Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:01:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084404.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_SRR3084404 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084404.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:01:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084404.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,536,056
Mapped reads	2,329,989 / 91.87%
Unmapped reads	206,067 / 8.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,446 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	81,756 / 3.22%
Duplication rate	2.99%
Clipped reads	1,019,125 / 40.19%

2.2. ACGT Content

Number/percentage of A's	44,708,854 / 28.52%
Number/percentage of C's	29,765,665 / 18.98%
Number/percentage of T's	48,682,182 / 31.05%
Number/percentage of G's	33,425,769 / 21.32%
Number/percentage of N's	202,787 / 0.13%
GC Percentage	40.3%

2.3. Coverage

Mean	0.0507

Standard Deviation	0.3243

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

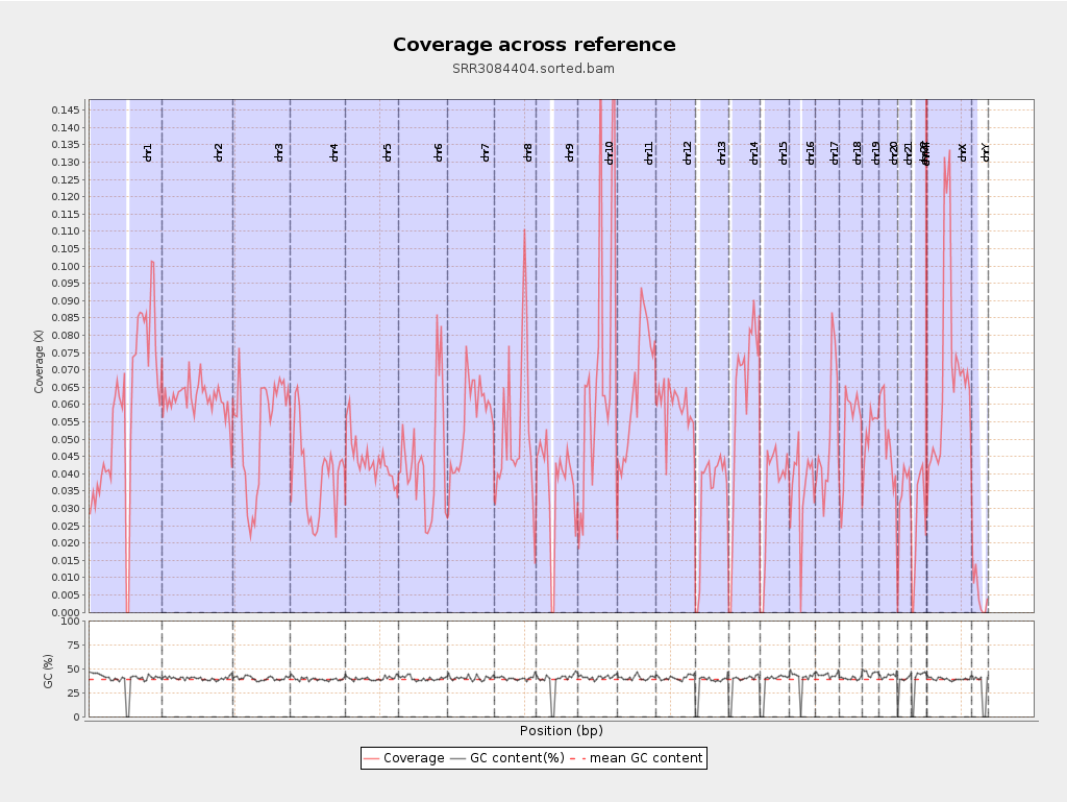
General error rate	1%
Mismatches	1,555,055
Insertions	11,150
Mapped reads with at least one insertion	0.47%
Deletions	30,548
Mapped reads with at least one deletion	1.3%
Homopolymer indels	47.36%

2.6. Chromosome stats

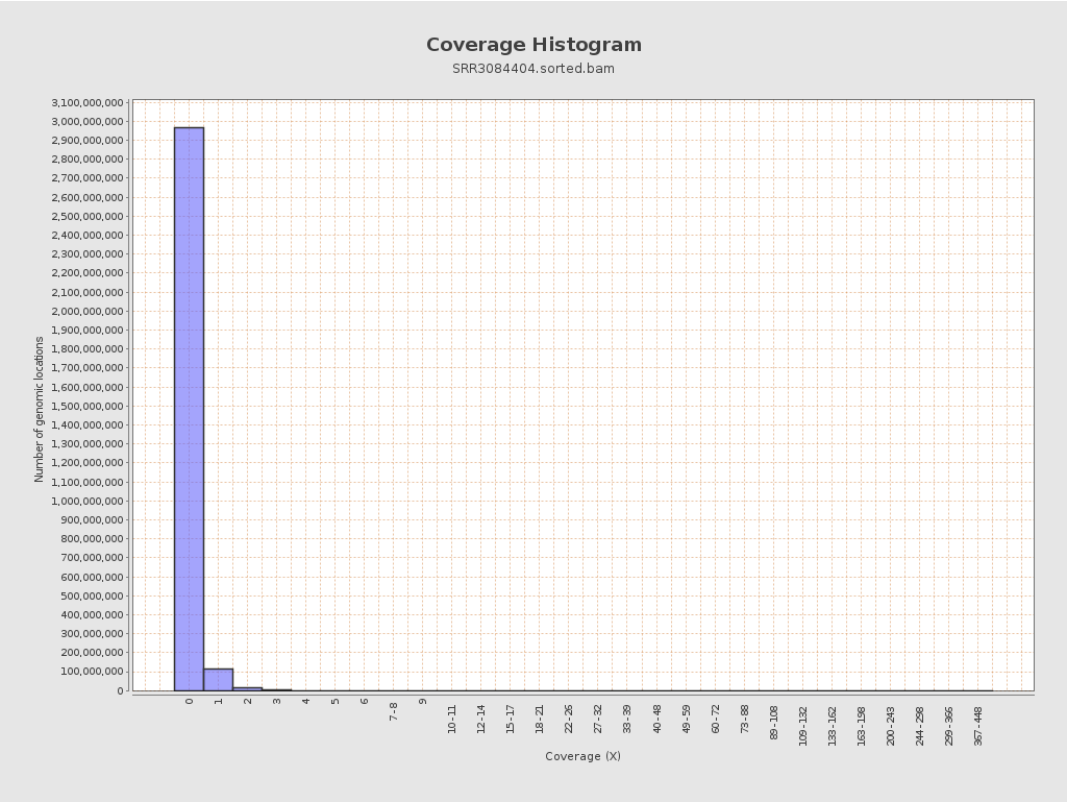
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14415664	0.0578	0.4864
chr2	243199373	15011686	0.0617	0.368
chr3	198022430	10539268	0.0532	0.2669
chr4	191154276	7576066	0.0396	0.2356
chr5	180915260	7952488	0.044	0.242
chr6	171115067	7511041	0.0439	0.2692
chr7	159138663	8852104	0.0556	0.4395

chr8	146364022	7616049	0.052	0.337
chr9	141213431	5229383	0.037	0.2714
chr10	135534747	9693528	0.0715	0.3976
chr11	135006516	8780114	0.065	0.3487
chr12	133851895	7961225	0.0595	0.2822
chr13	115169878	3893399	0.0338	0.2109
chr14	107349540	6644589	0.0619	0.2955
chr15	102531392	3558025	0.0347	0.218
chr16	90354753	3270932	0.0362	0.2352
chr17	81195210	4132064	0.0509	0.2748
chr18	78077248	4156833	0.0532	0.4261
chr19	59128983	3073698	0.052	0.3622
chr20	63025520	3123825	0.0496	0.2598
chr21	48129895	1583046	0.0329	0.2191
chr22	51304566	1329528	0.0259	0.1837
chrMT	16571	8545	0.5157	0.9409
chrX	155270560	10607172	0.0683	0.3384
chrY	59373566	318156	0.0054	0.1103

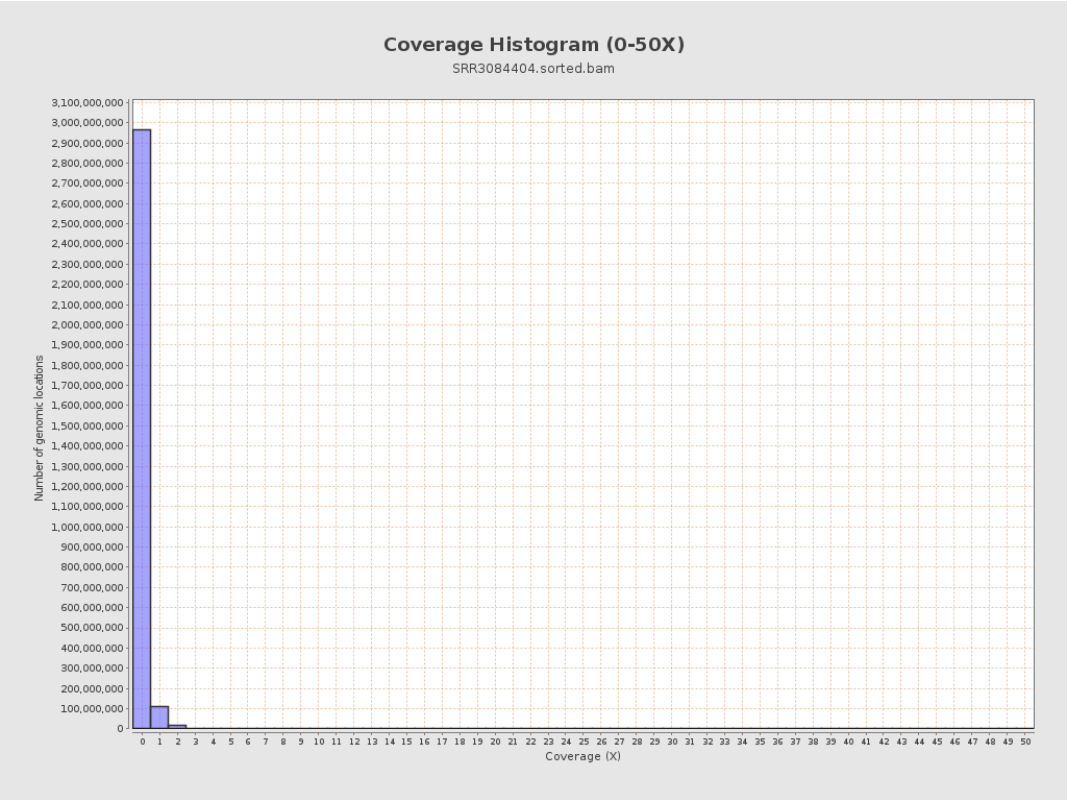
3. Results : Coverage across reference



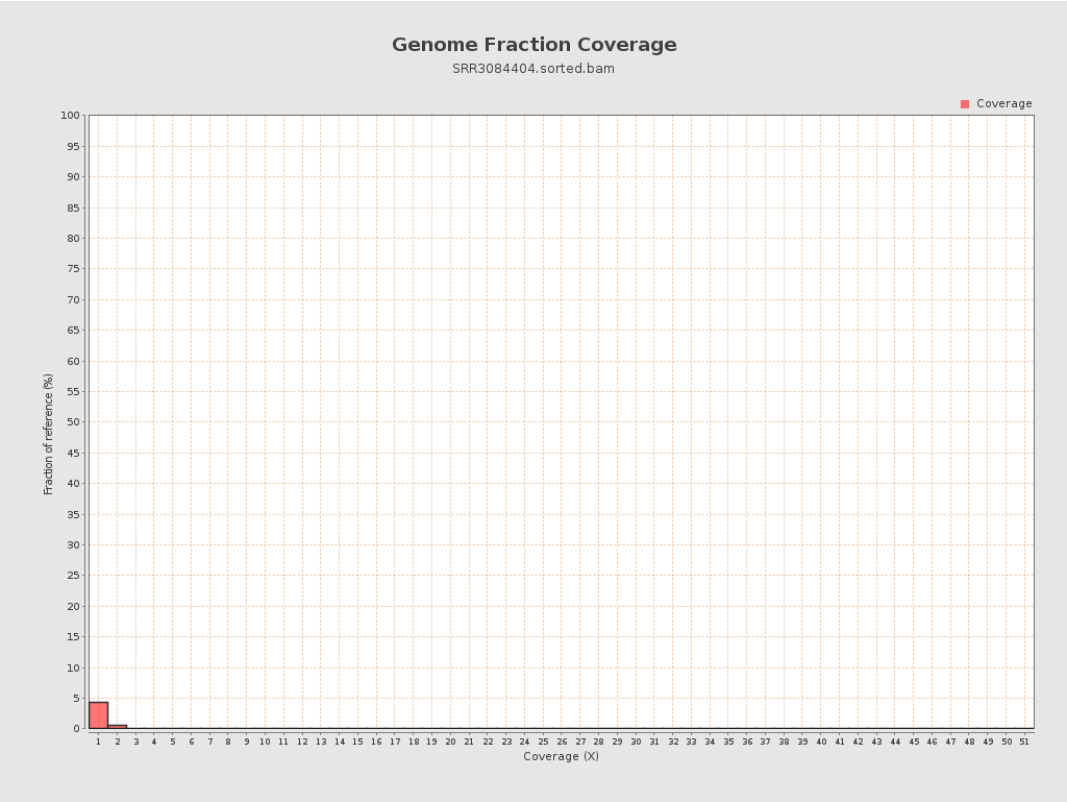
4. Results : Coverage Histogram



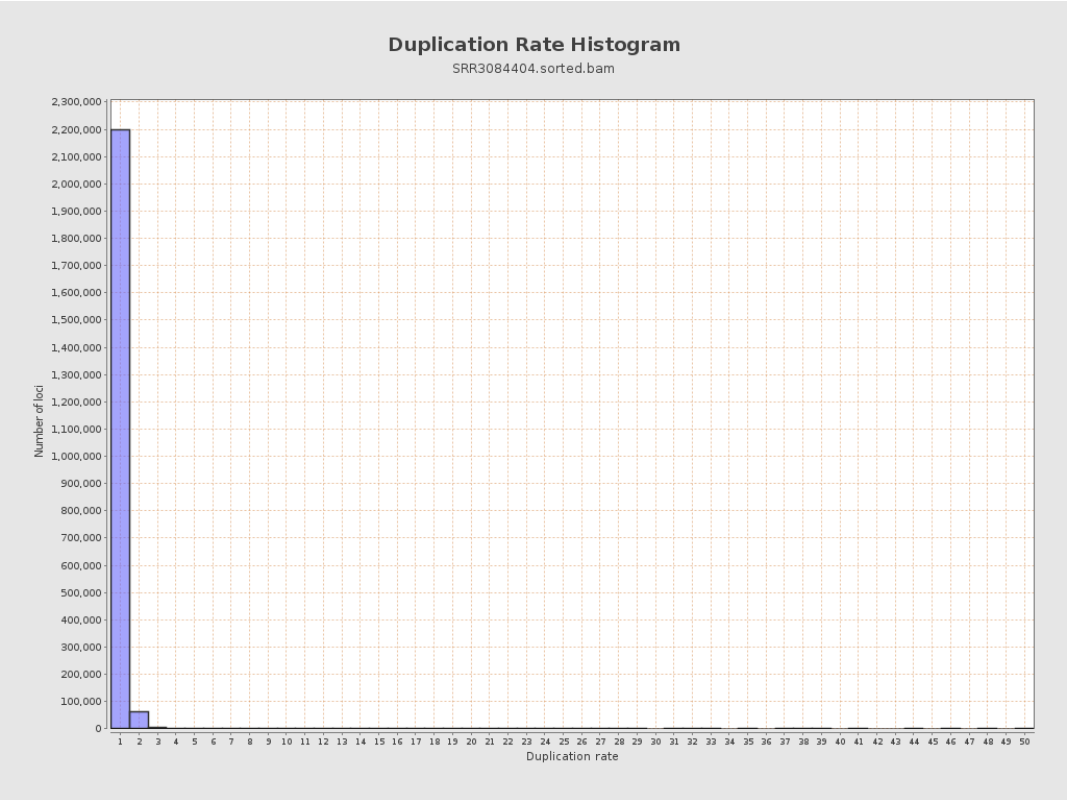
5. Results : Coverage Histogram (0-50X)



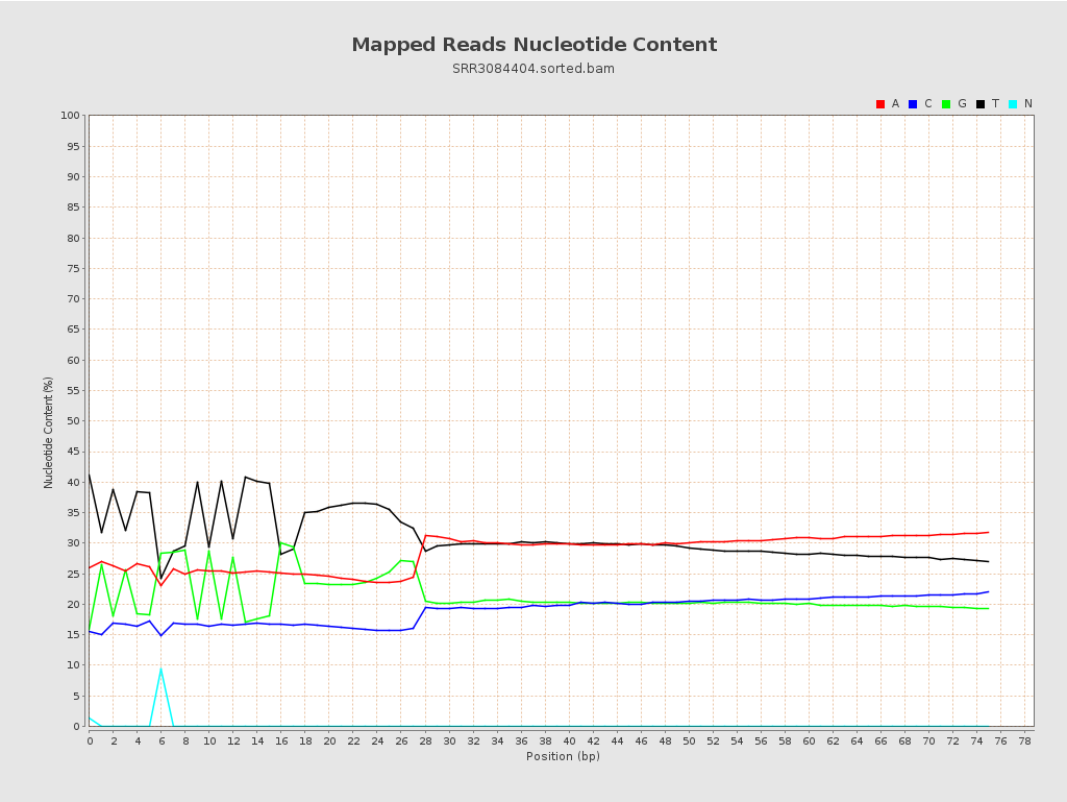
6. Results : Genome Fraction Coverage



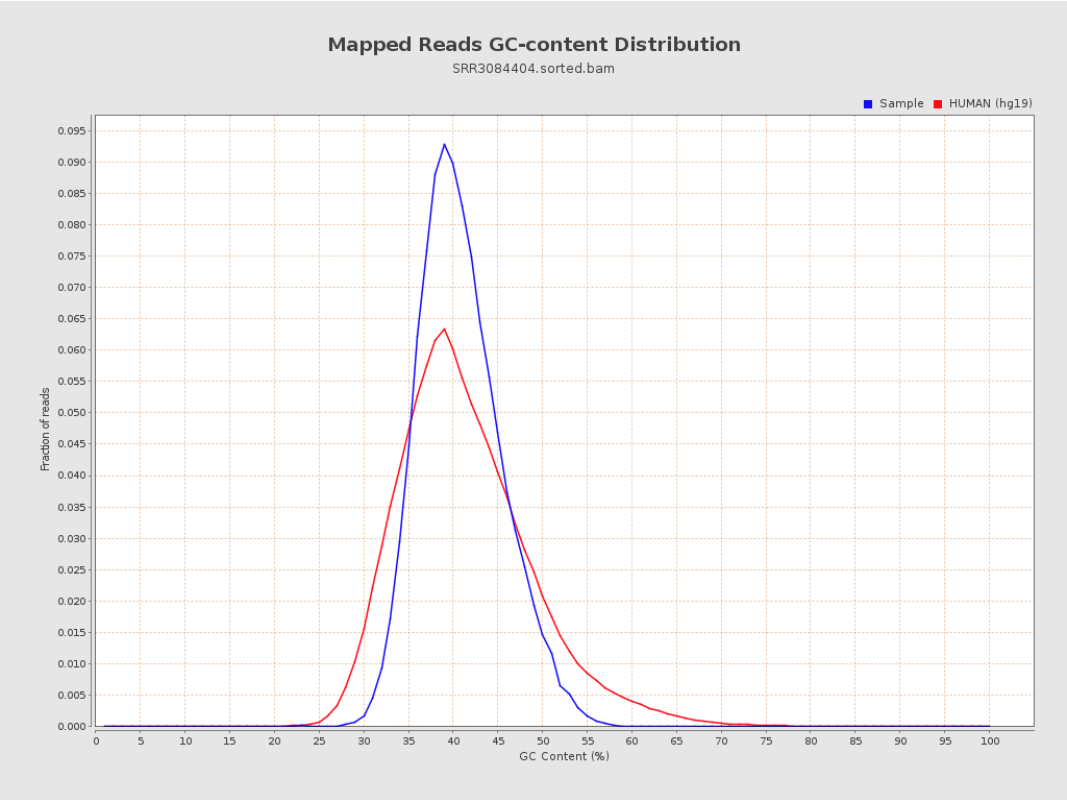
7. Results : Duplication Rate Histogram



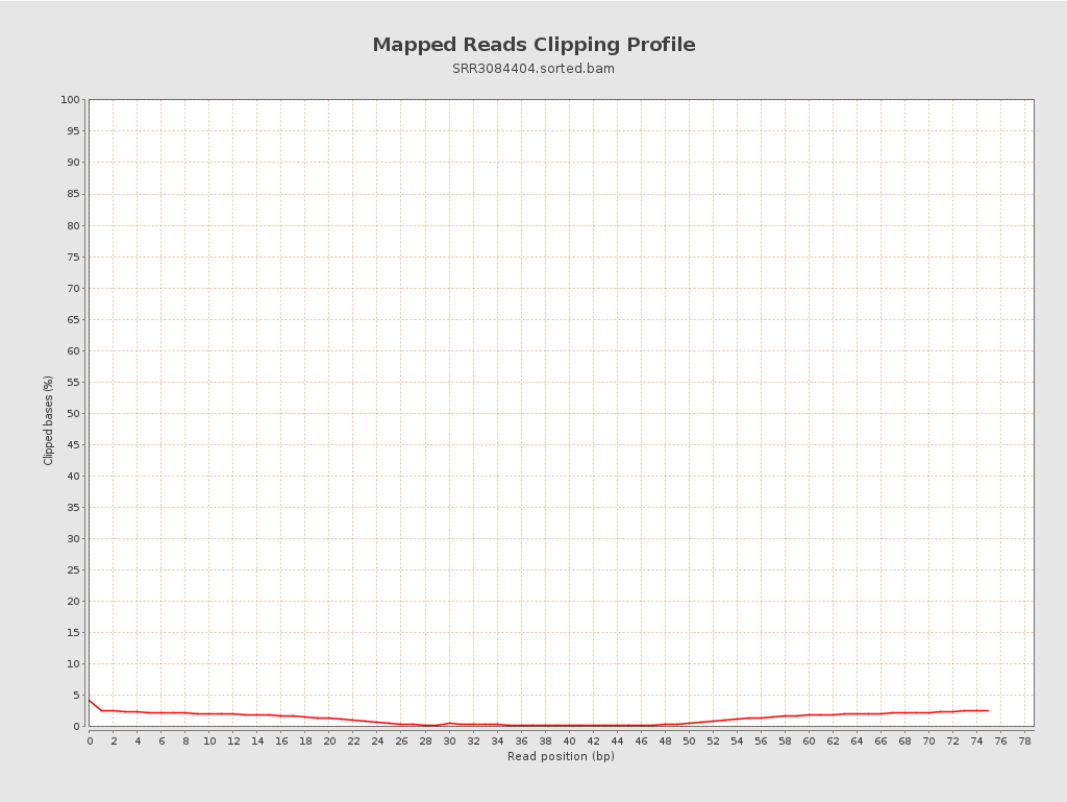
8. Results : Mapped Reads Nucleotide Content



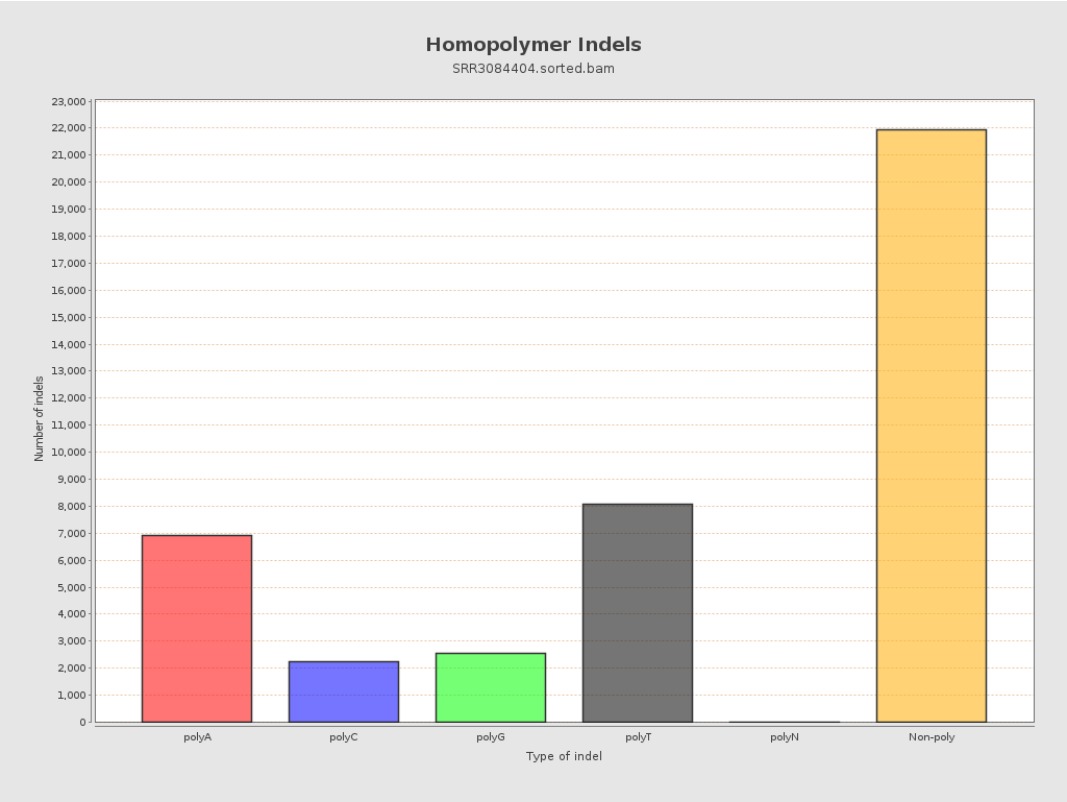
9. Results : Mapped Reads GC-content Distribution



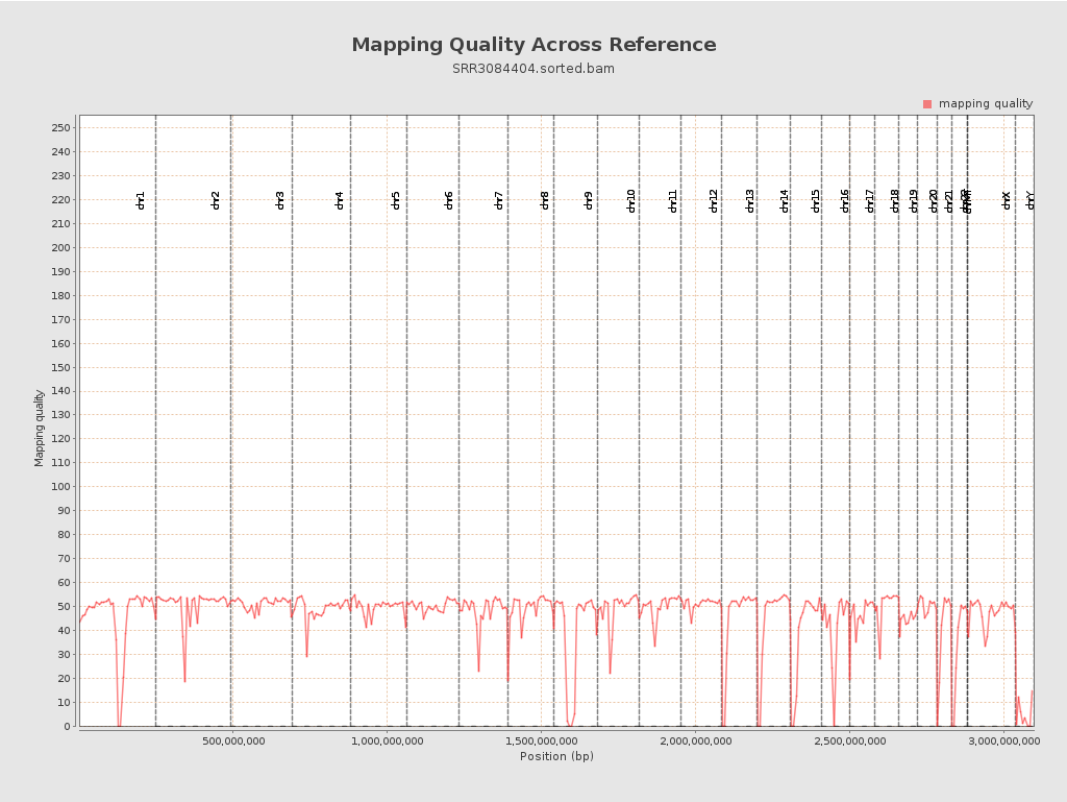
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram