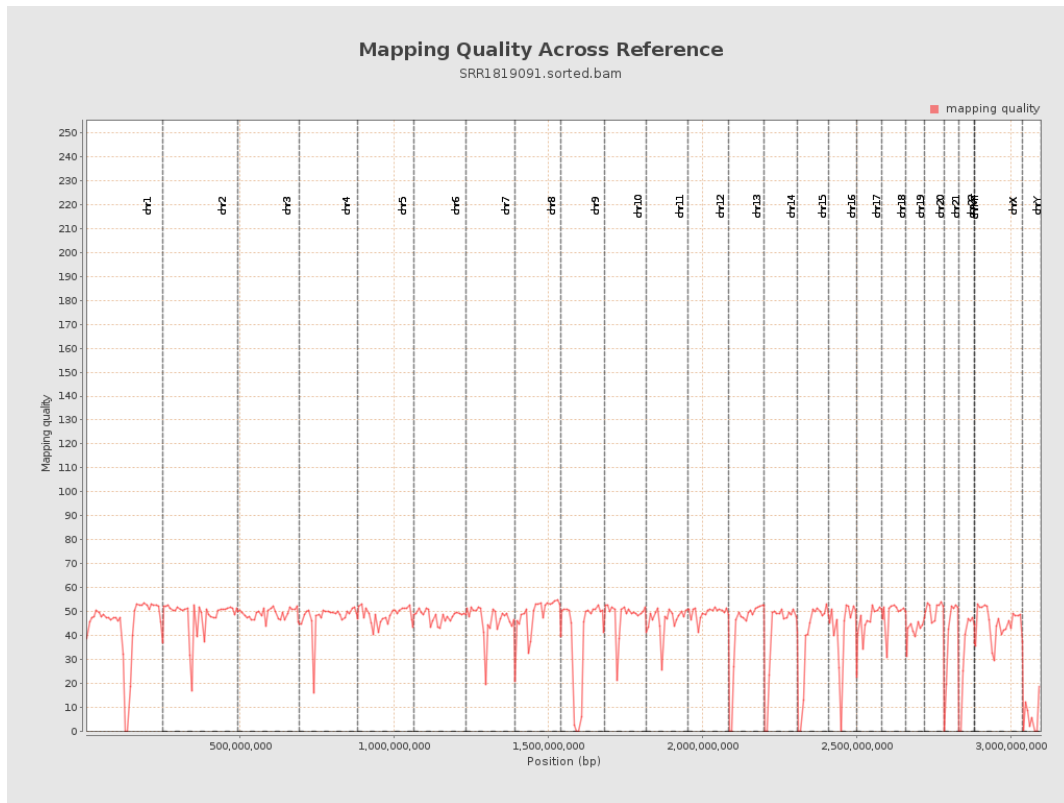
## 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram

