Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 09:24:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472833.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_SRR3472833 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472833.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 09:24:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472833.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,453,604
Mapped reads	2,810,648 / 81.38%
Unmapped reads	642,956 / 18.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,889 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	102,737 / 2.97%
Duplication rate	2.79%
Clipped reads	1,385,165 / 40.11%

2.2. ACGT Content

Number/percentage of A's	49,512,010 / 26.92%
Number/percentage of C's	36,511,870 / 19.85%
Number/percentage of T's	54,957,824 / 29.89%
Number/percentage of G's	42,911,685 / 23.33%
Number/percentage of N's	4,247 / 0%
GC Percentage	43.19%

2.3. Coverage

Mean	0.0594

Standard Deviation	0.4103

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

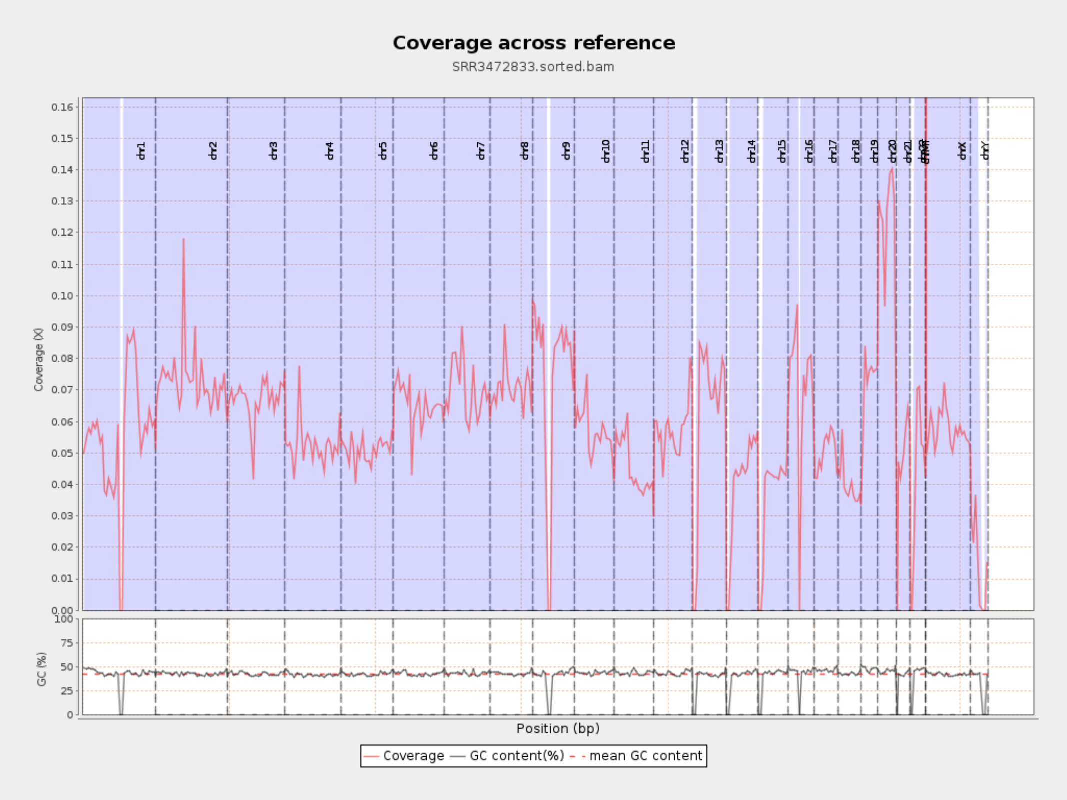
General error rate	0.82%
Mismatches	1,490,040
Insertions	14,065
Mapped reads with at least one insertion	0.5%
Deletions	41,948
Mapped reads with at least one deletion	1.48%
Homopolymer indels	45.72%

2.6. Chromosome stats

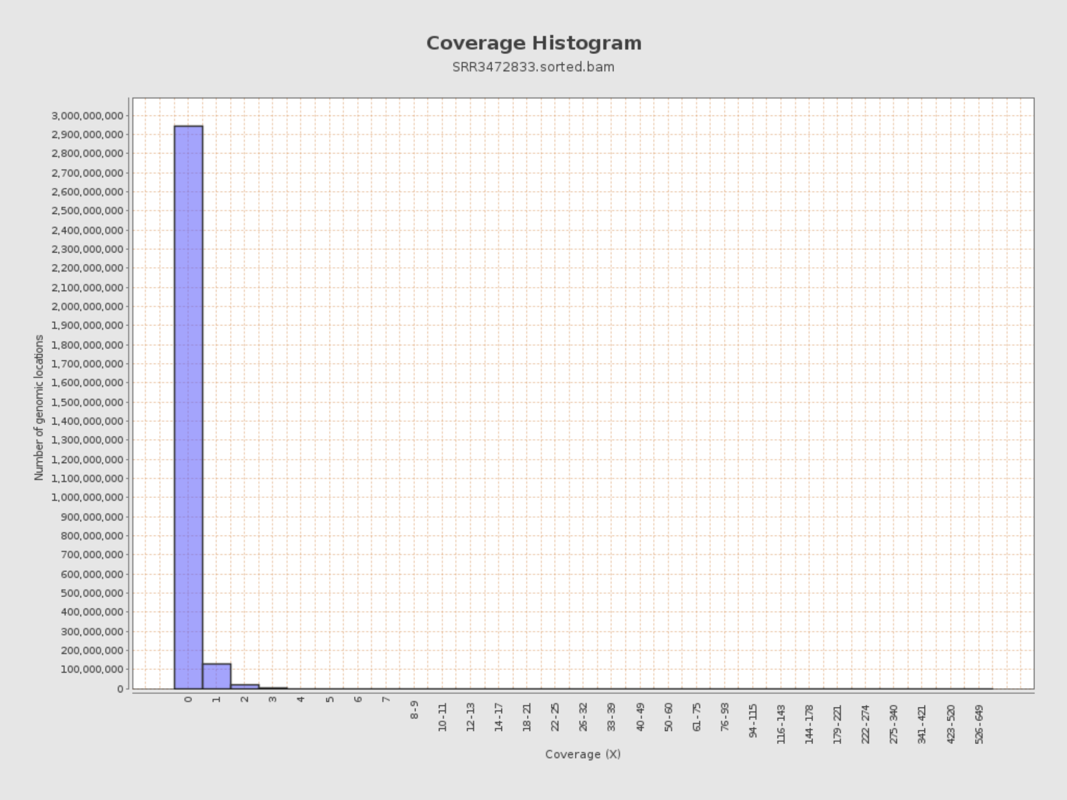
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13648331	0.0548	0.5365
chr2	243199373	17848356	0.0734	0.592
chr3	198022430	13178377	0.0665	0.3039
chr4	191154276	10102482	0.0528	0.298
chr5	180915260	9247849	0.0511	0.2607
chr6	171115067	11184160	0.0654	0.33
chr7	159138663	11195334	0.0703	0.5582

chr8	146364022	10319175	0.0705	0.4116
chr9	141213431	10507744	0.0744	0.4967
chr10	135534747	7711309	0.0569	0.3807
chr11	135006516	6118259	0.0453	0.3791
chr12	133851895	7747287	0.0579	0.2852
chr13	115169878	7212725	0.0626	0.3043
chr14	107349540	4282549	0.0399	0.2655
chr15	102531392	3565093	0.0348	0.233
chr16	90354753	6265682	0.0693	0.3385
chr17	81195210	4112730	0.0507	0.2837
chr18	78077248	3123369	0.04	0.7599
chr19	59128983	4260849	0.0721	0.4362
chr20	63025520	7873839	0.1249	0.4377
chr21	48129895	2305530	0.0479	0.3078
chr22	51304566	2155164	0.042	0.2501
chrMT	16571	195015	11.7685	8.7687
chrX	155270560	8937307	0.0576	0.3131
chrY	59373566	874429	0.0147	0.1971

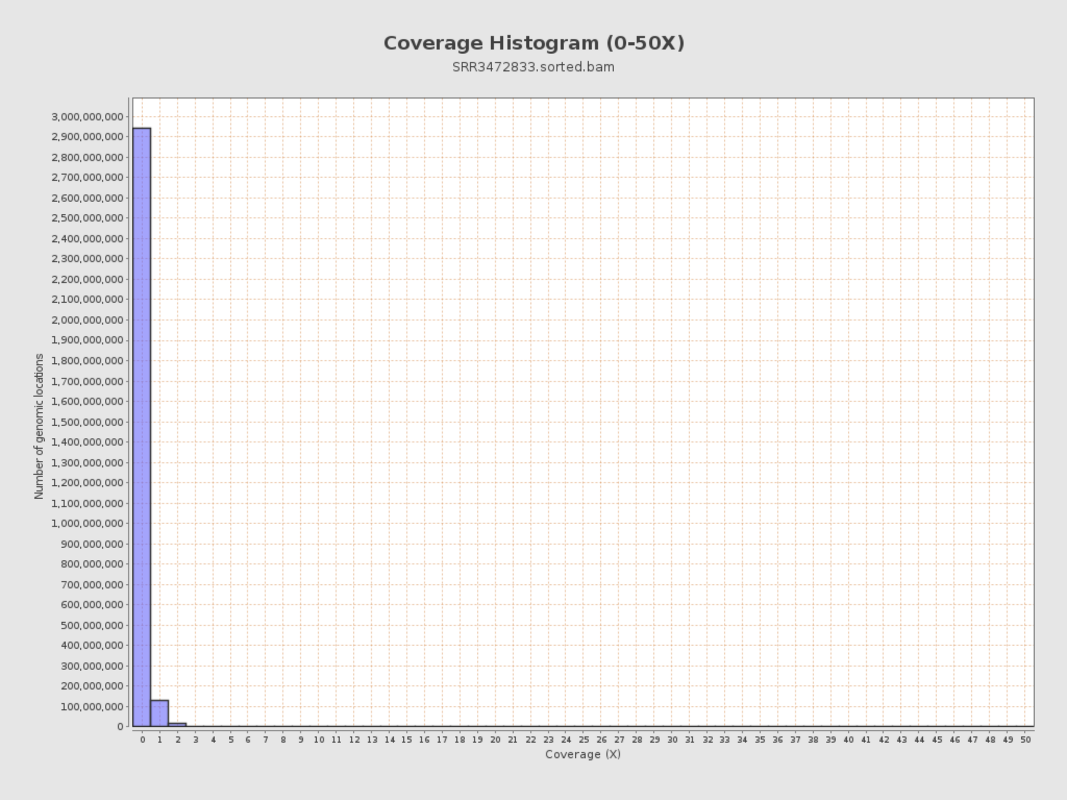
3. Results : Coverage across reference



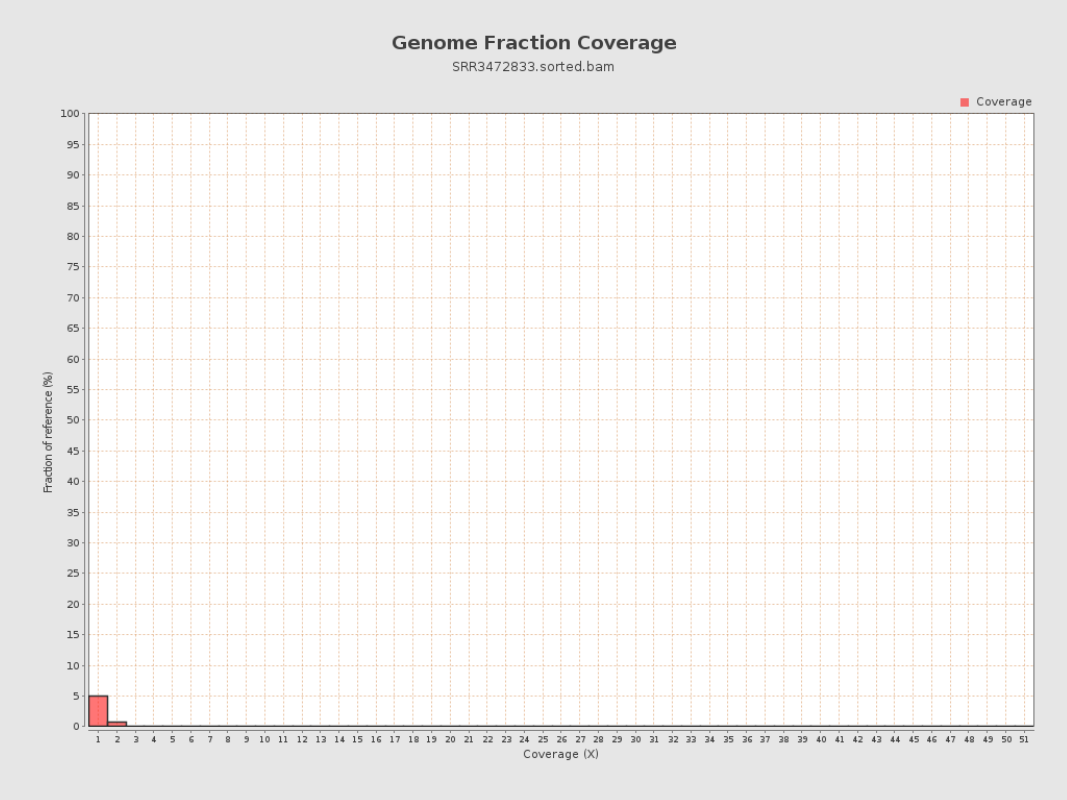
4. Results : Coverage Histogram



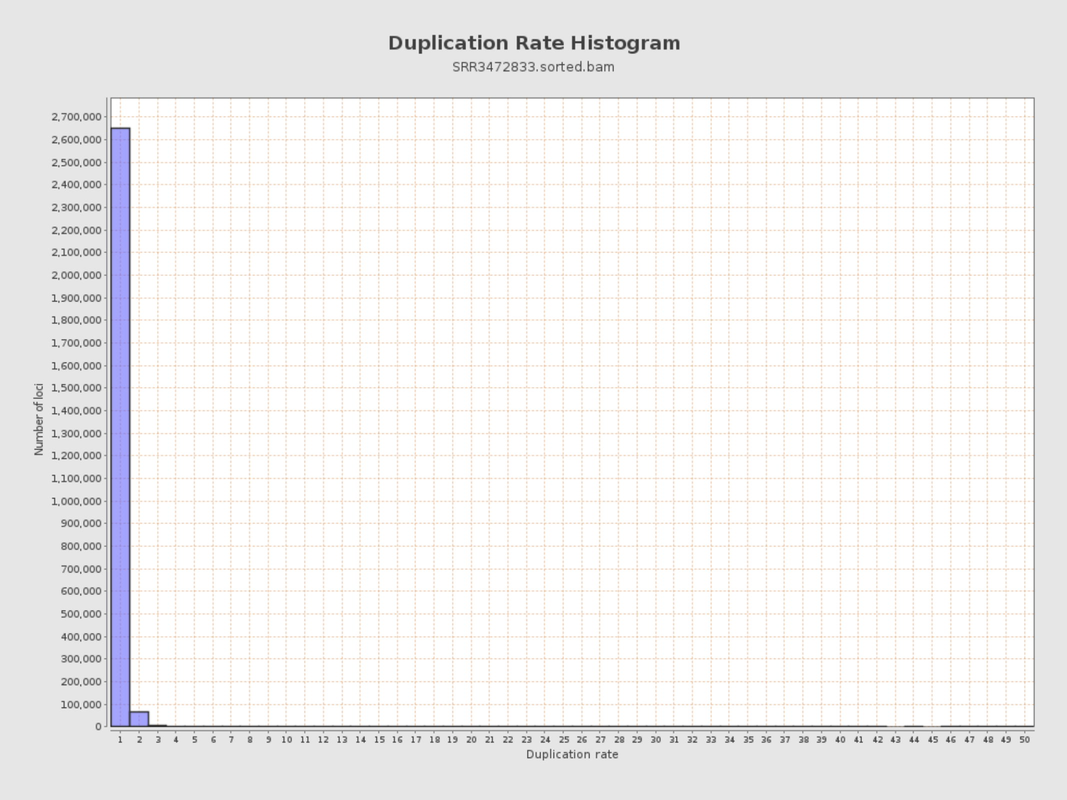
5. Results : Coverage Histogram (0-50X)



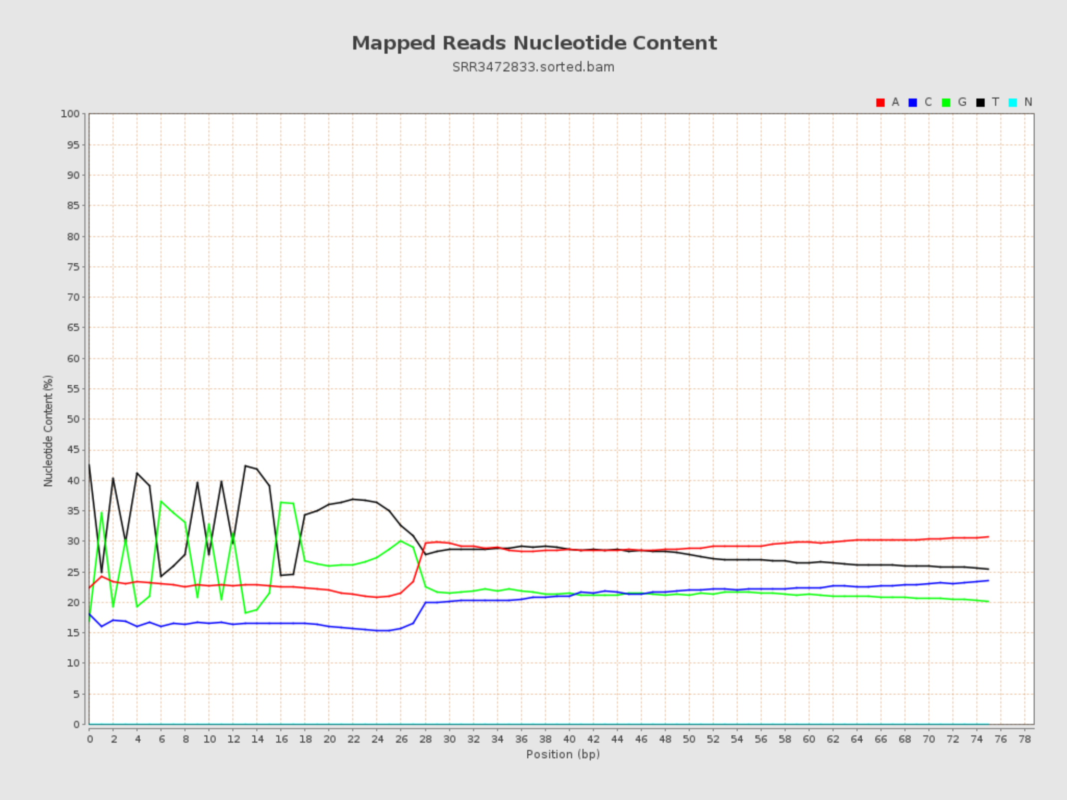
6. Results : Genome Fraction Coverage



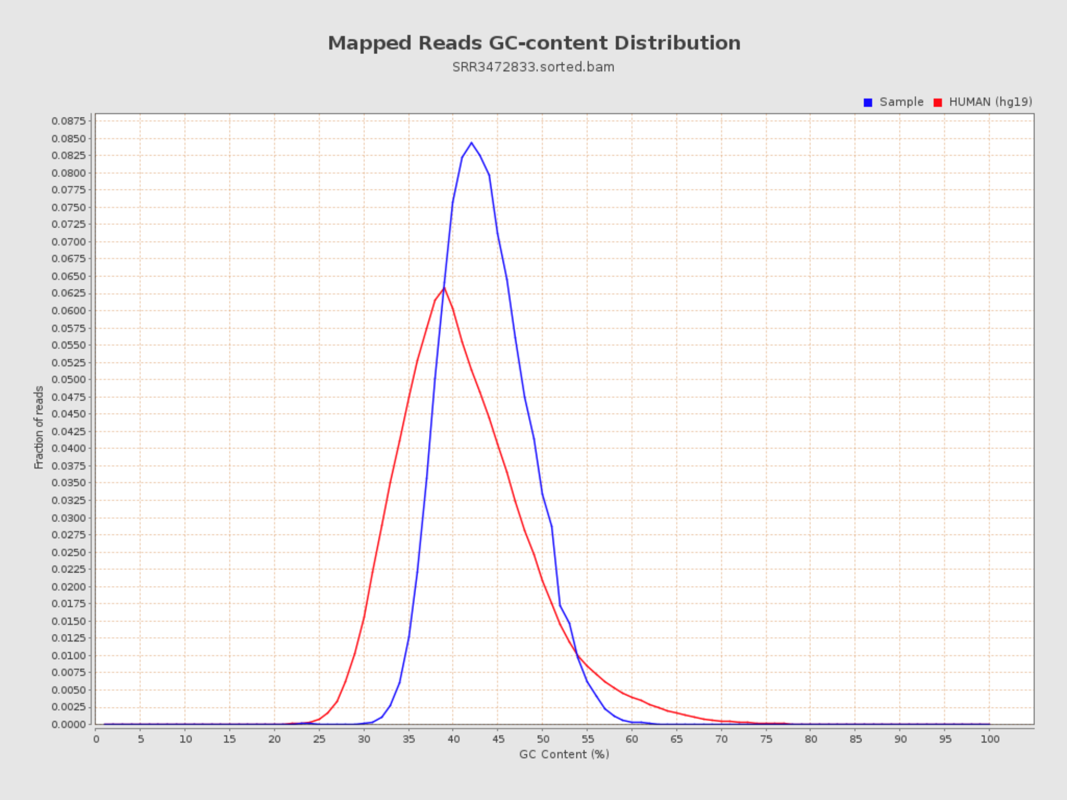
7. Results : Duplication Rate Histogram



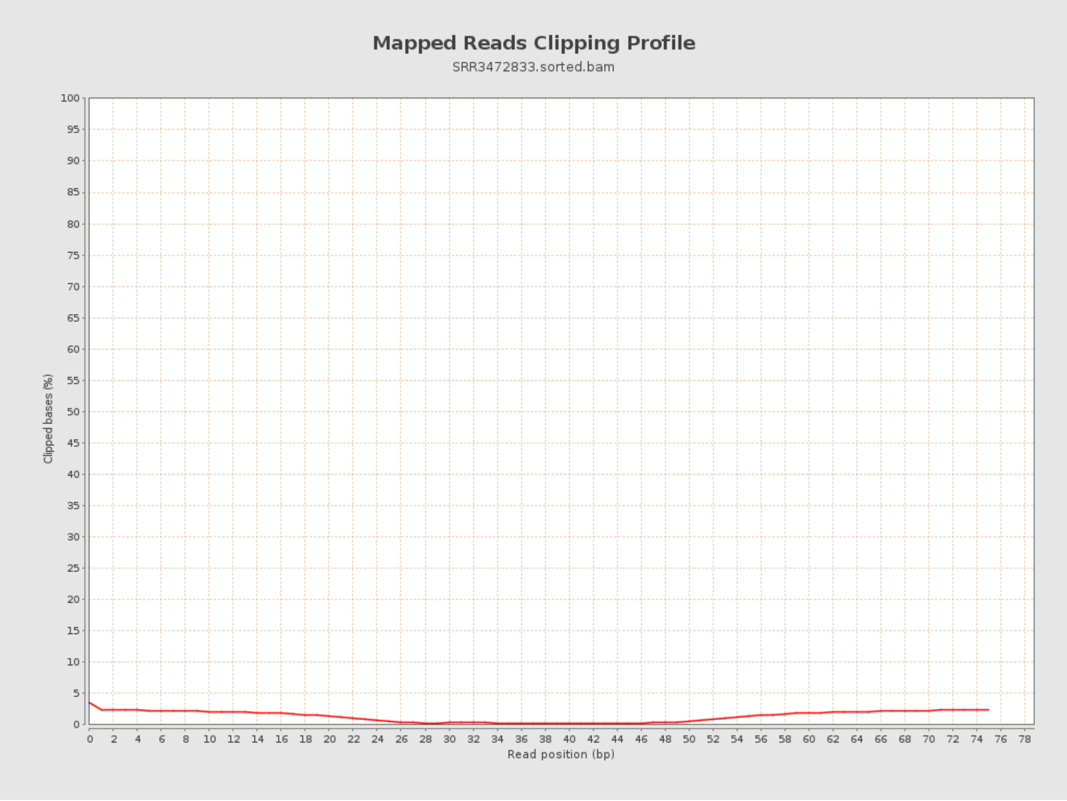
8. Results : Mapped Reads Nucleotide Content



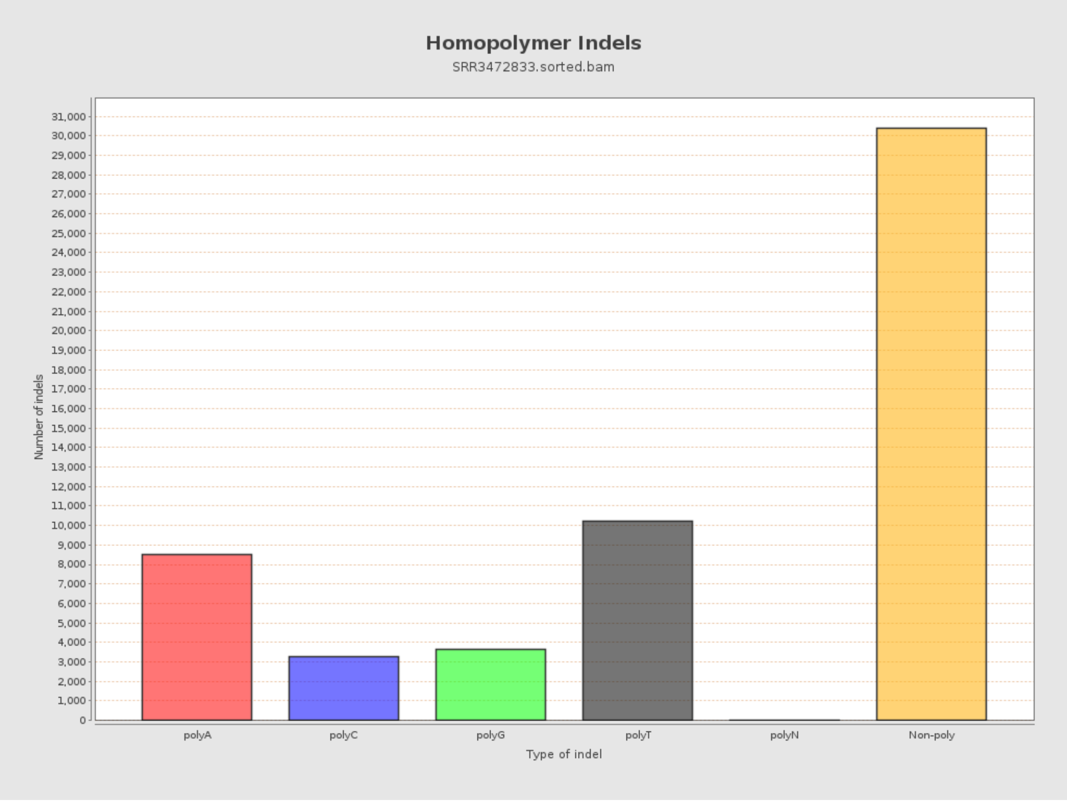
9. Results : Mapped Reads GC-content Distribution



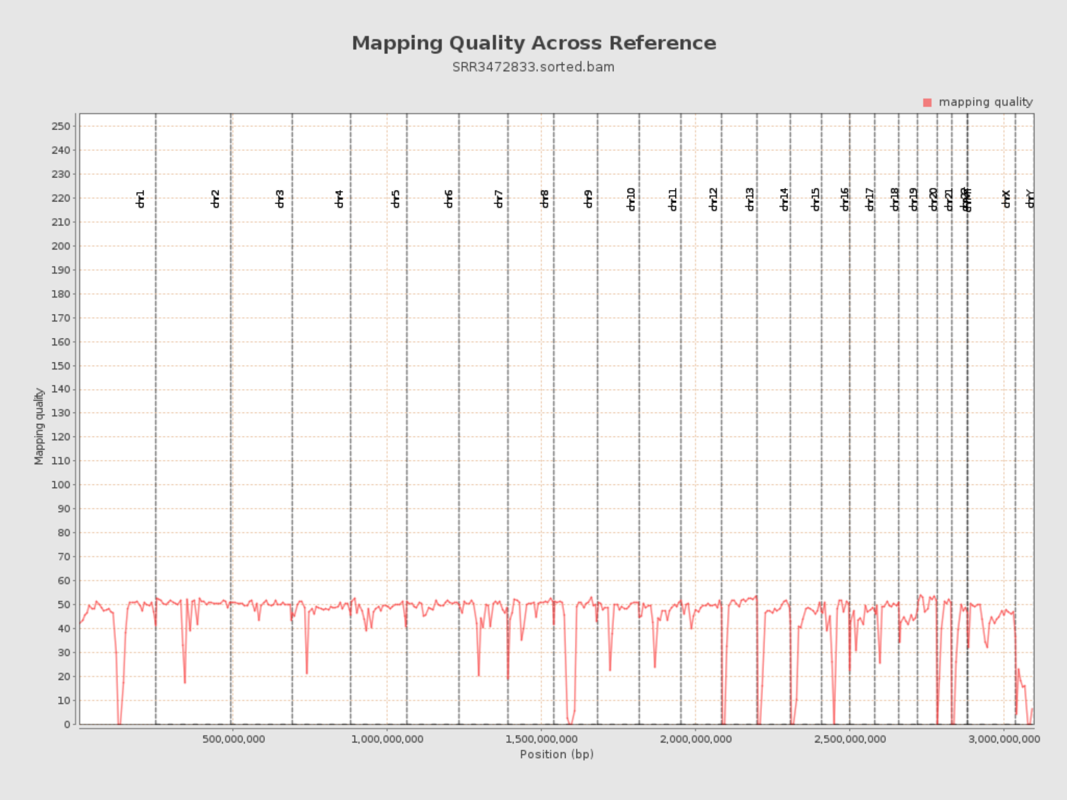
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram