Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:08:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081108.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_SRR3081108 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081108.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:08:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081108.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,265,123
Mapped reads	2,067,268 / 91.27%
Unmapped reads	197,855 / 8.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,635 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	87,905 / 3.88%
Duplication rate	3.34%
Clipped reads	891,965 / 39.38%

2.2. ACGT Content

Number/percentage of A's	38,628,788 / 27.73%
Number/percentage of C's	26,502,628 / 19.02%
Number/percentage of T's	43,218,616 / 31.02%
Number/percentage of G's	30,957,160 / 22.22%
Number/percentage of N's	1,583 / 0%
GC Percentage	41.25%

2.3. Coverage

Mean	0.045

Standard Deviation	0.3843

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

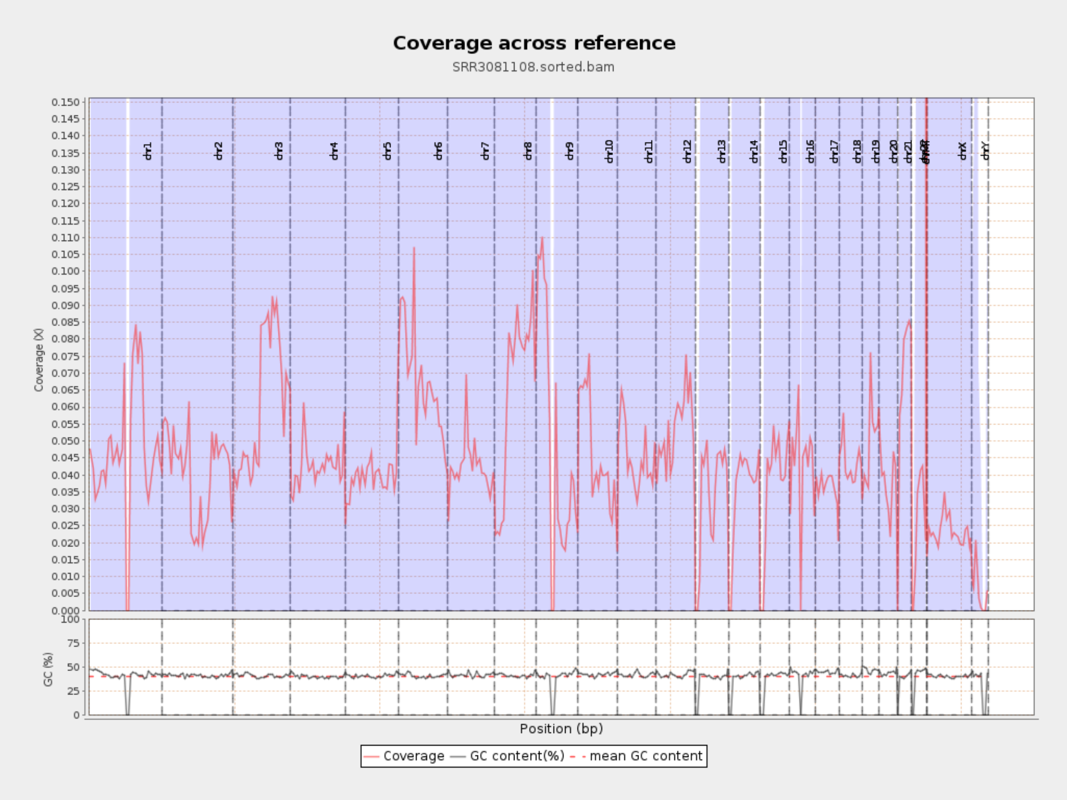
General error rate	0.91%
Mismatches	1,247,574
Insertions	11,232
Mapped reads with at least one insertion	0.54%
Deletions	31,070
Mapped reads with at least one deletion	1.49%
Homopolymer indels	46.26%

2.6. Chromosome stats

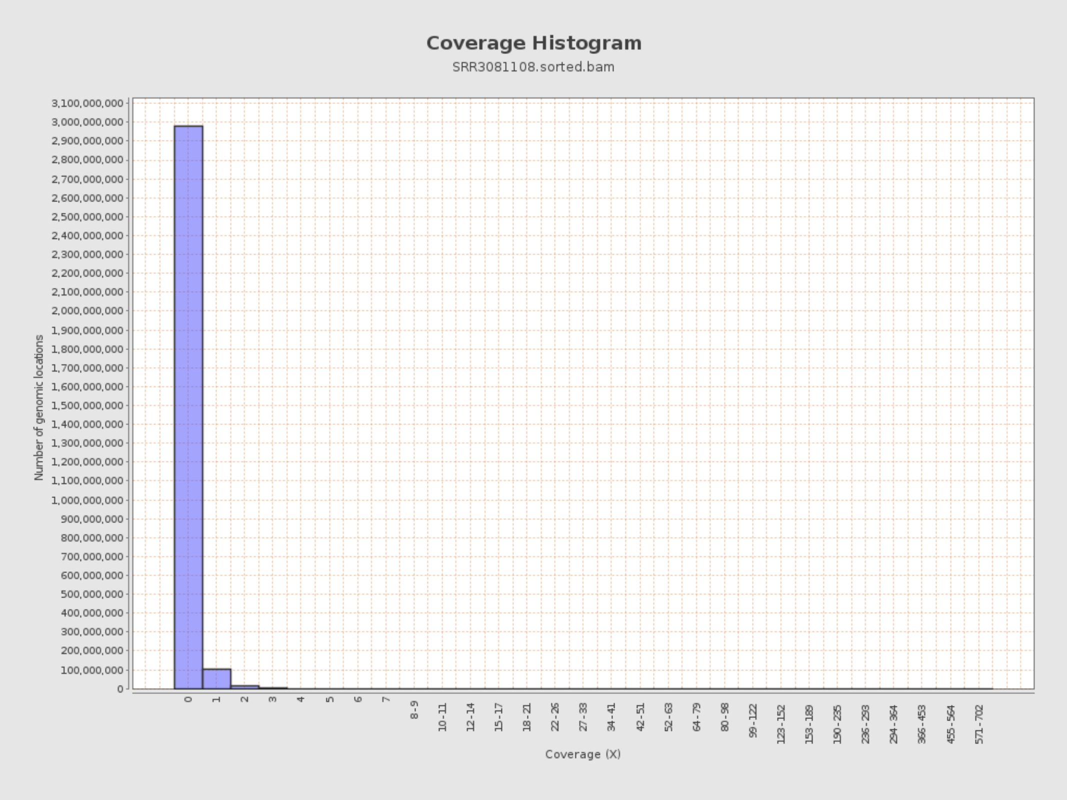
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11761704	0.0472	0.6623
chr2	243199373	10054598	0.0413	0.3979
chr3	198022430	12105509	0.0611	0.2811
chr4	191154276	8155593	0.0427	0.2531
chr5	180915260	7105569	0.0393	0.2278
chr6	171115067	11609070	0.0678	0.4491
chr7	159138663	6798351	0.0427	0.4564

chr8	146364022	9522566	0.0651	0.4135
chr9	141213431	6956364	0.0493	0.4116
chr10	135534747	6354692	0.0469	0.3816
chr11	135006516	6048418	0.0448	0.3015
chr12	133851895	7129448	0.0533	0.2747
chr13	115169878	3835619	0.0333	0.2079
chr14	107349540	3735580	0.0348	0.2781
chr15	102531392	3764598	0.0367	0.2171
chr16	90354753	3840981	0.0425	0.2859
chr17	81195210	2940229	0.0362	0.2234
chr18	78077248	3427523	0.0439	0.6826
chr19	59128983	2949178	0.0499	0.5163
chr20	63025520	2365227	0.0375	0.2367
chr21	48129895	3269870	0.0679	0.3372
chr22	51304566	1265688	0.0247	0.176
chrMT	16571	416113	25.1109	12.9103
chrX	155270560	3611565	0.0233	0.1967
chrY	59373566	335447	0.0056	0.1524

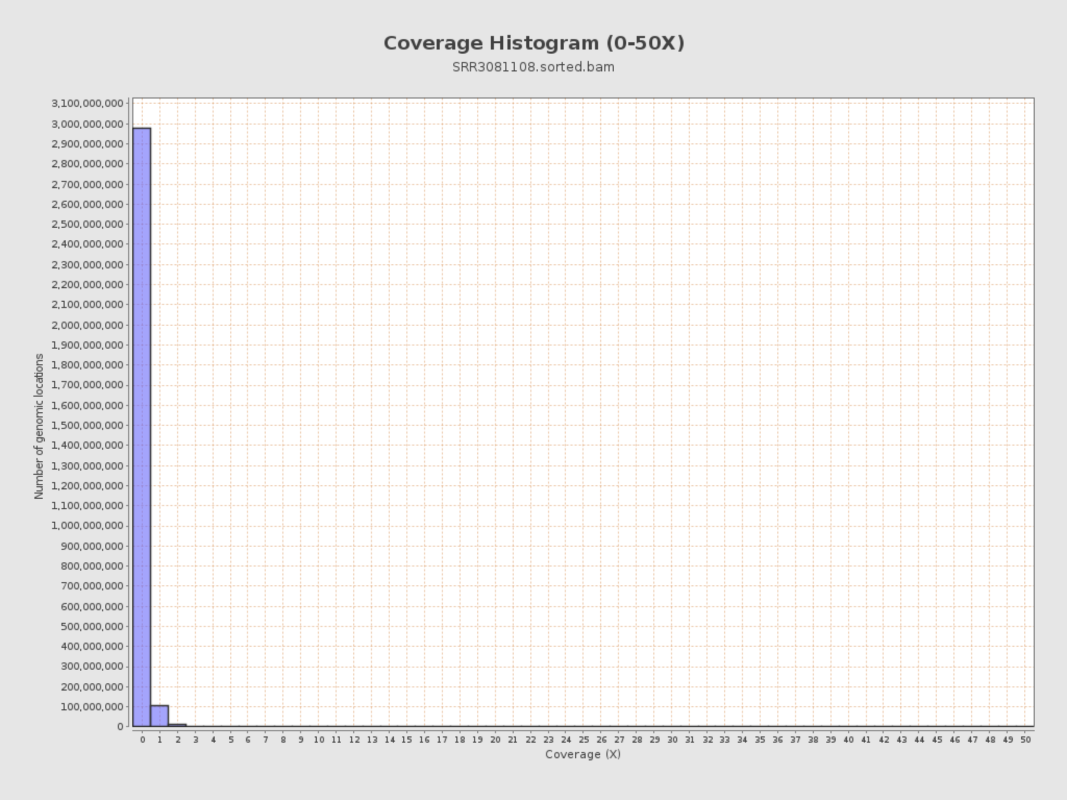
3. Results : Coverage across reference



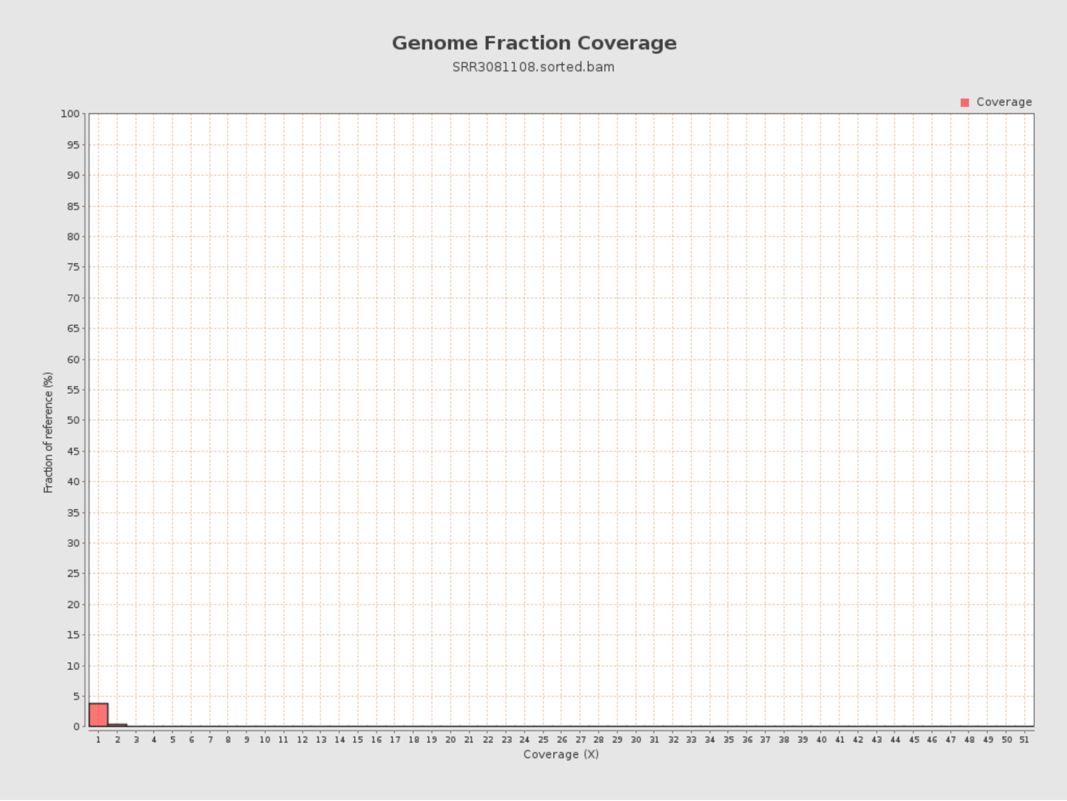
4. Results : Coverage Histogram



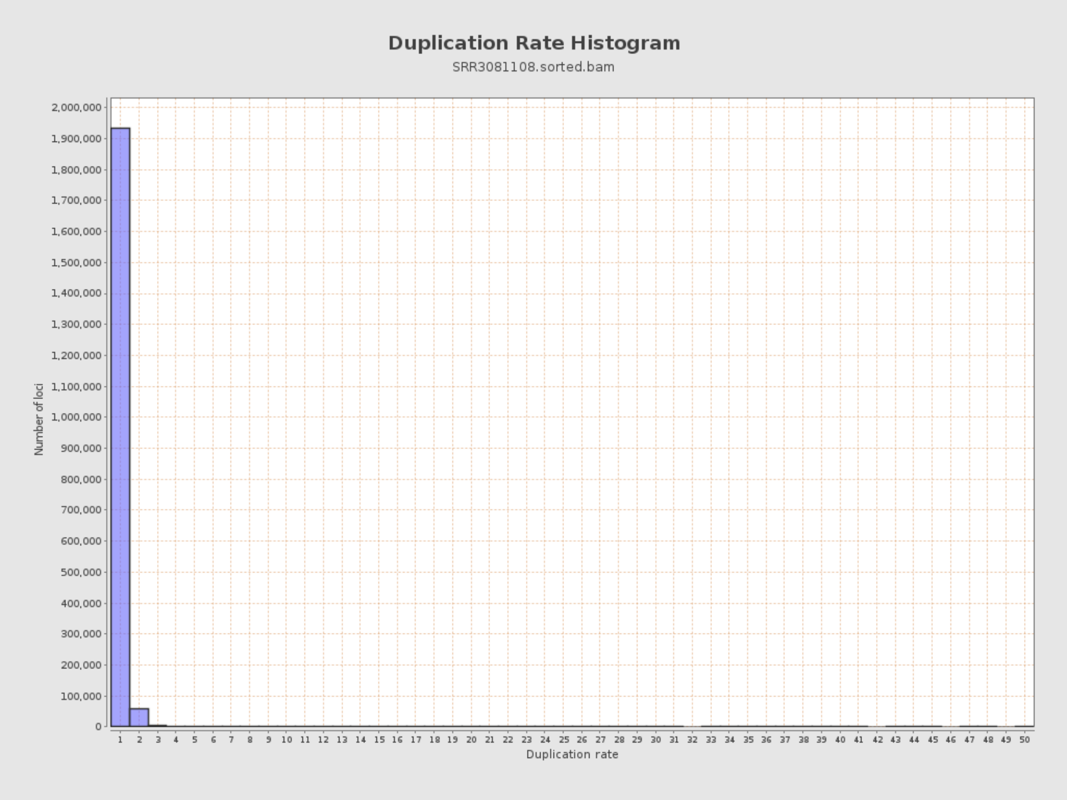
5. Results : Coverage Histogram (0-50X)



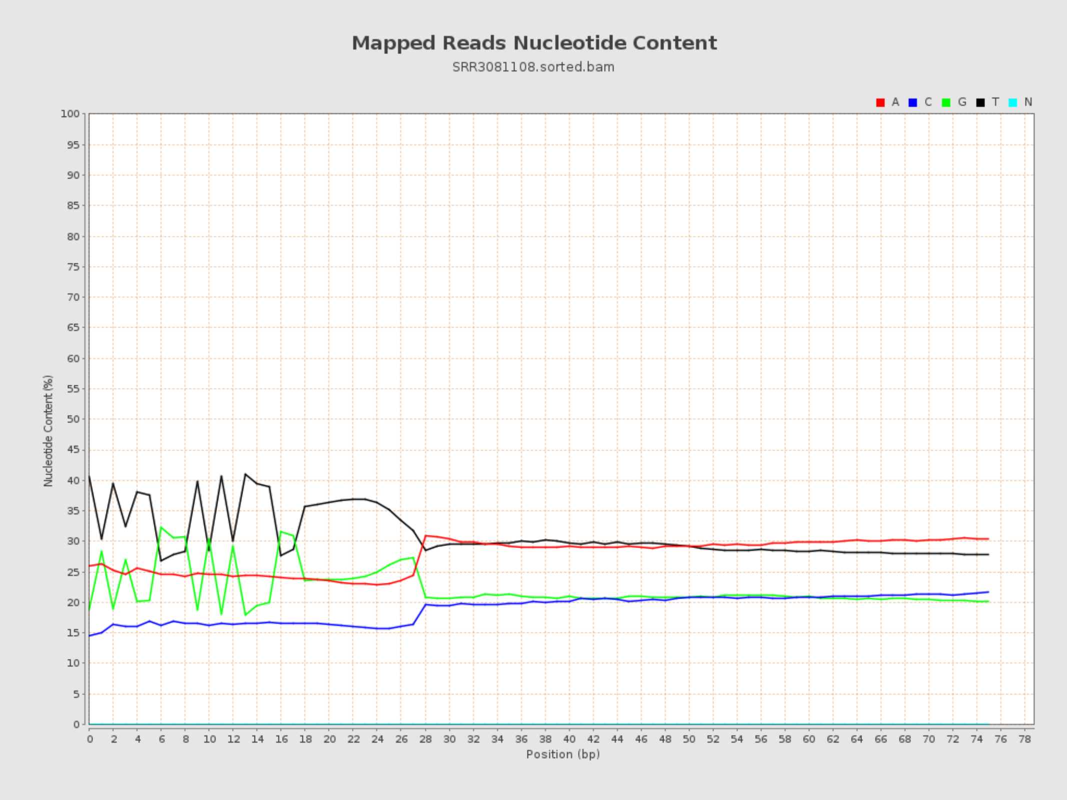
6. Results : Genome Fraction Coverage



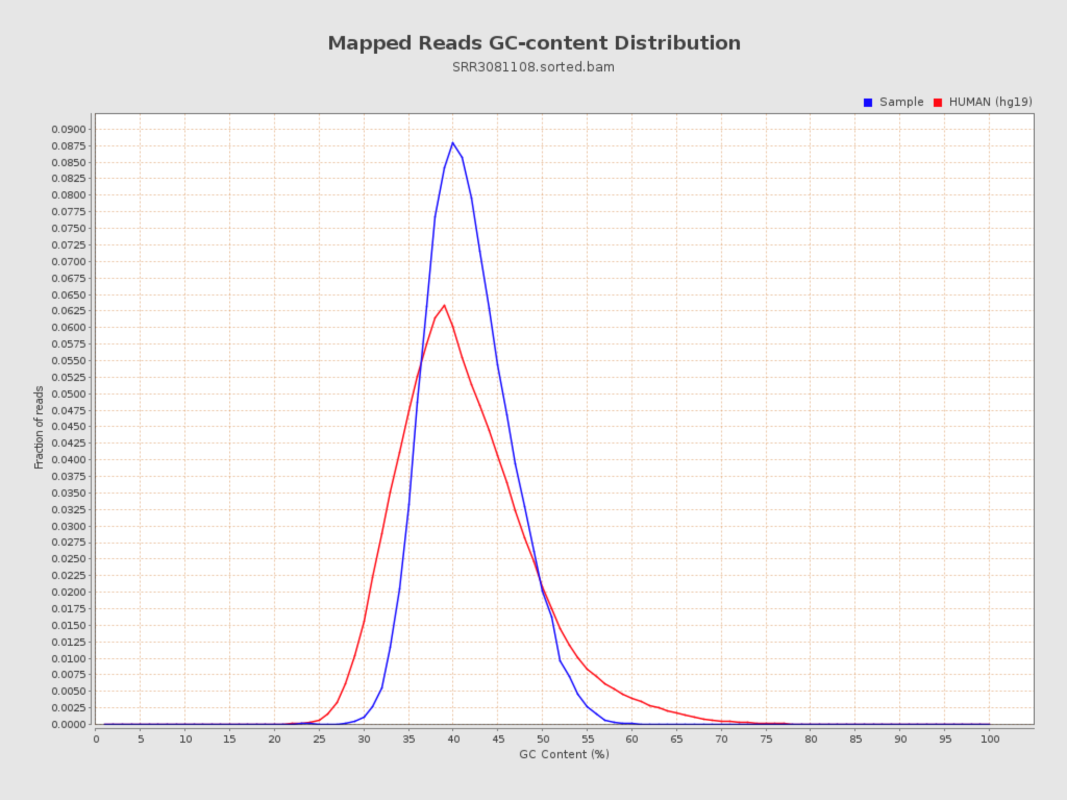
7. Results : Duplication Rate Histogram



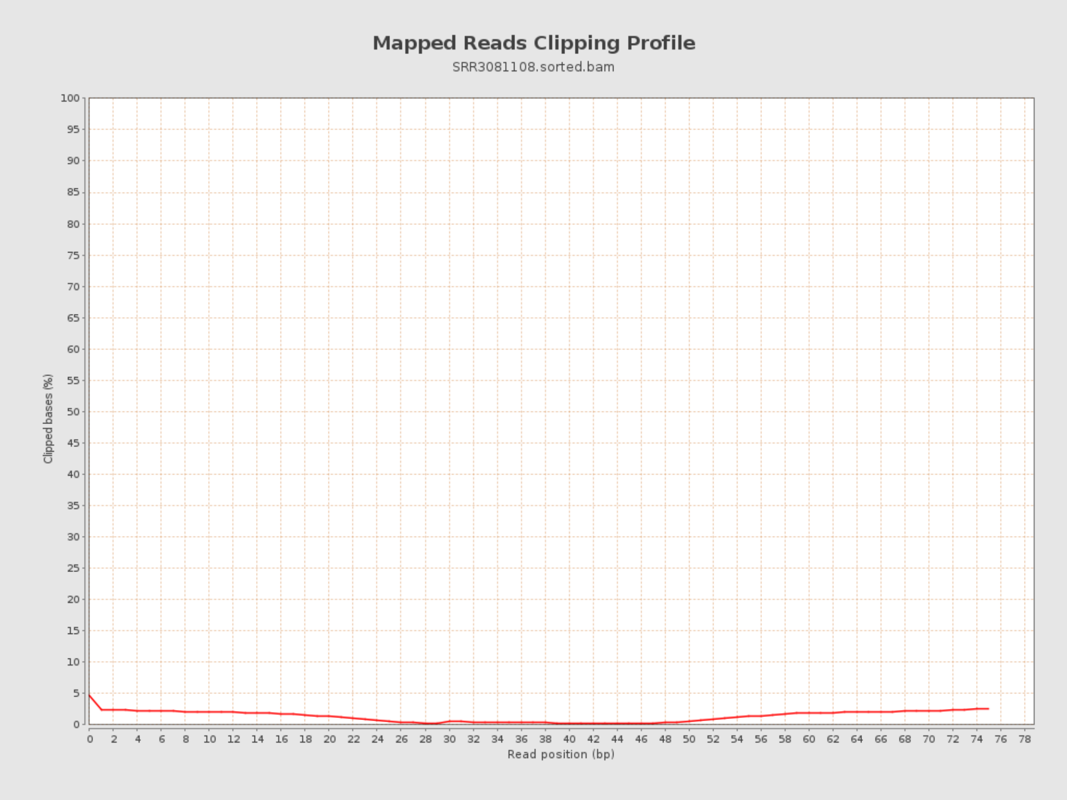
8. Results : Mapped Reads Nucleotide Content



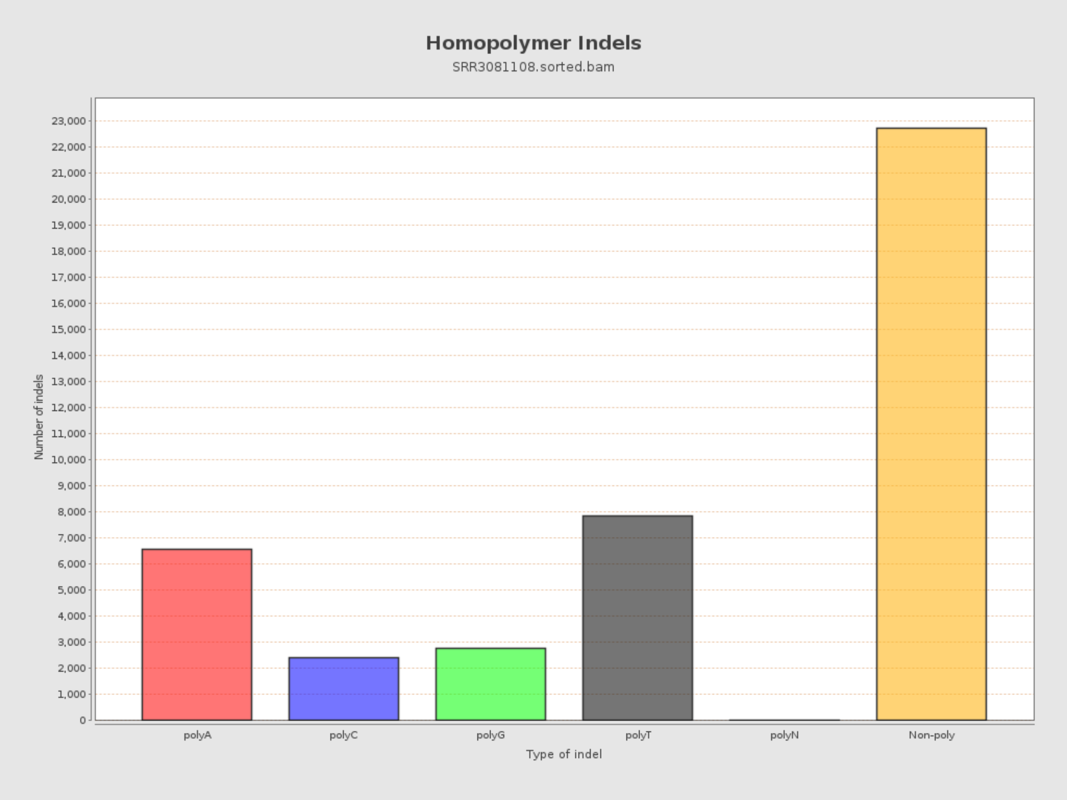
9. Results : Mapped Reads GC-content Distribution



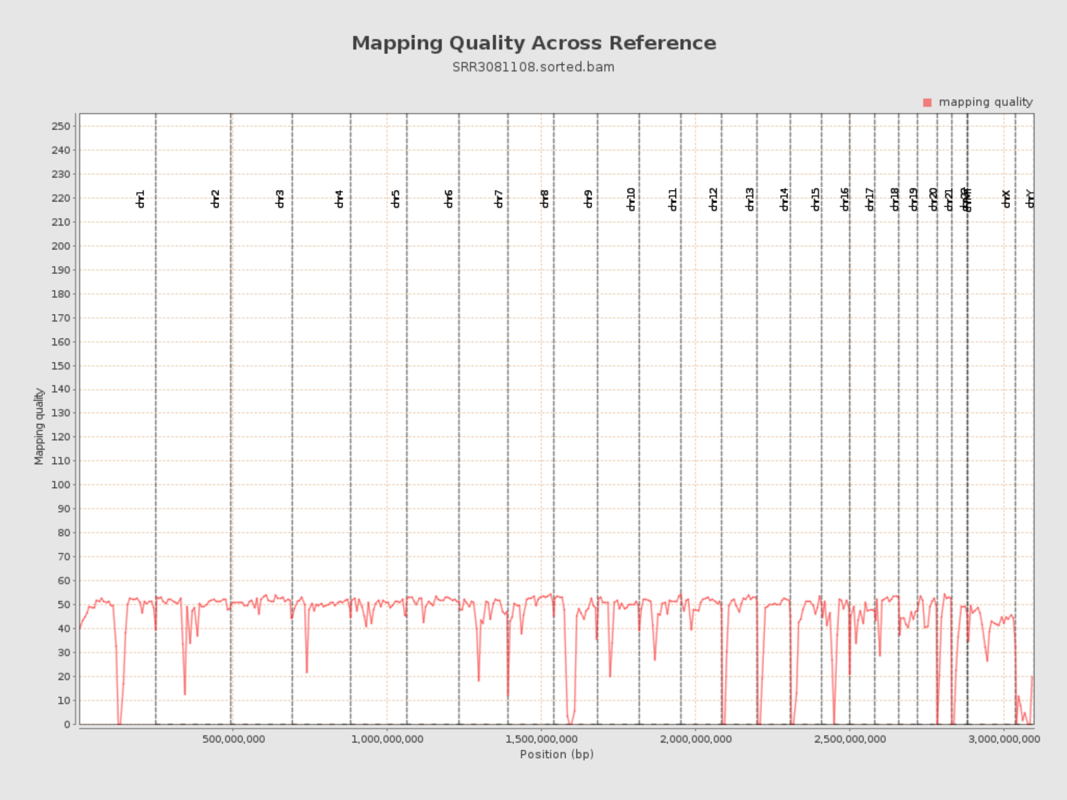
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram