

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/13 22:57:00*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004053.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_SRR6004053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004053.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:56:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004053.sorted.bam

## 2. Summary

### 2.1. Globals

Reference size	3,095,693,983
Number of reads	3,362,631
Mapped reads	3,080,236 / 91.6%
Unmapped reads	282,395 / 8.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,605 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	209,288 / 6.22%
Duplication rate	5.62%
Clipped reads	1,306,581 / 38.86%

### 2.2. ACGT Content

Number/percentage of A's	56,506,179 / 27.32%
Number/percentage of C's	38,879,849 / 18.8%
Number/percentage of T's	64,653,553 / 31.26%
Number/percentage of G's	46,570,773 / 22.52%
Number/percentage of N's	227,906 / 0.11%
GC Percentage	41.31%

### 2.3. Coverage

Mean	0.0668

Standard Deviation	0.4806
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## 2.4. Mapping Quality

Mean Mapping Quality	45.3
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## 2.5. Mismatches and indels

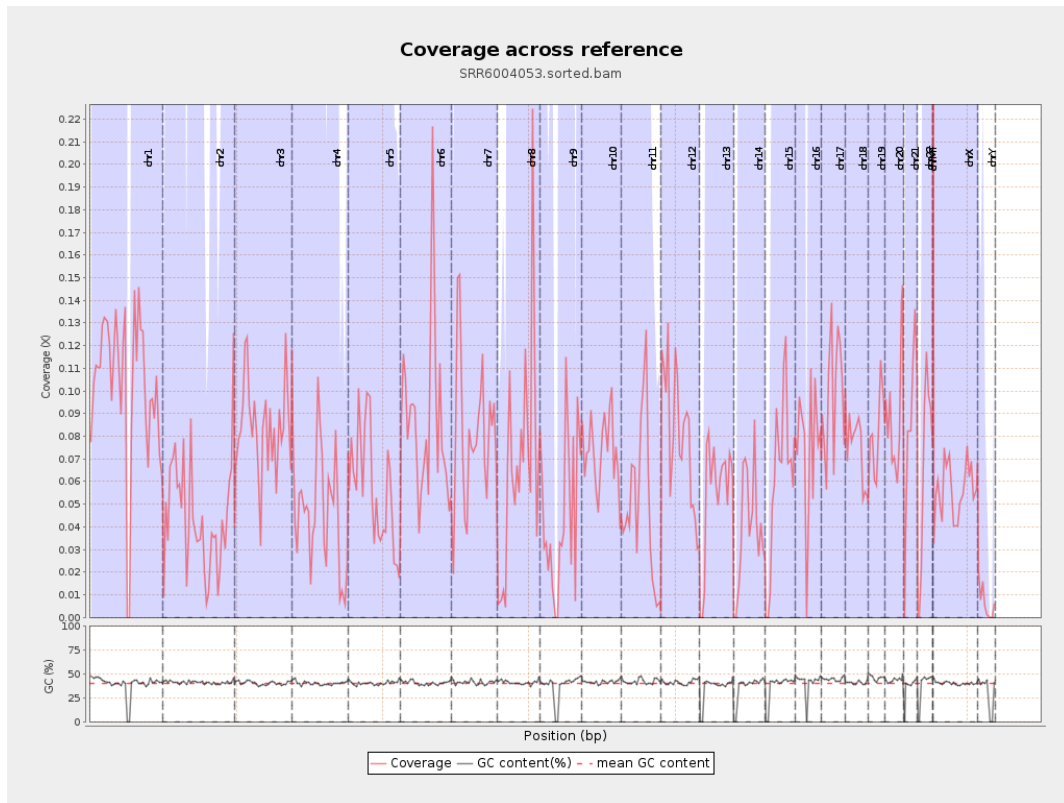
General error rate	0.79%
Mismatches	1,611,543
Insertions	13,939
Mapped reads with at least one insertion	0.45%
Deletions	49,690
Mapped reads with at least one deletion	1.6%
Homopolymer indels	47.5%

## 2.6. Chromosome stats

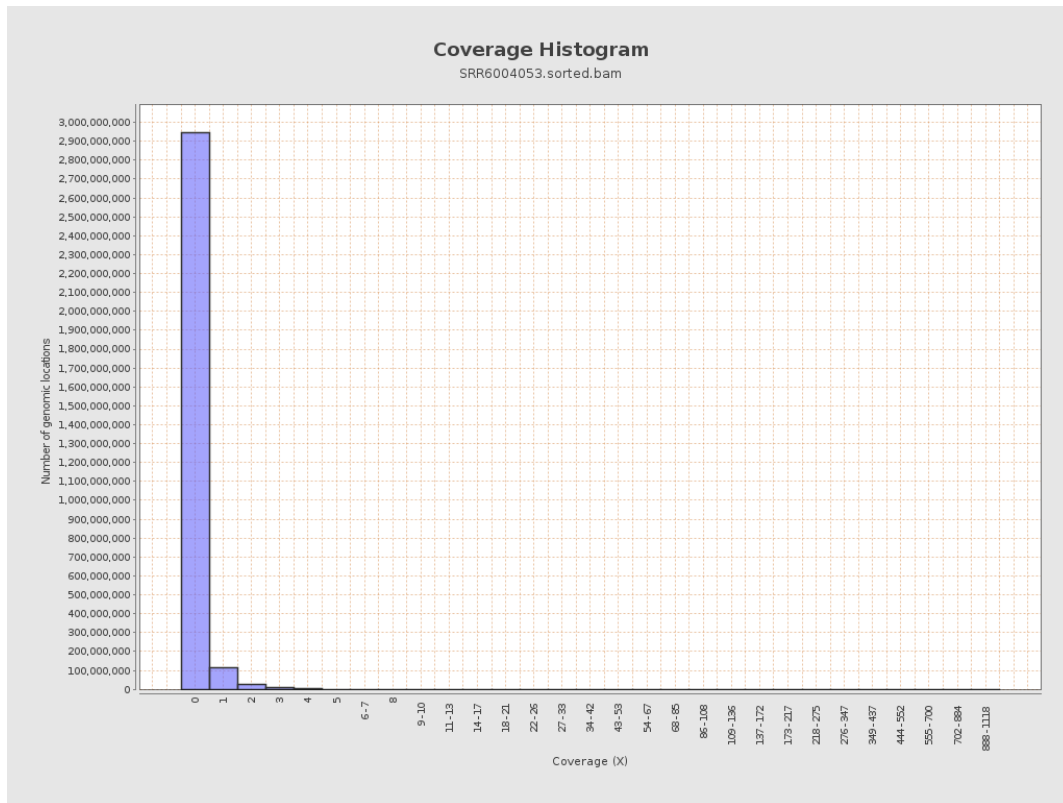
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25291850	0.1015	0.932
chr2	243199373	10732742	0.0441	0.5762
chr3	198022430	16541018	0.0835	0.3733
chr4	191154276	8871751	0.0464	0.2882
chr5	180915260	10242578	0.0566	0.315
chr6	171115067	14778627	0.0864	0.4123
chr7	159138663	12761817	0.0802	0.5235

chr8	146364022	9898461	0.0676	0.6004
chr9	141213431	6030118	0.0427	0.3425
chr10	135534747	9899331	0.073	0.4095
chr11	135006516	6590991	0.0488	0.3287
chr12	133851895	10818461	0.0808	0.3707
chr13	115169878	6311354	0.0548	0.3071
chr14	107349540	4359384	0.0406	0.2687
chr15	102531392	6277112	0.0612	0.3257
chr16	90354753	6717266	0.0743	0.3662
chr17	81195210	7996999	0.0985	0.4315
chr18	78077248	5874561	0.0752	0.6948
chr19	59128983	4748452	0.0803	0.6164
chr20	63025520	5621327	0.0892	0.4044
chr21	48129895	4020867	0.0835	0.3809
chr22	51304566	3420761	0.0667	0.3343
chrMT	16571	13758	0.8302	1.1375
chrX	155270560	8724369	0.0562	0.326
chrY	59373566	381799	0.0064	0.1163

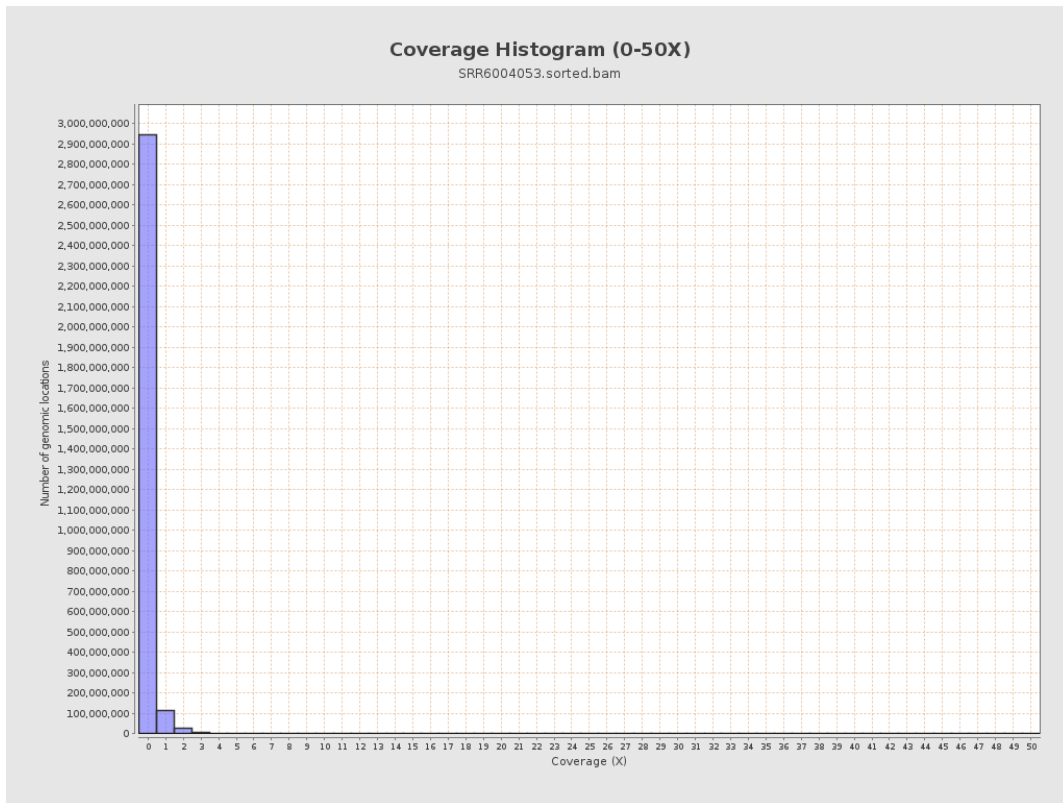
### 3. Results : Coverage across reference



# 4. Results : Coverage Histogram

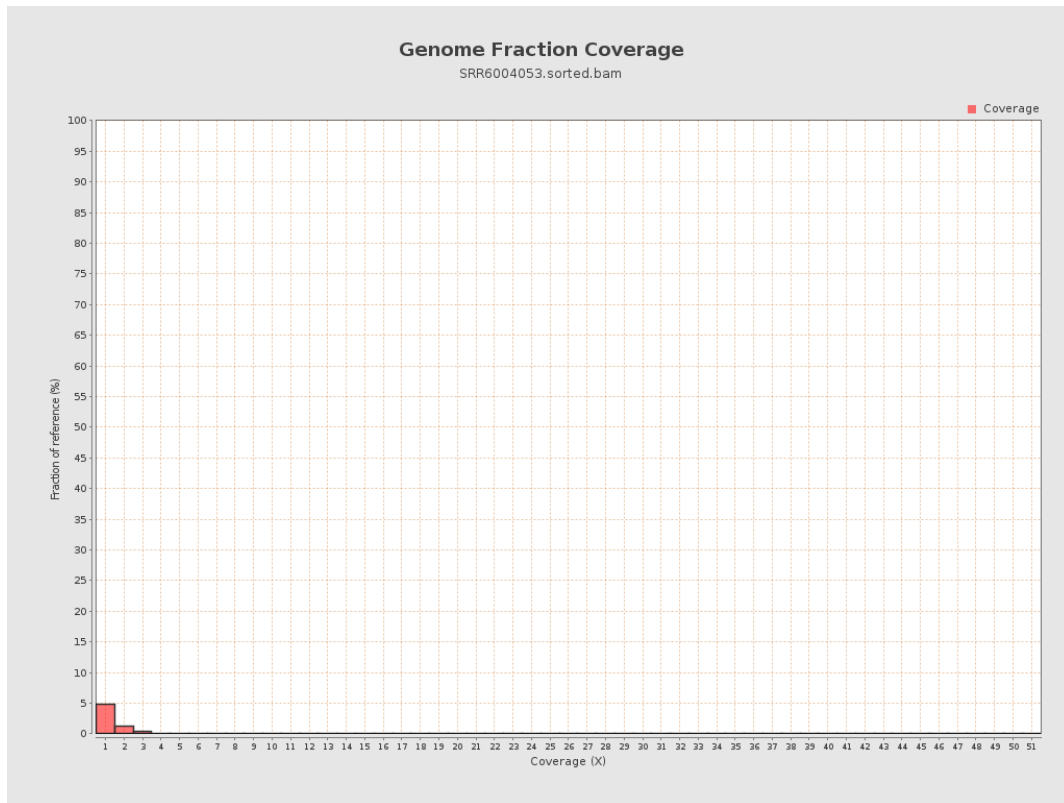


## 5. Results : Coverage Histogram (0-50X)

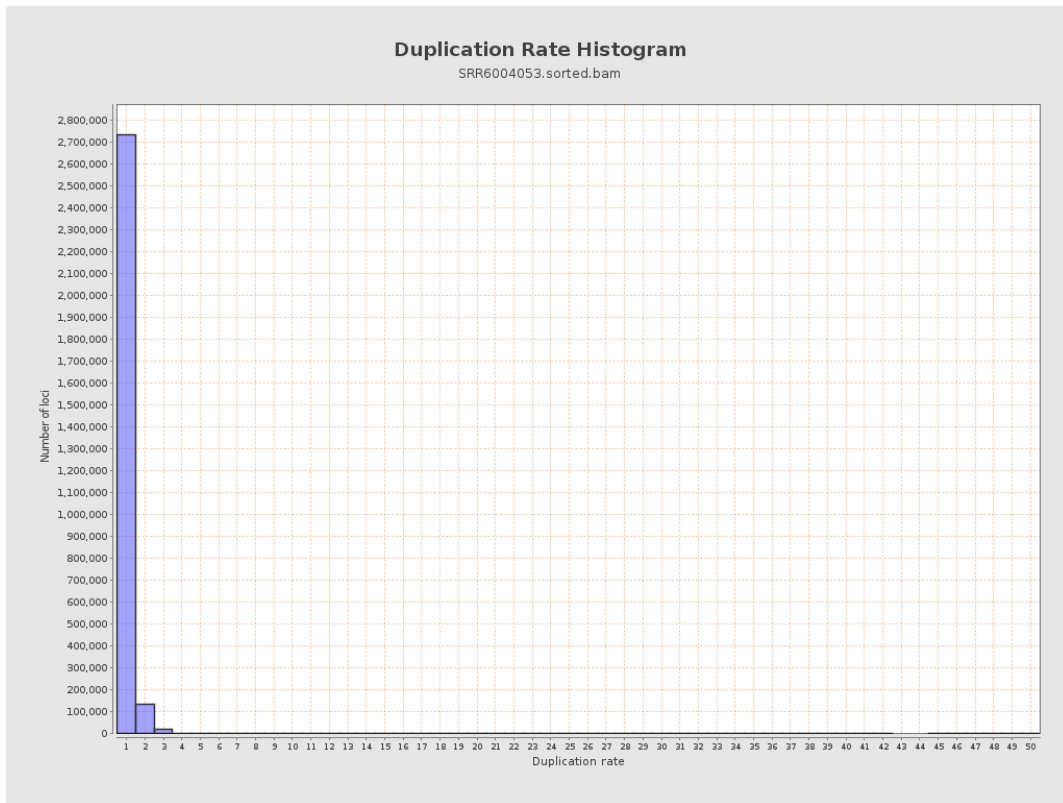




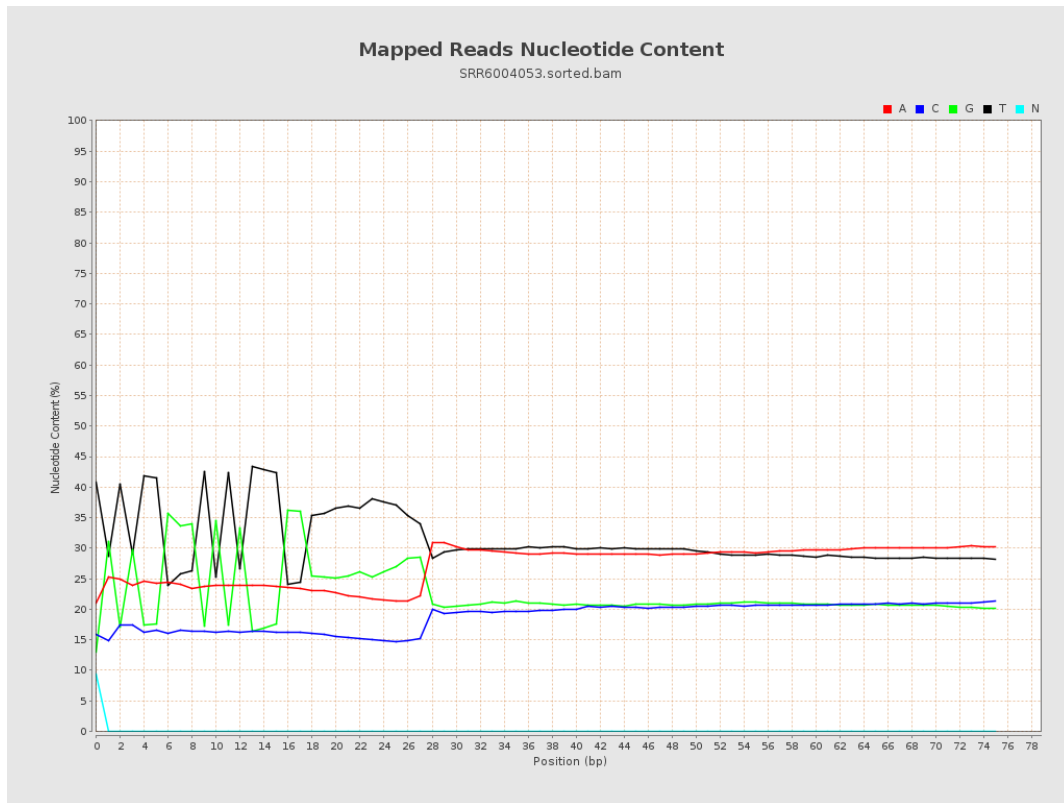
## 6. Results : Genome Fraction Coverage



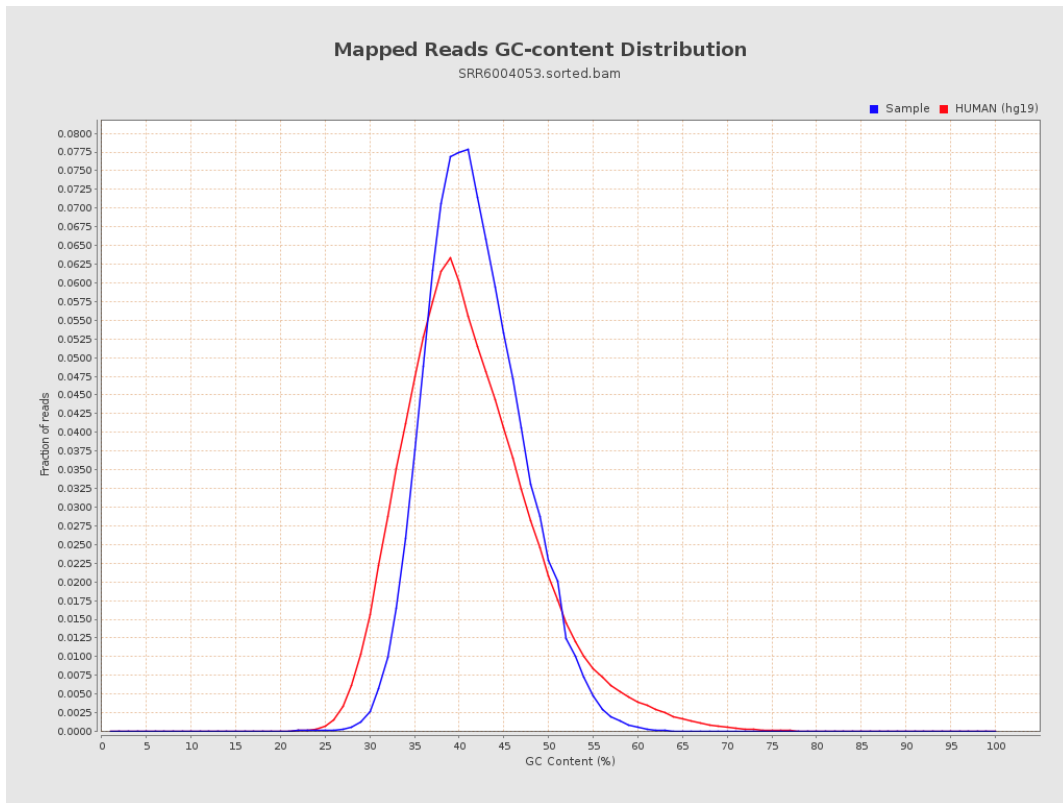
# 7. Results : Duplication Rate Histogram



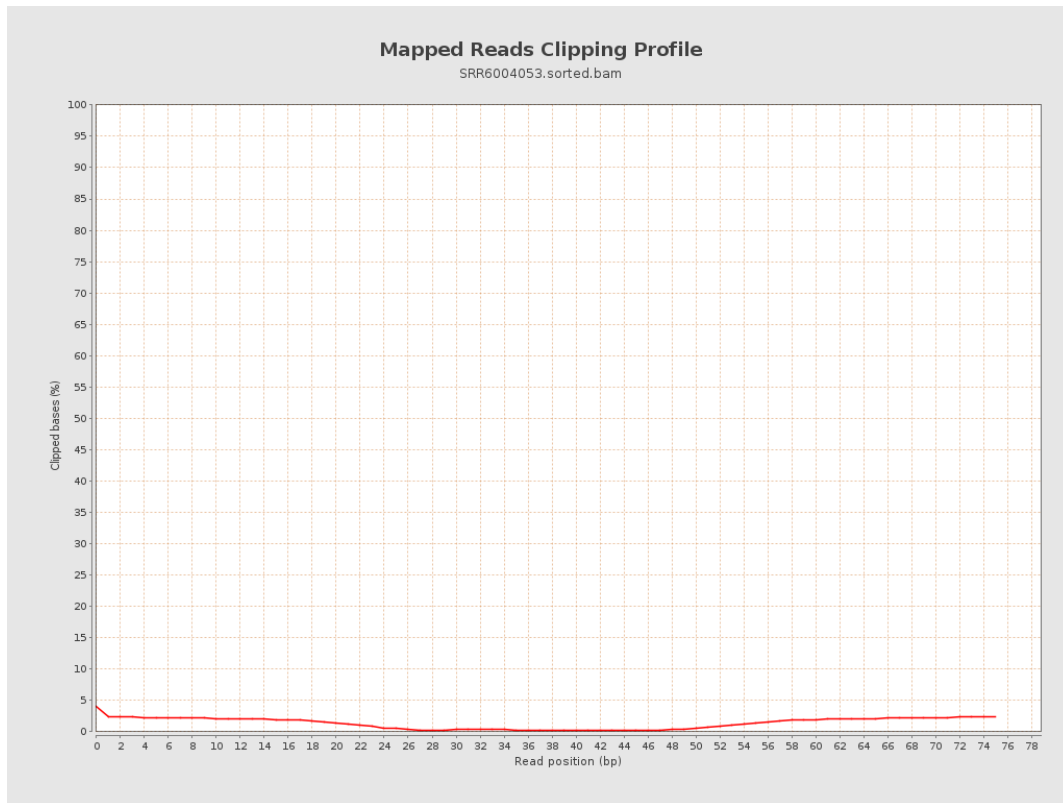
# 8. Results : Mapped Reads Nucleotide Content



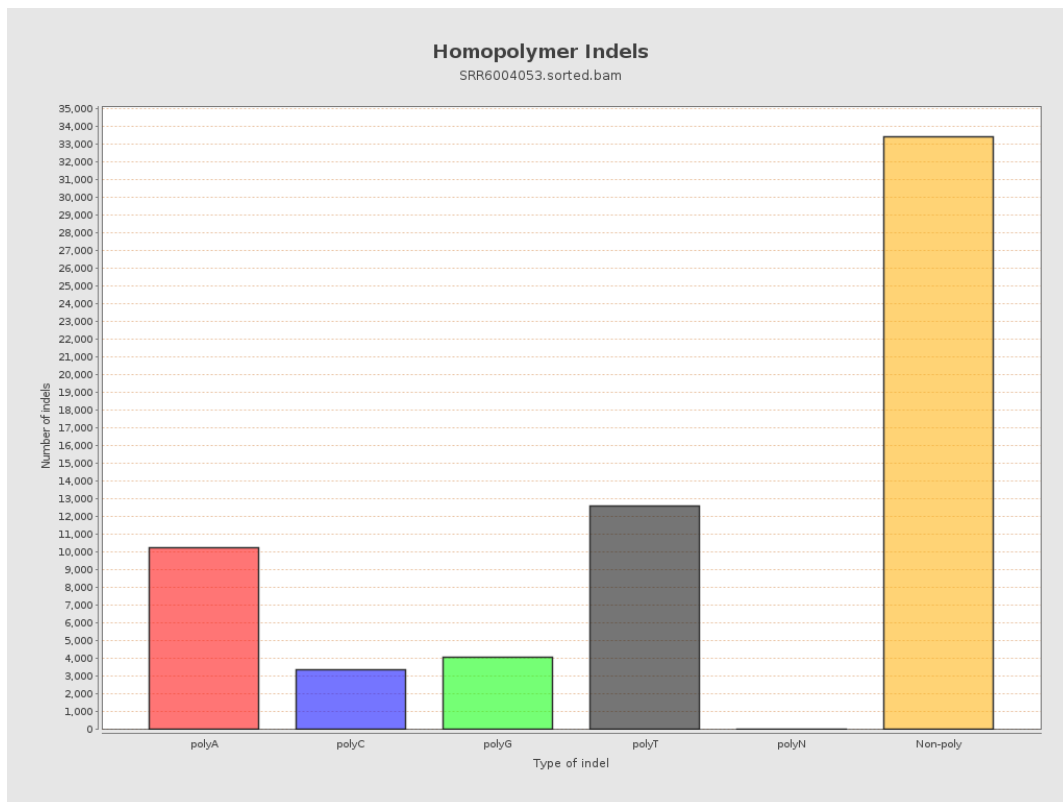
# 9. Results : Mapped Reads GC-content Distribution



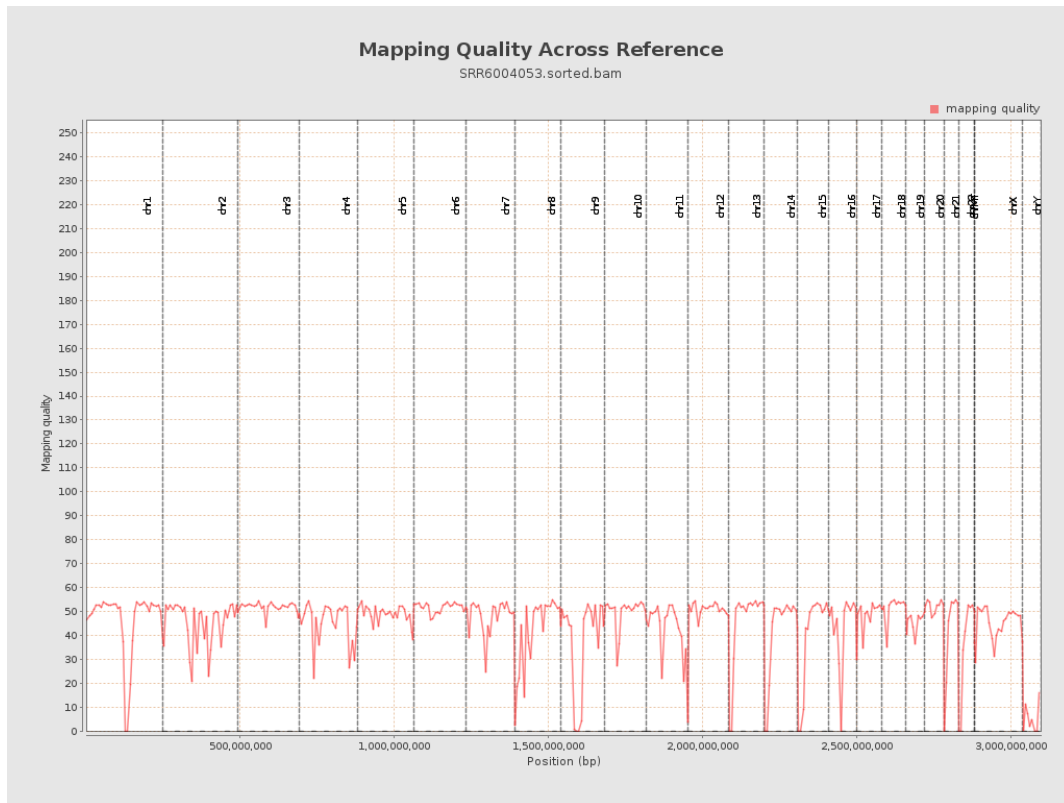
## 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram

