Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:55:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068098.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_SRR6068098 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068098.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:55:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068098.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,387,099
Mapped reads	1,932,778 / 80.97%
Unmapped reads	454,321 / 19.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,934 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	298,117 / 12.49%
Duplication rate	11.88%
Clipped reads	1,157,361 / 48.48%

2.2. ACGT Content

Number/percentage of A's	32,633,447 / 26.76%
Number/percentage of C's	21,835,191 / 17.91%
Number/percentage of T's	39,411,427 / 32.32%
Number/percentage of G's	28,055,549 / 23.01%
Number/percentage of N's	2,346 / 0%
GC Percentage	40.91%

2.3. Coverage

Mean	0.0394

Standard Deviation	0.4482

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

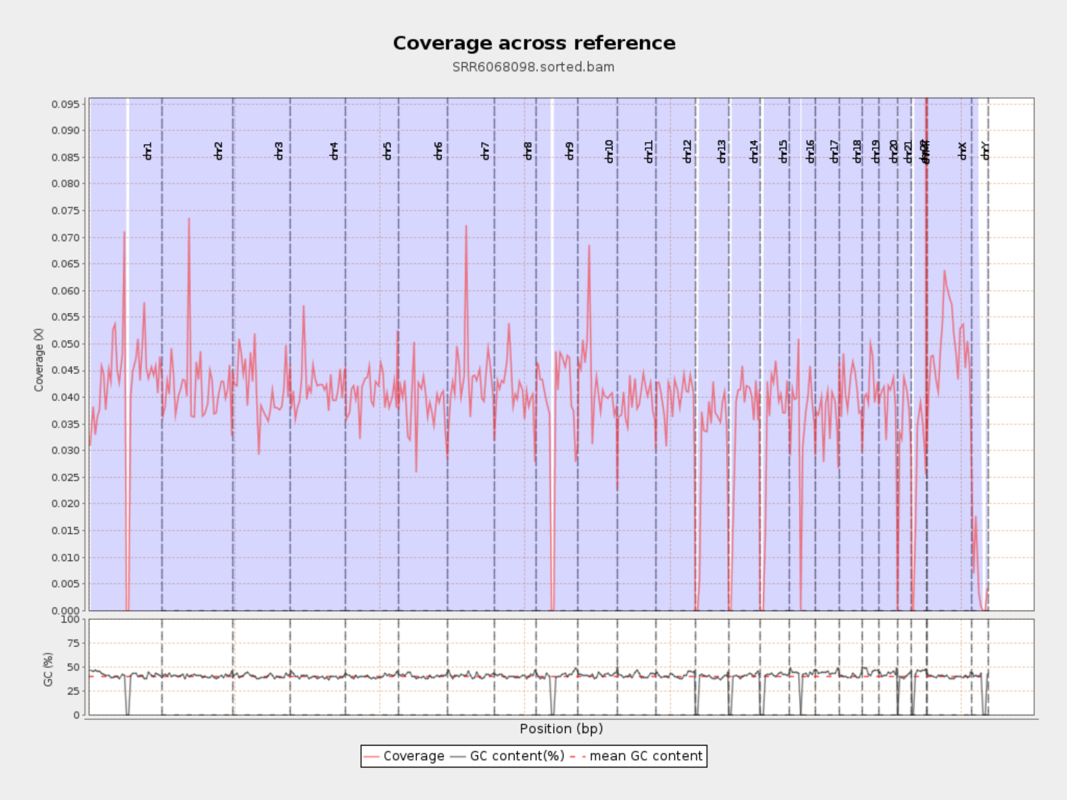
General error rate	0.78%
Mismatches	934,917
Insertions	9,260
Mapped reads with at least one insertion	0.47%
Deletions	28,244
Mapped reads with at least one deletion	1.45%
Homopolymer indels	46.63%

2.6. Chromosome stats

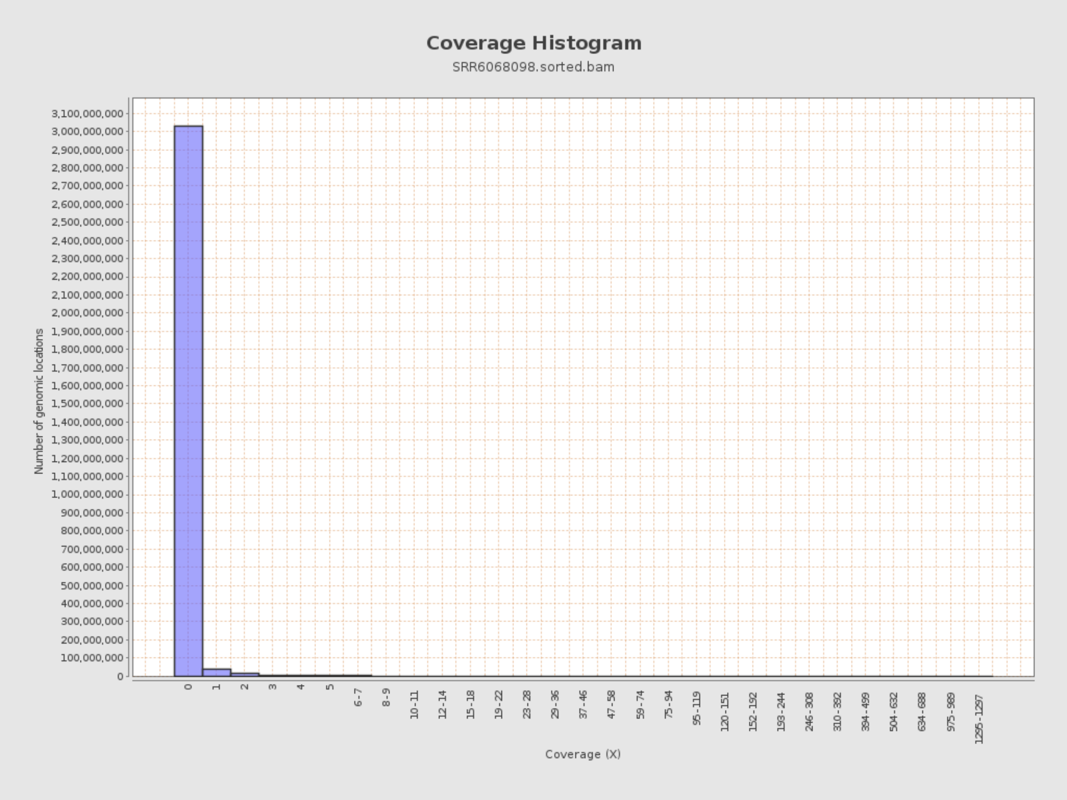
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10537221	0.0423	0.6552
chr2	243199373	10245375	0.0421	0.6816
chr3	198022430	8223229	0.0415	0.3499
chr4	191154276	8018595	0.0419	0.3706
chr5	180915260	7411114	0.041	0.3437
chr6	171115067	6635521	0.0388	0.3915
chr7	159138663	7048179	0.0443	0.5431

chr8	146364022	6018660	0.0411	0.4876
chr9	141213431	5343612	0.0378	0.3948
chr10	135534747	5874087	0.0433	0.4293
chr11	135006516	5268682	0.039	0.3947
chr12	133851895	5393663	0.0403	0.3456
chr13	115169878	3533954	0.0307	0.3019
chr14	107349540	3614483	0.0337	0.328
chr15	102531392	3388730	0.0331	0.3374
chr16	90354753	3251936	0.036	0.3287
chr17	81195210	2945009	0.0363	0.3291
chr18	78077248	3268485	0.0419	0.5978
chr19	59128983	2482655	0.042	0.486
chr20	63025520	2474431	0.0393	0.3414
chr21	48129895	1598162	0.0332	0.3168
chr22	51304566	1235553	0.0241	0.2496
chrMT	16571	162385	9.7993	6.7758
chrX	155270560	7672671	0.0494	0.4002
chrY	59373566	336035	0.0057	0.1427

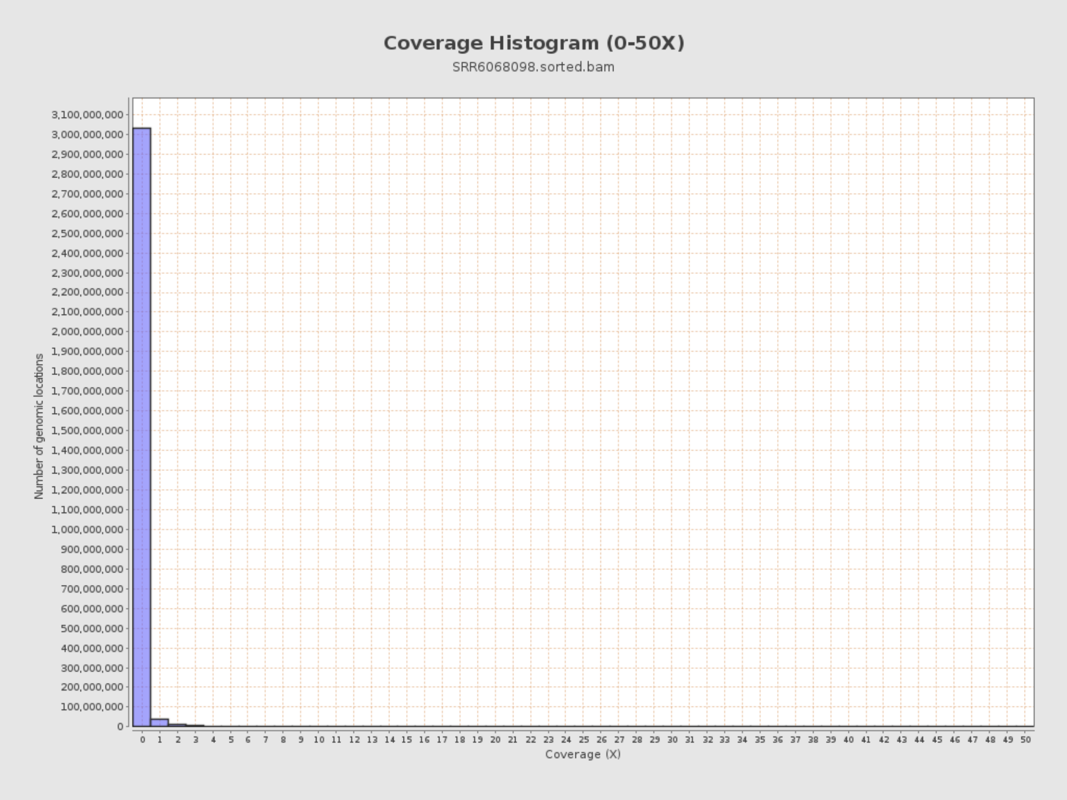
3. Results : Coverage across reference



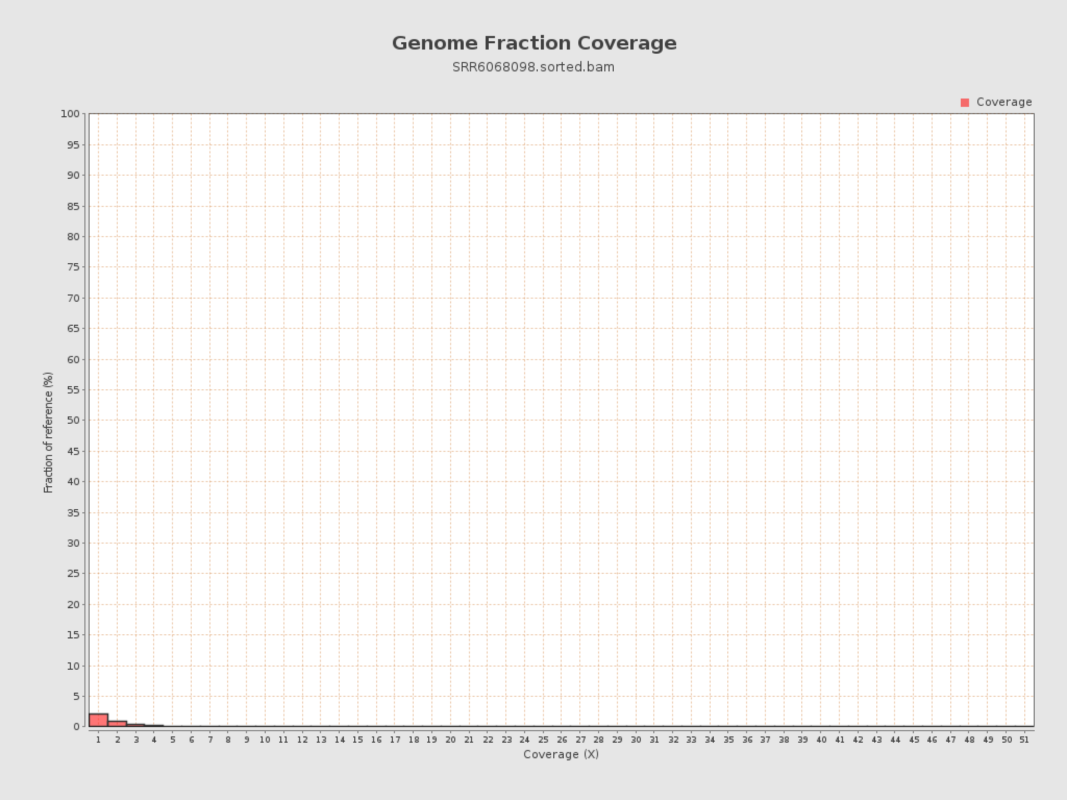
4. Results : Coverage Histogram



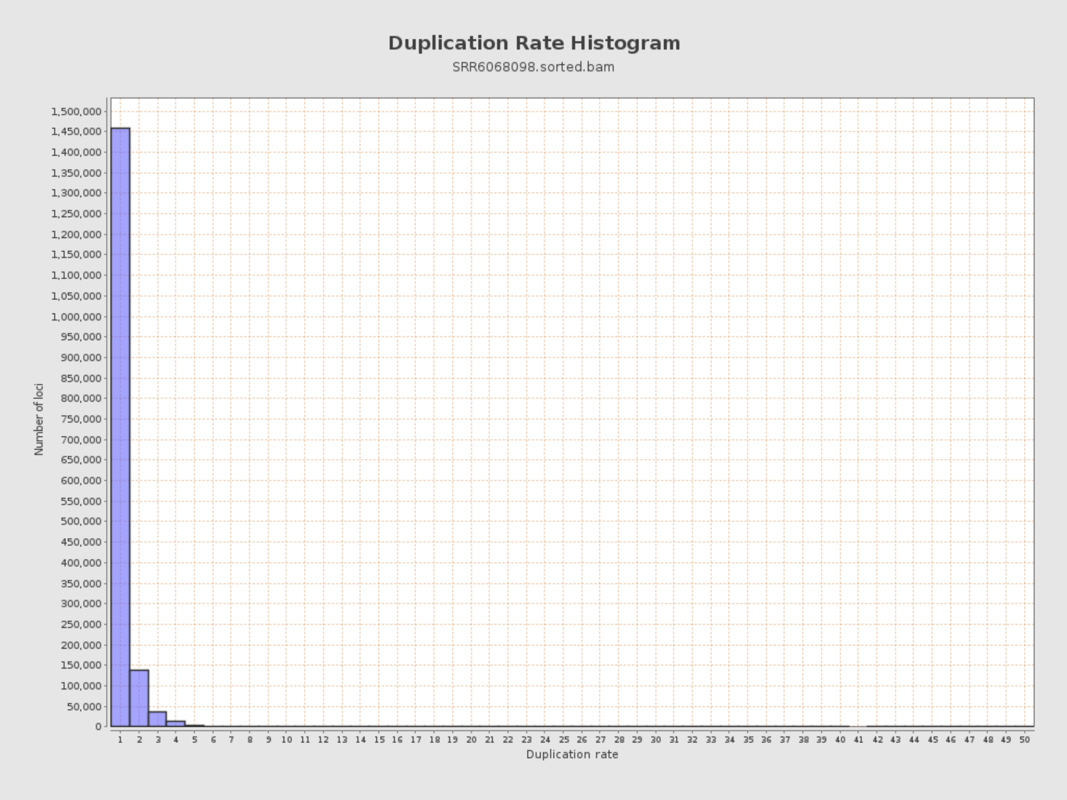
5. Results : Coverage Histogram (0-50X)



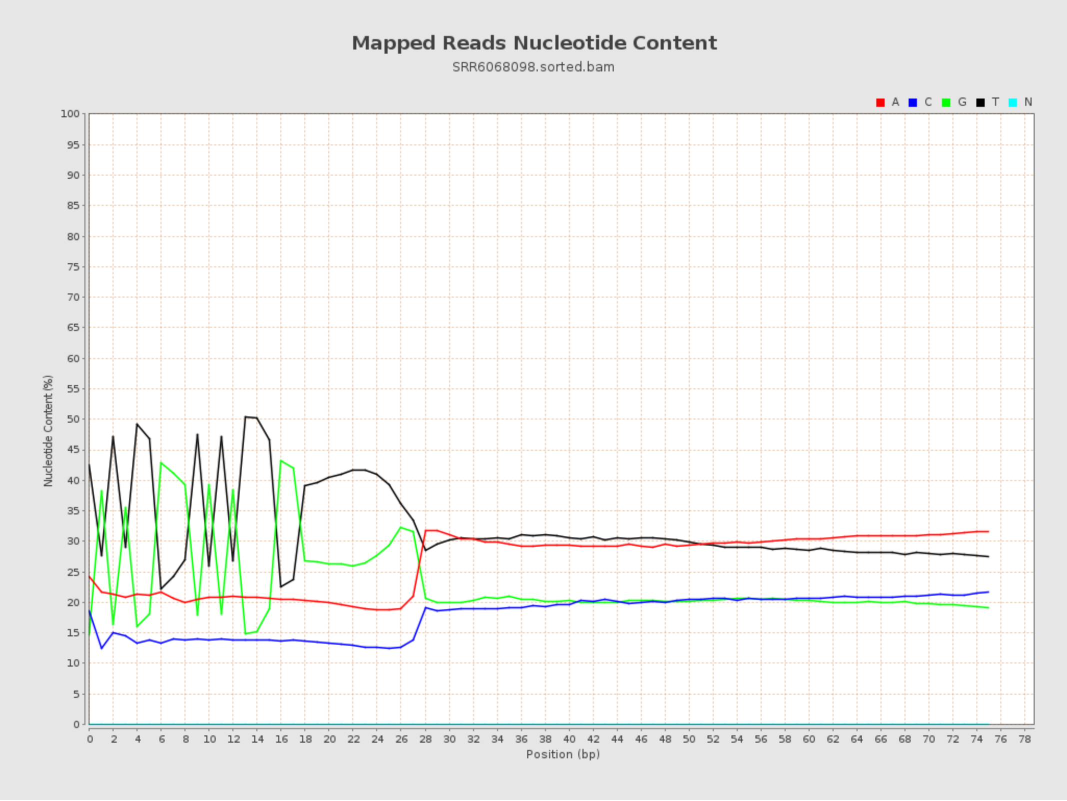
6. Results : Genome Fraction Coverage



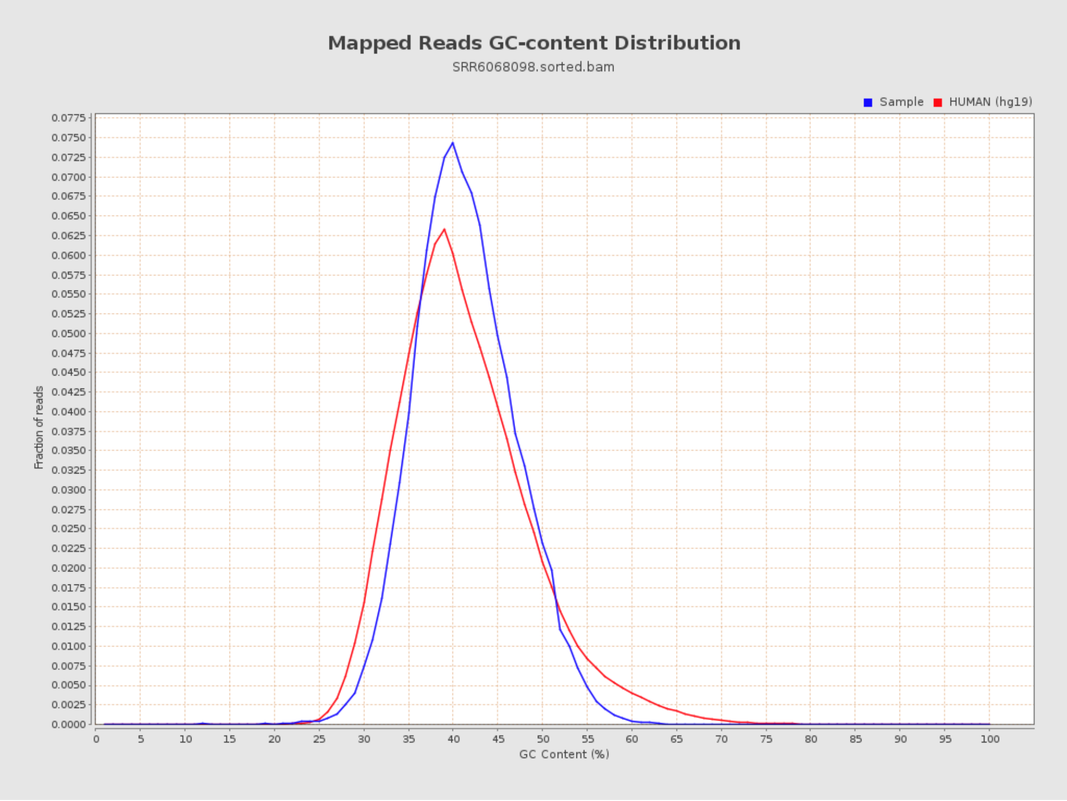
7. Results : Duplication Rate Histogram



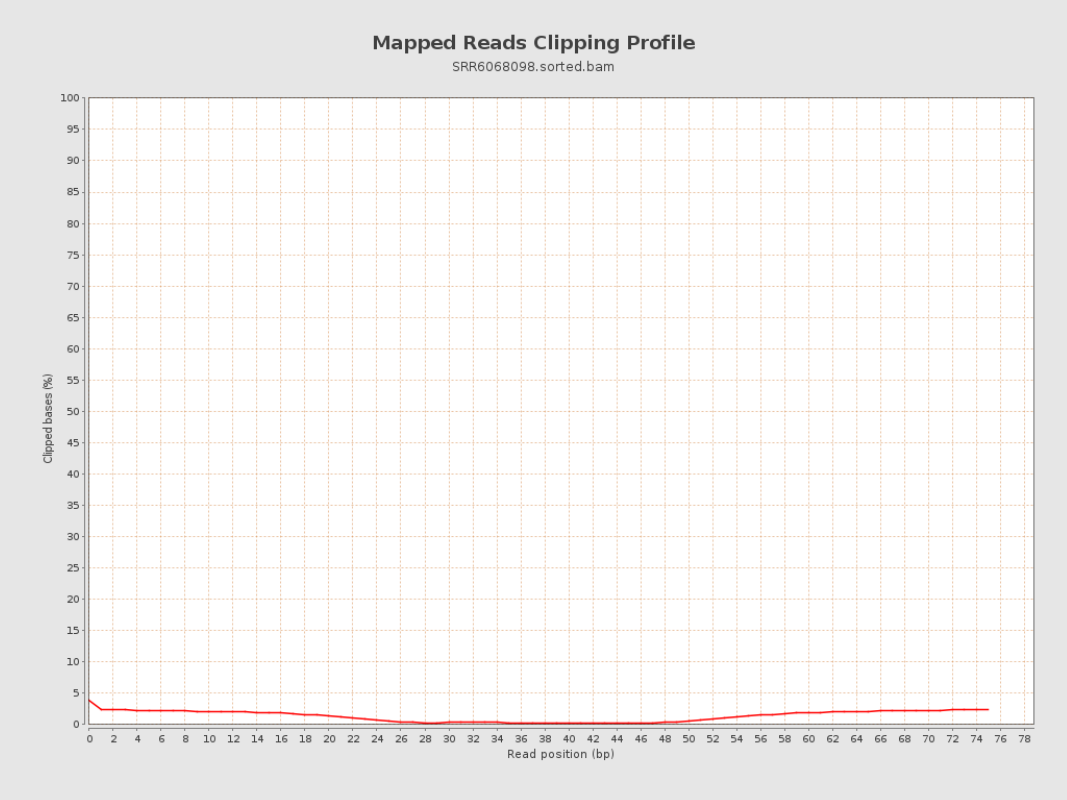
8. Results : Mapped Reads Nucleotide Content



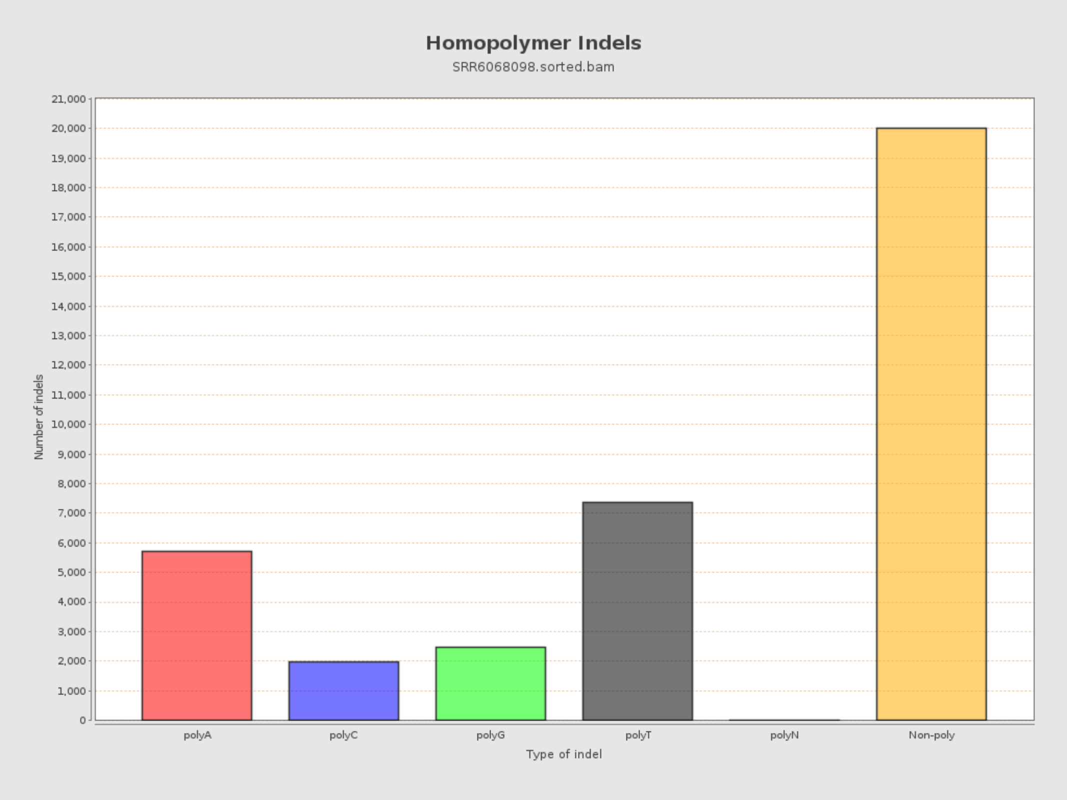
9. Results : Mapped Reads GC-content Distribution



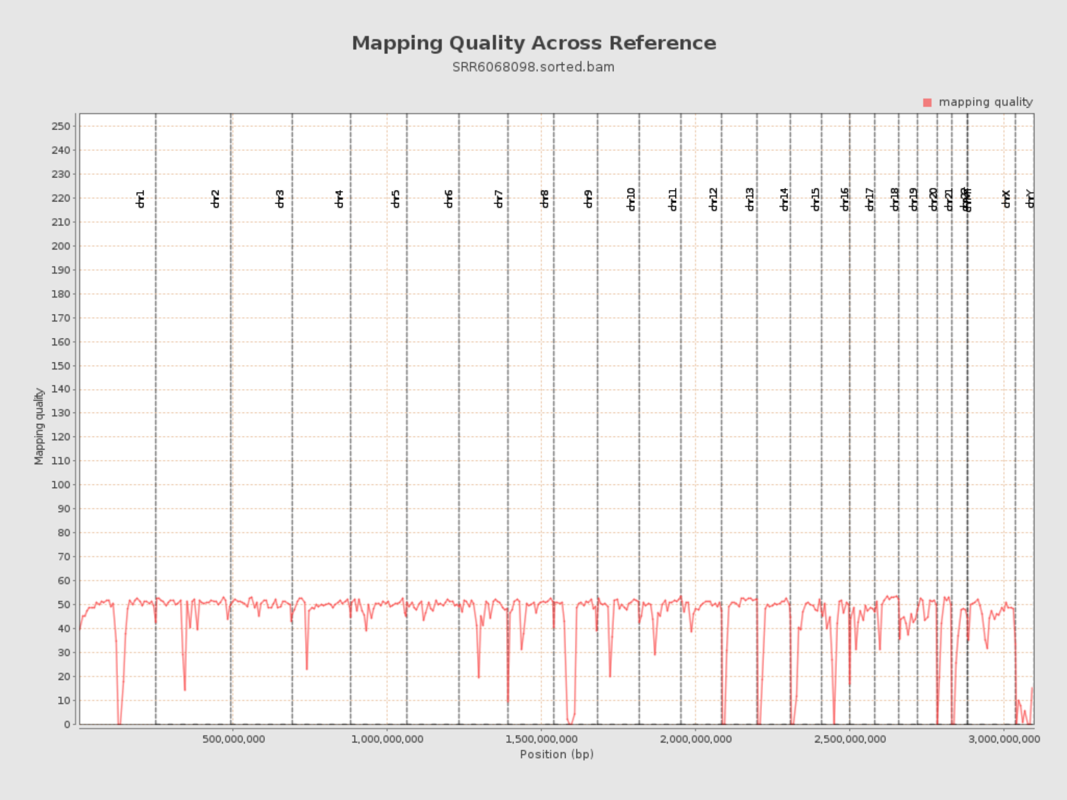
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram