Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:23:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082471.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_SRR3082471 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082471.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:23:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082471.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,444,876
Mapped reads	1,264,409 / 87.51%
Unmapped reads	180,467 / 12.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,552 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	36,053 / 2.5%
Duplication rate	2.19%
Clipped reads	533,930 / 36.95%

2.2. ACGT Content

Number/percentage of A's	24,578,003 / 28.65%
Number/percentage of C's	16,063,764 / 18.72%
Number/percentage of T's	26,156,957 / 30.49%
Number/percentage of G's	18,993,768 / 22.14%
Number/percentage of N's	1,707 / 0%
GC Percentage	40.86%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2605

2.4. Mapping Quality

Mean Mapping Quality	45.79

2.5. Mismatches and indels

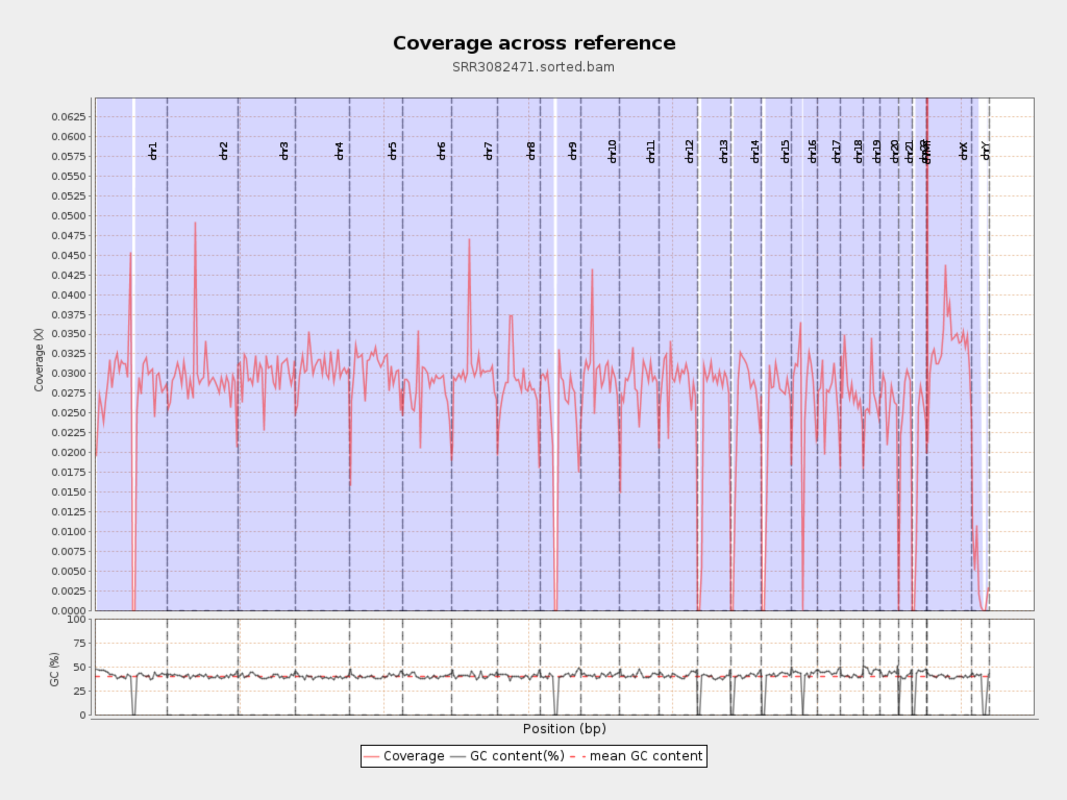
General error rate	0.89%
Mismatches	749,050
Insertions	7,250
Mapped reads with at least one insertion	0.57%
Deletions	20,019
Mapped reads with at least one deletion	1.57%
Homopolymer indels	46.64%

2.6. Chromosome stats

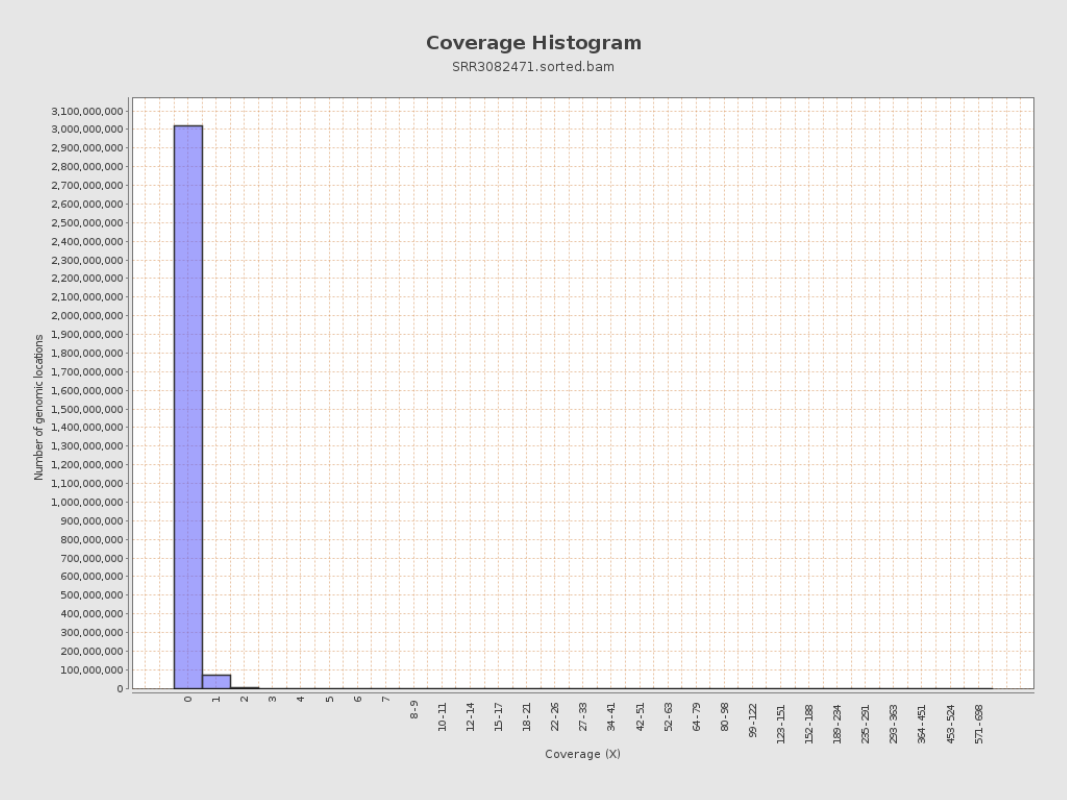
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6860295	0.0275	0.4041
chr2	243199373	7169030	0.0295	0.3004
chr3	198022430	5943654	0.03	0.1841
chr4	191154276	5849723	0.0306	0.1898
chr5	180915260	5543099	0.0306	0.1865
chr6	171115067	4810248	0.0281	0.1978
chr7	159138663	4849322	0.0305	0.3309

chr8	146364022	4167150	0.0285	0.4528
chr9	141213431	3444001	0.0244	0.2311
chr10	135534747	4052834	0.0299	0.2426
chr11	135006516	3871366	0.0287	0.2364
chr12	133851895	3889074	0.0291	0.1819
chr13	115169878	2829554	0.0246	0.1661
chr14	107349540	2614774	0.0244	0.1716
chr15	102531392	2410553	0.0235	0.1666
chr16	90354753	2394258	0.0265	0.1898
chr17	81195210	2200081	0.0271	0.1919
chr18	78077248	2181015	0.0279	0.3956
chr19	59128983	1568679	0.0265	0.3322
chr20	63025520	1633148	0.0259	0.1732
chr21	48129895	1153848	0.024	0.1707
chr22	51304566	923970	0.018	0.1422
chrMT	16571	24647	1.4874	1.3998
chrX	155270560	5222089	0.0336	0.2087
chrY	59373566	220484	0.0037	0.0878

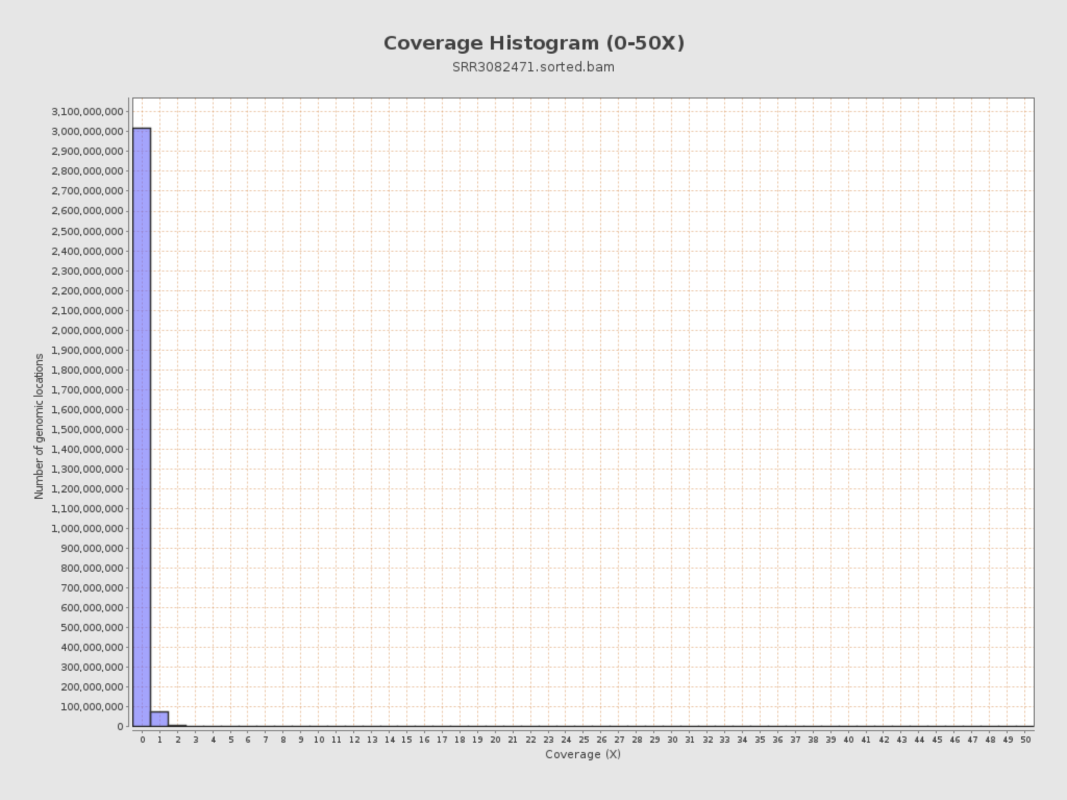
3. Results : Coverage across reference



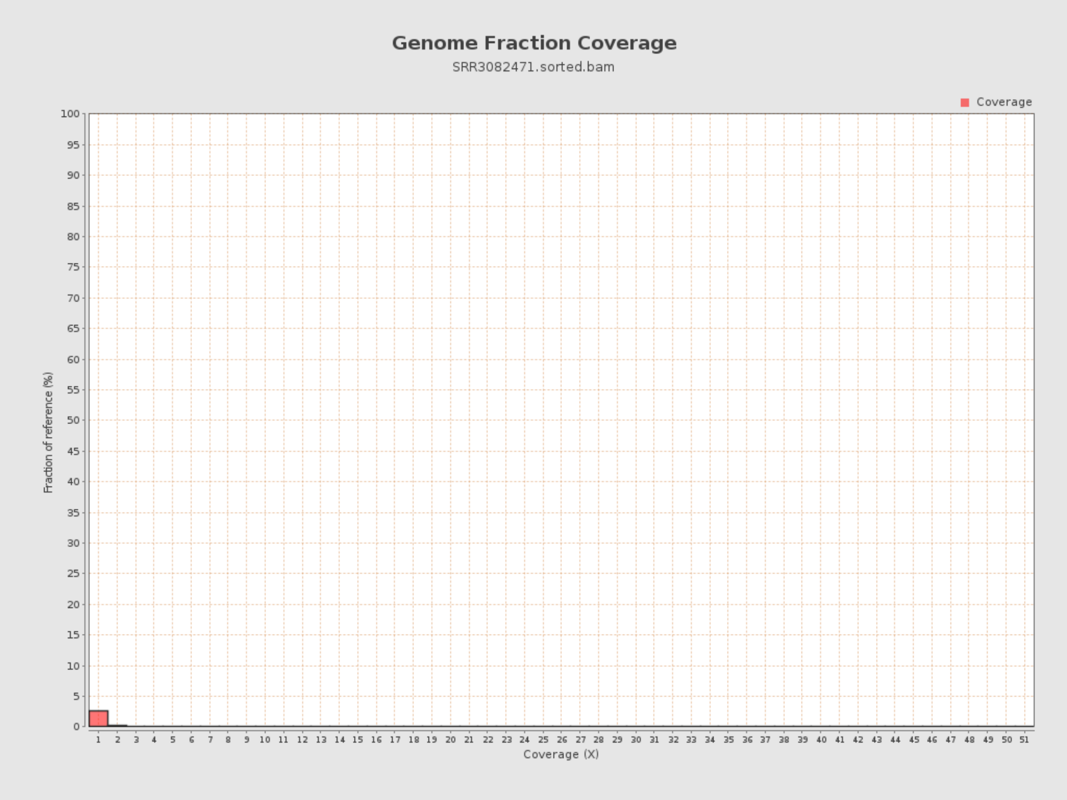
4. Results : Coverage Histogram



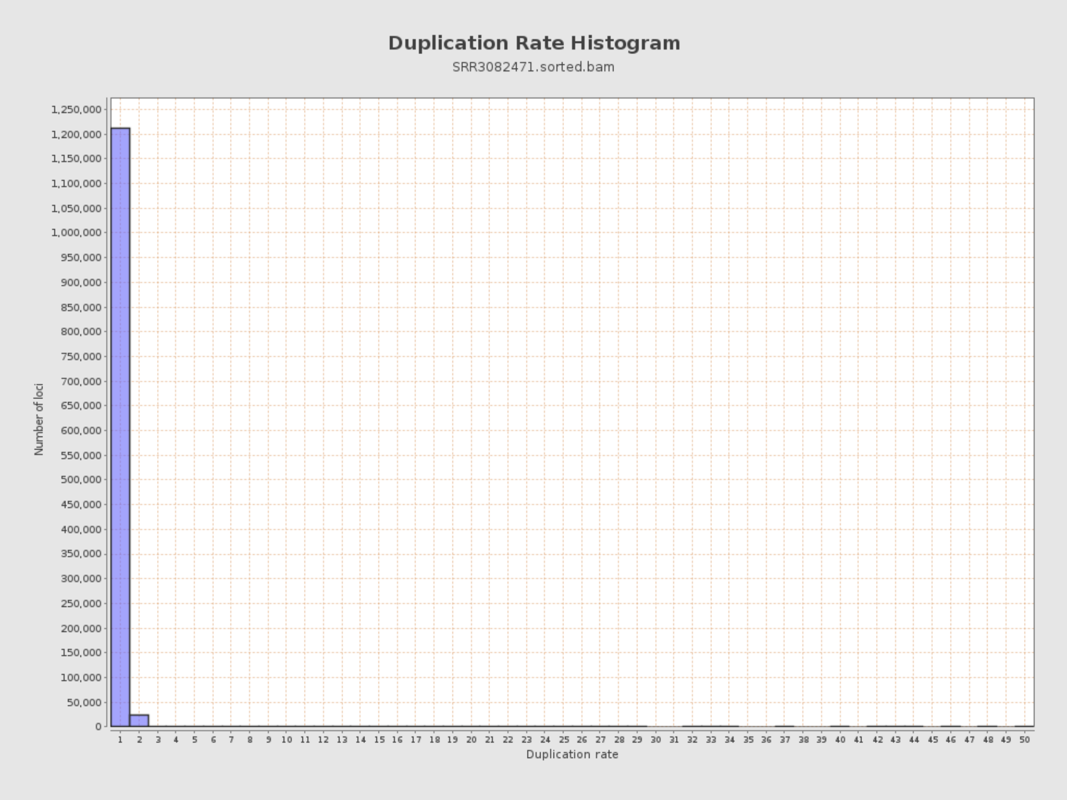
5. Results : Coverage Histogram (0-50X)



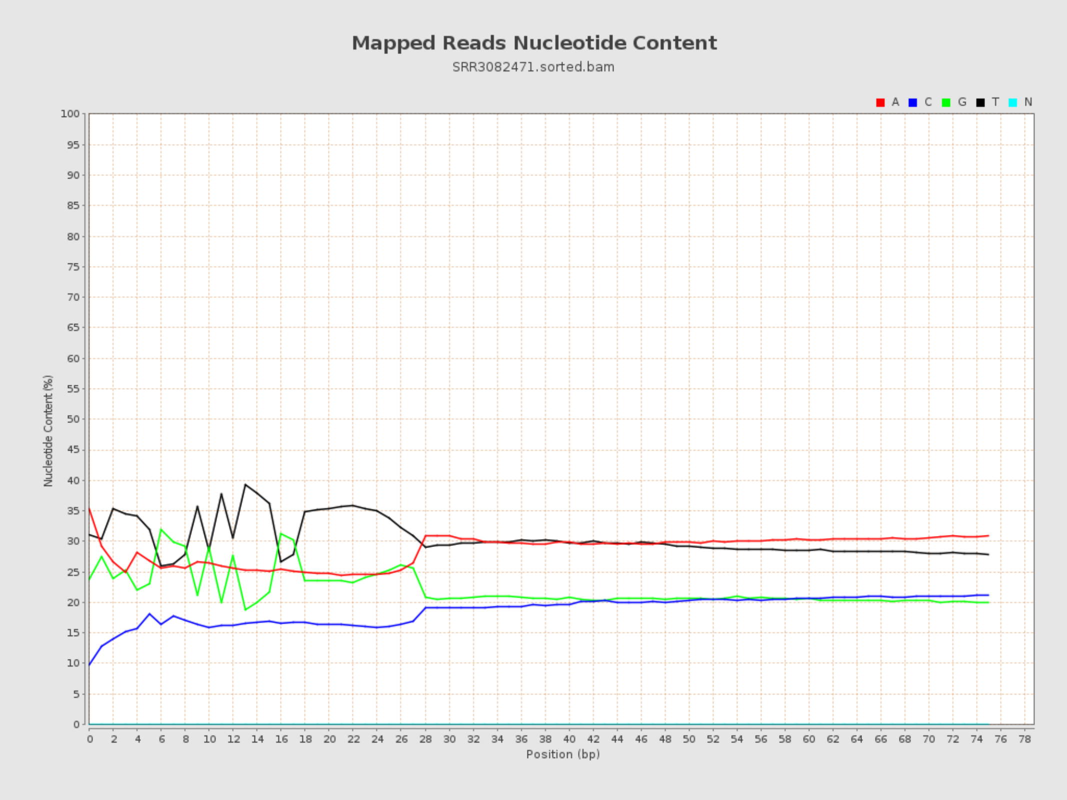
6. Results : Genome Fraction Coverage



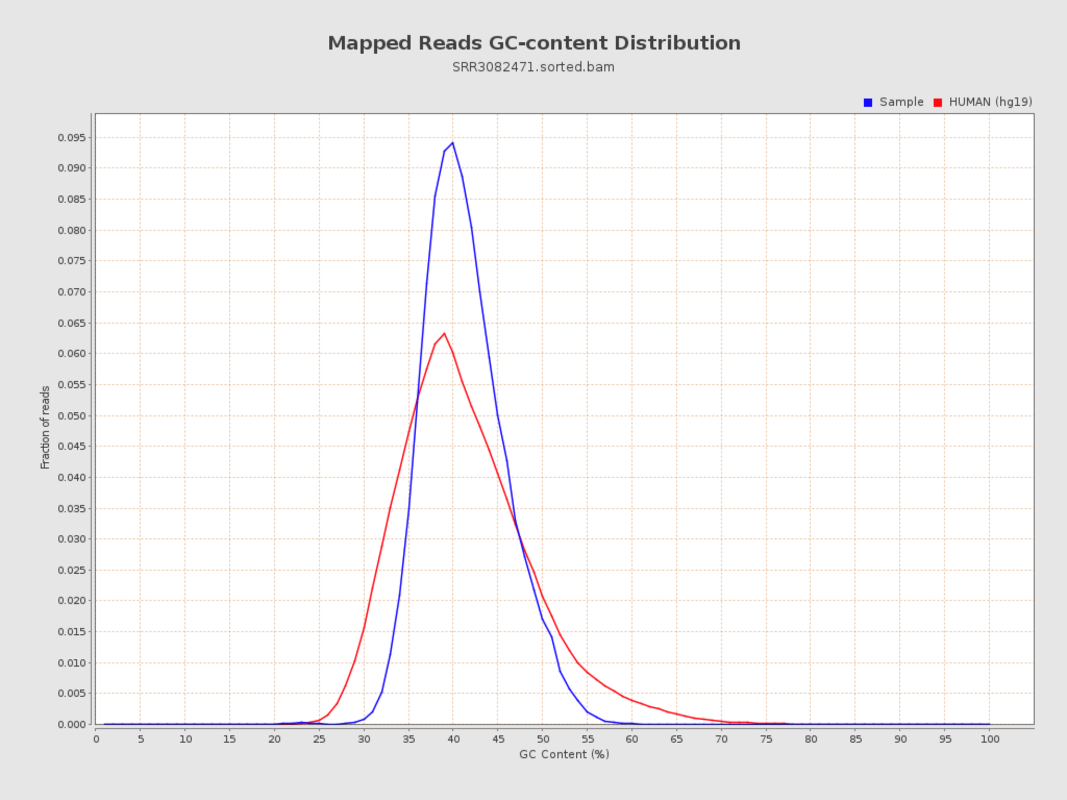
7. Results : Duplication Rate Histogram



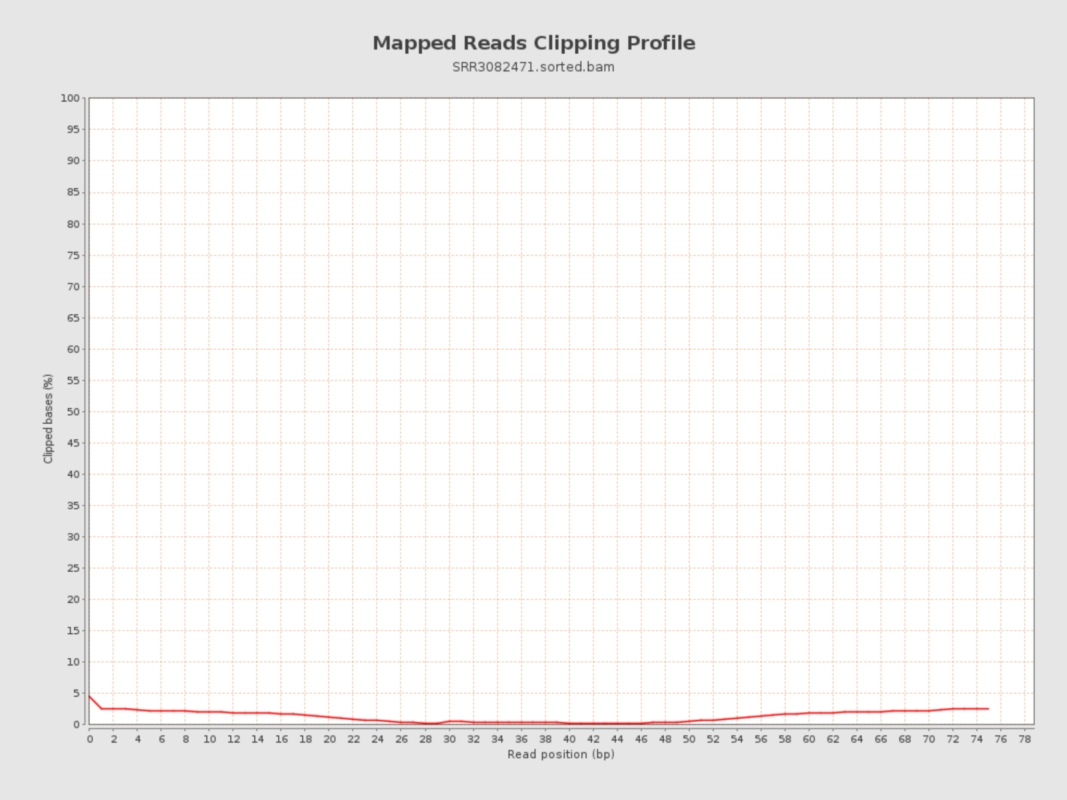
8. Results : Mapped Reads Nucleotide Content



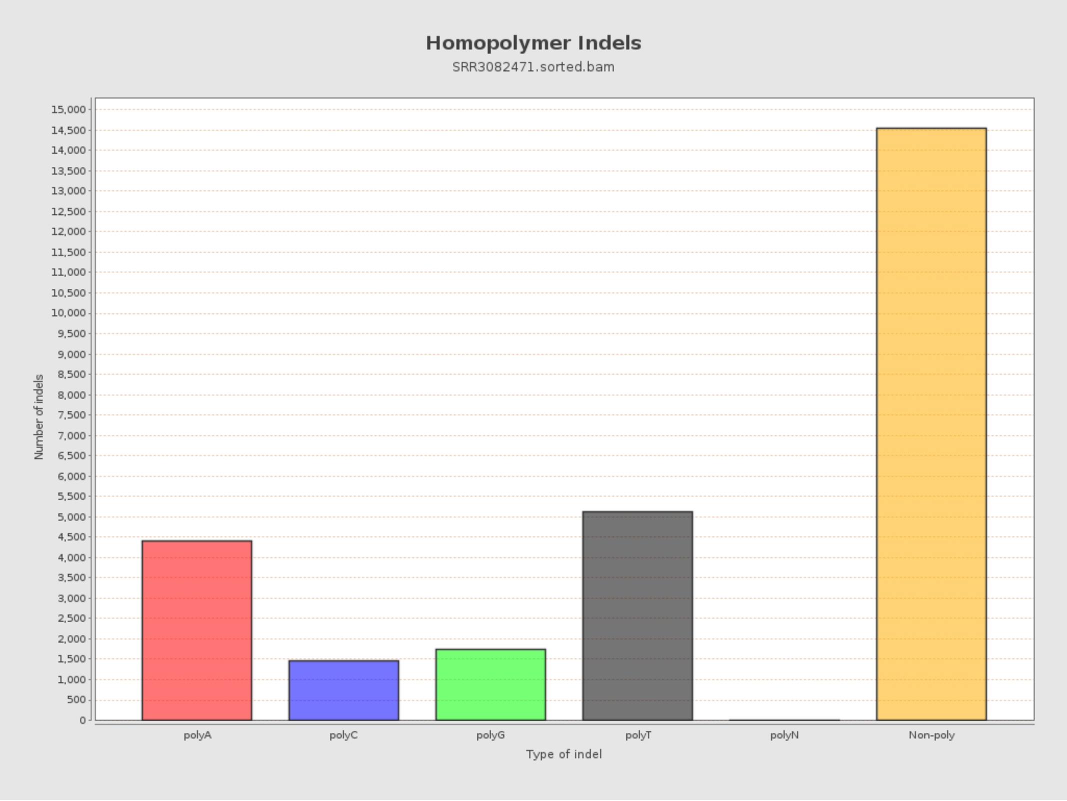
9. Results : Mapped Reads GC-content Distribution



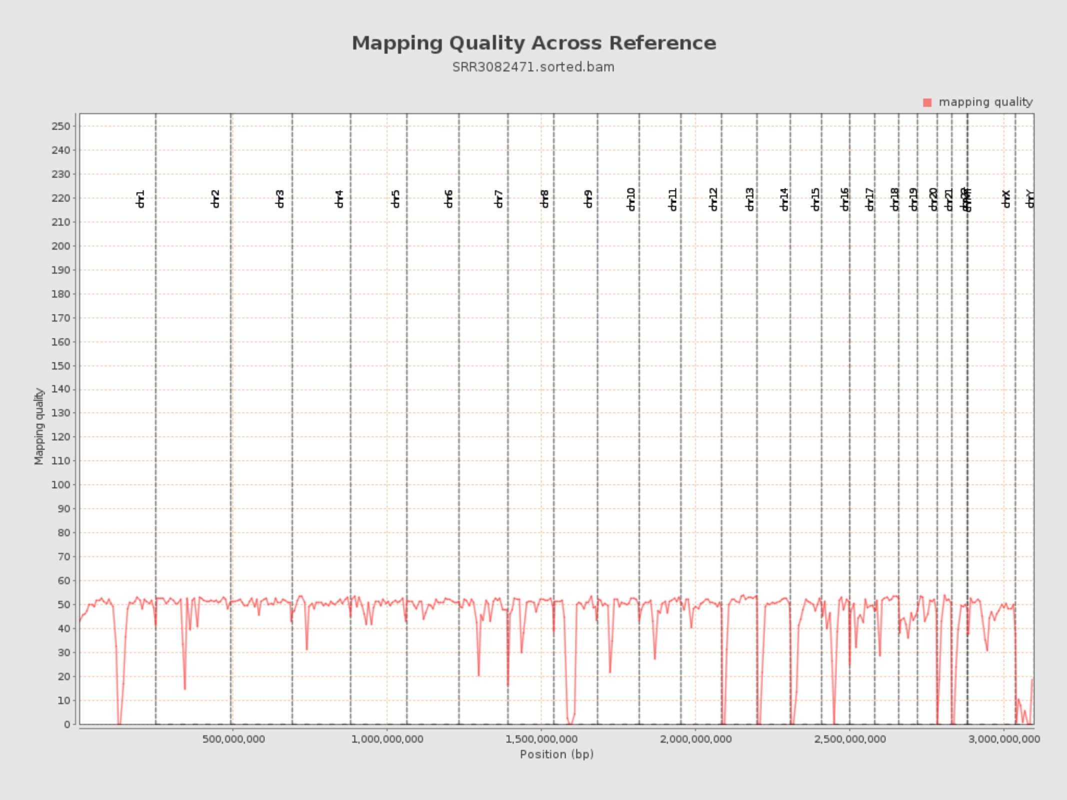
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram