Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:55:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080951.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_SRR3080951 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080951.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:55:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080951.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,099,259
Mapped reads	3,734,923 / 91.11%
Unmapped reads	364,336 / 8.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	47,378 / 1.16%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	184,472 / 4.5%
Duplication rate	3.88%
Clipped reads	1,254,046 / 30.59%

2.2. ACGT Content

Number/percentage of A's	75,357,176 / 29.11%
Number/percentage of C's	46,260,139 / 17.87%
Number/percentage of T's	82,317,436 / 31.8%
Number/percentage of G's	53,634,835 / 20.72%
Number/percentage of N's	1,272,075 / 0.49%
GC Percentage	38.59%

2.3. Coverage

Mean	0.0836

Standard Deviation	0.6157

2.4. Mapping Quality

Mean Mapping Quality	47.68

2.5. Mismatches and indels

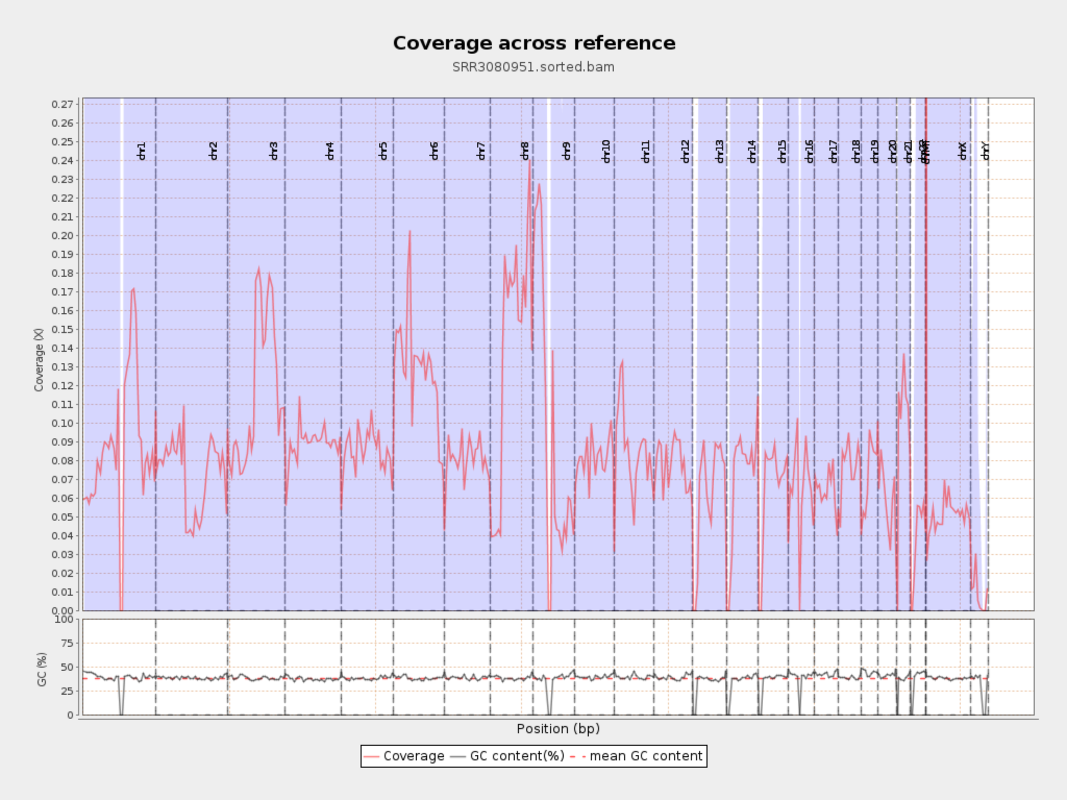
General error rate	1.15%
Mismatches	2,938,824
Insertions	19,391
Mapped reads with at least one insertion	0.52%
Deletions	57,223
Mapped reads with at least one deletion	1.52%
Homopolymer indels	49.73%

2.6. Chromosome stats

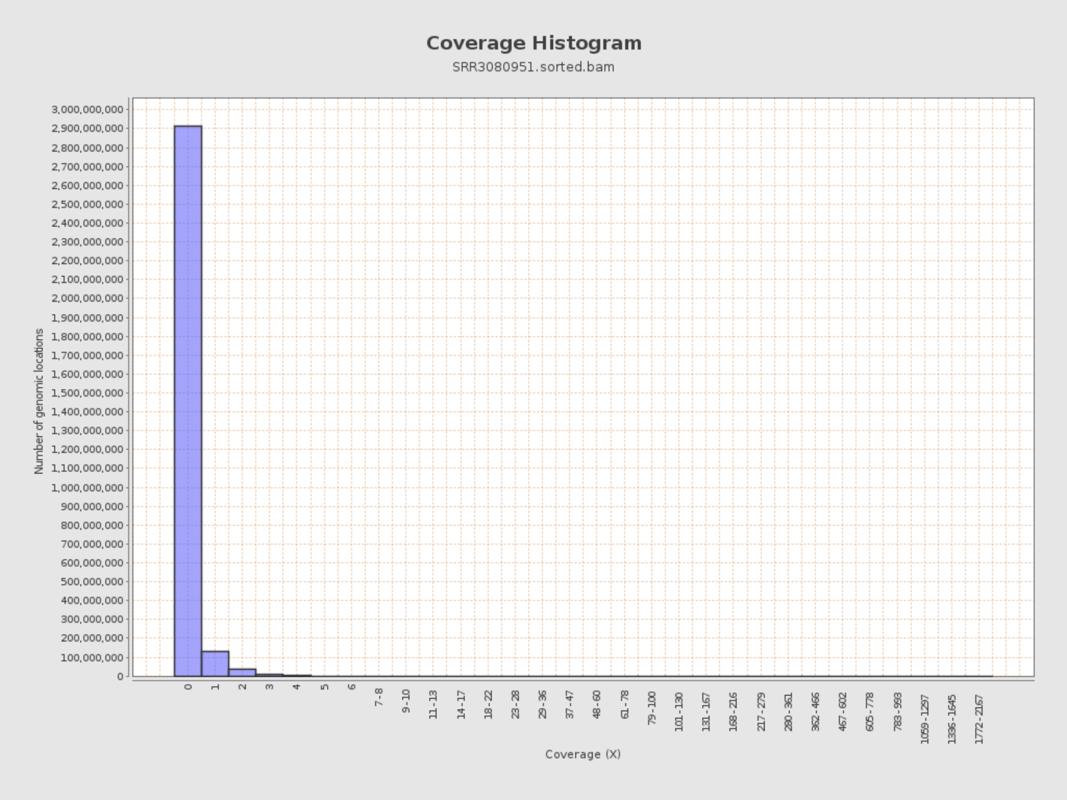
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21545092	0.0864	0.909
chr2	243199373	17841666	0.0734	0.5304
chr3	198022430	23076556	0.1165	0.4608
chr4	191154276	17051729	0.0892	0.4169
chr5	180915260	15420389	0.0852	0.3916
chr6	171115067	22348023	0.1306	0.6447
chr7	159138663	12849084	0.0807	0.5733

chr8	146364022	20492199	0.14	1.4221
chr9	141213431	13480475	0.0955	0.654
chr10	135534747	11118139	0.082	0.4703
chr11	135006516	11587551	0.0858	0.4754
chr12	133851895	10430929	0.0779	0.3871
chr13	115169878	7176059	0.0623	0.3298
chr14	107349540	7444686	0.0693	0.4092
chr15	102531392	6608270	0.0645	0.3369
chr16	90354753	5735434	0.0635	0.3989
chr17	81195210	5315531	0.0655	0.3554
chr18	78077248	5972845	0.0765	1.1374
chr19	59128983	4343760	0.0735	0.6316
chr20	63025520	3849387	0.0611	0.3525
chr21	48129895	4884330	0.1015	0.5196
chr22	51304566	1927398	0.0376	0.2513
chrMT	16571	25426	1.5344	1.6423
chrX	155270560	7871141	0.0507	0.3255
chrY	59373566	540224	0.0091	0.1796

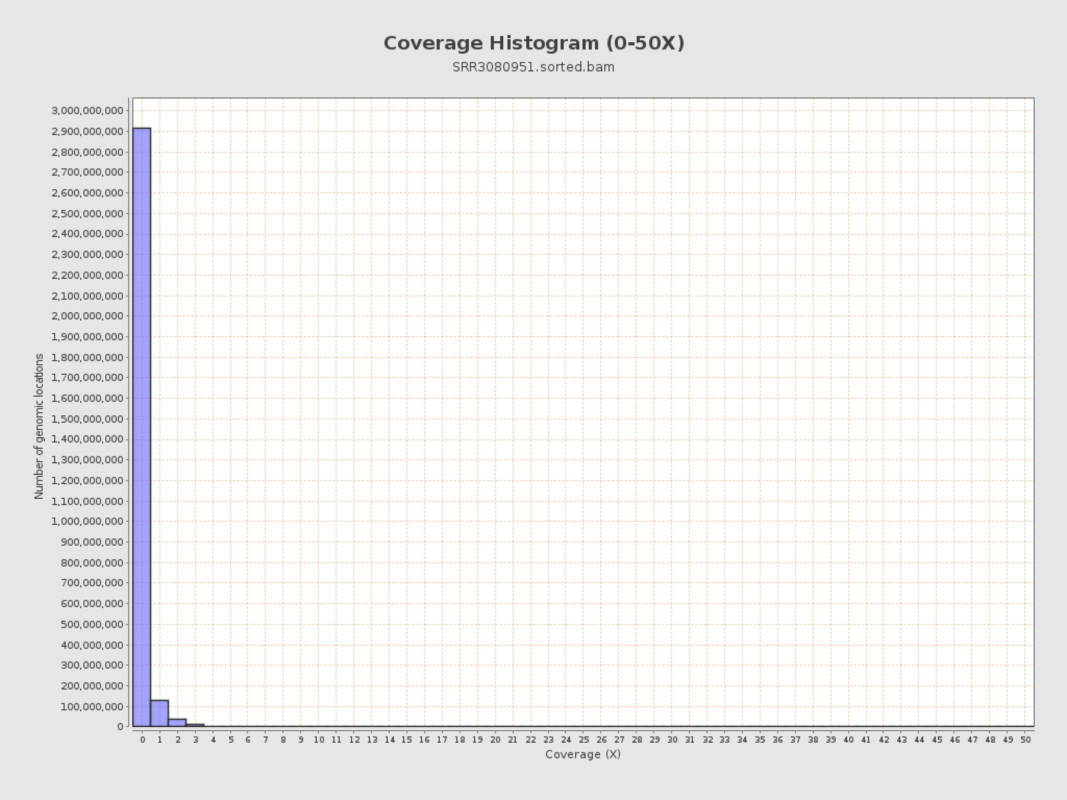
3. Results : Coverage across reference



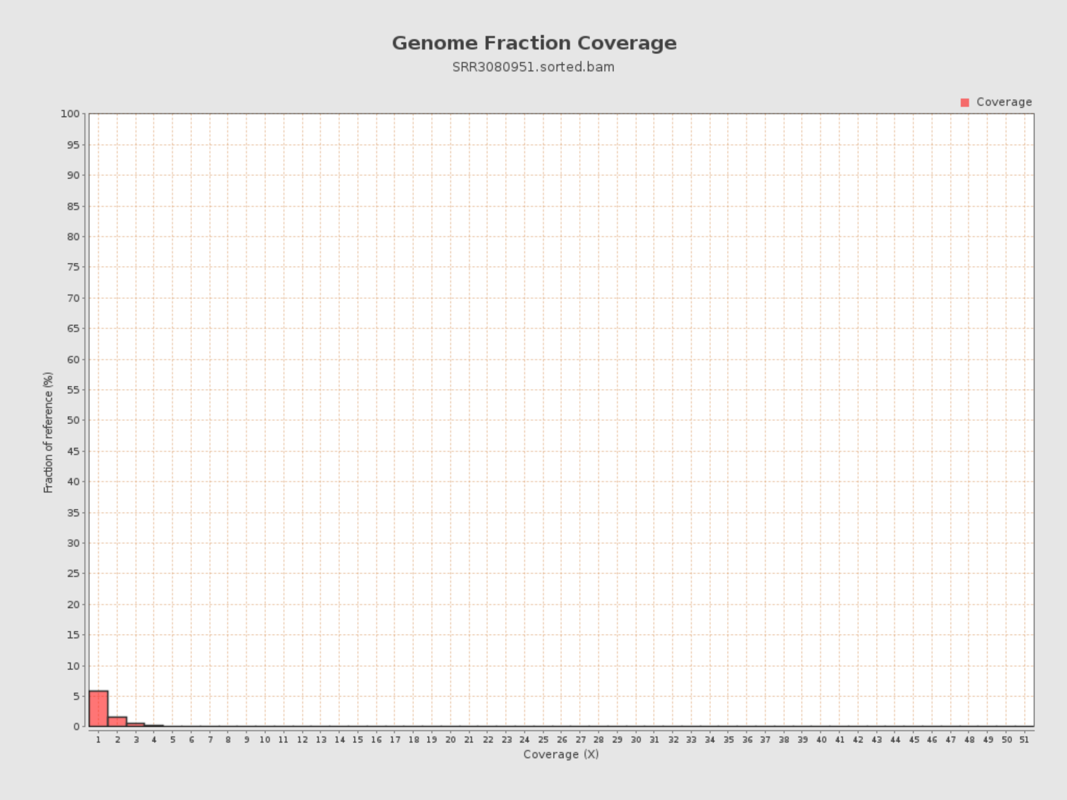
4. Results : Coverage Histogram



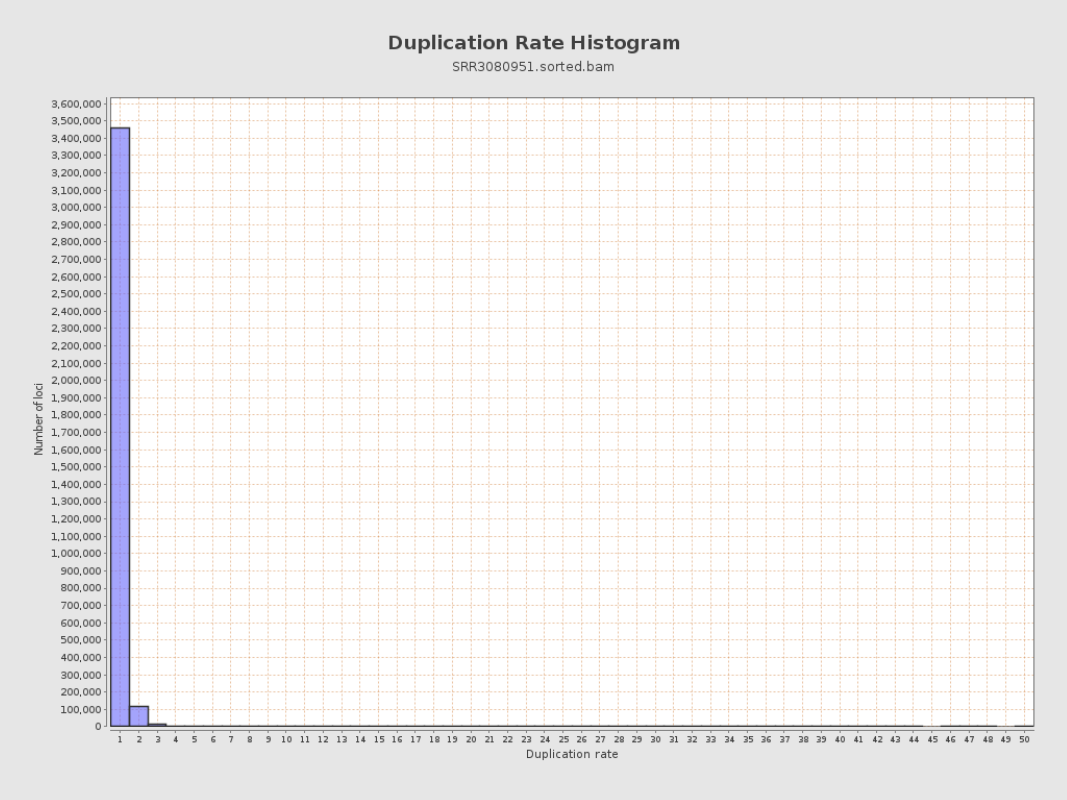
5. Results : Coverage Histogram (0-50X)



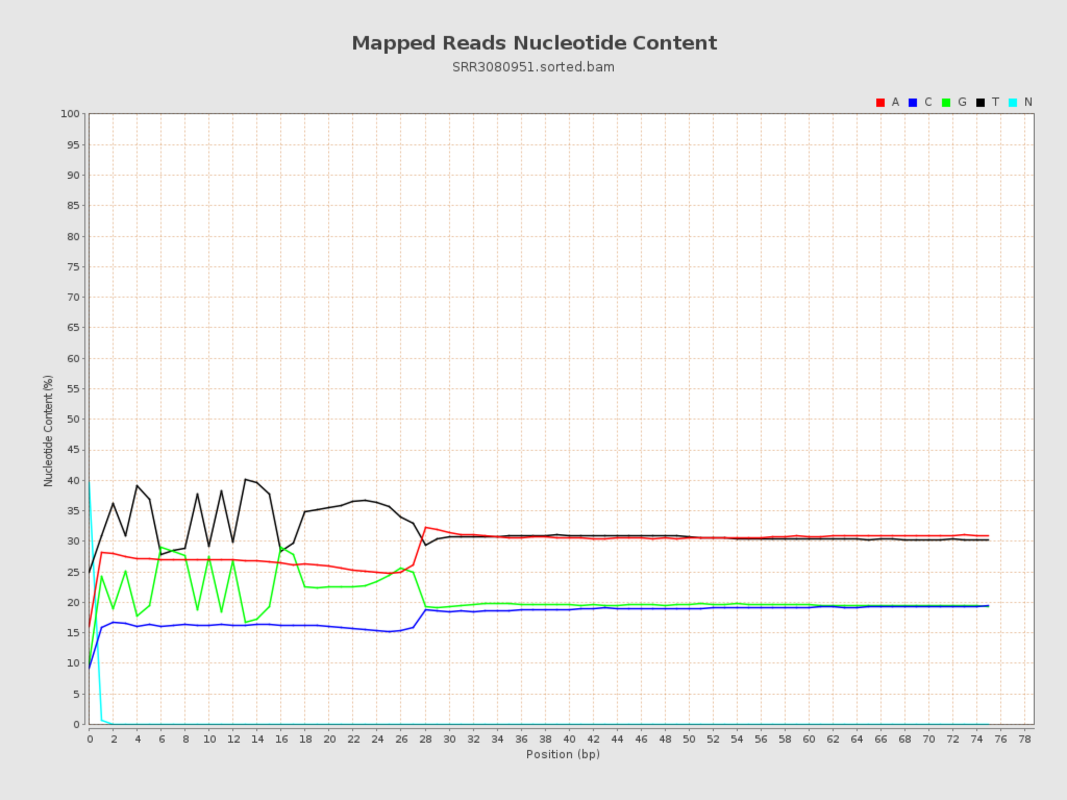
6. Results : Genome Fraction Coverage



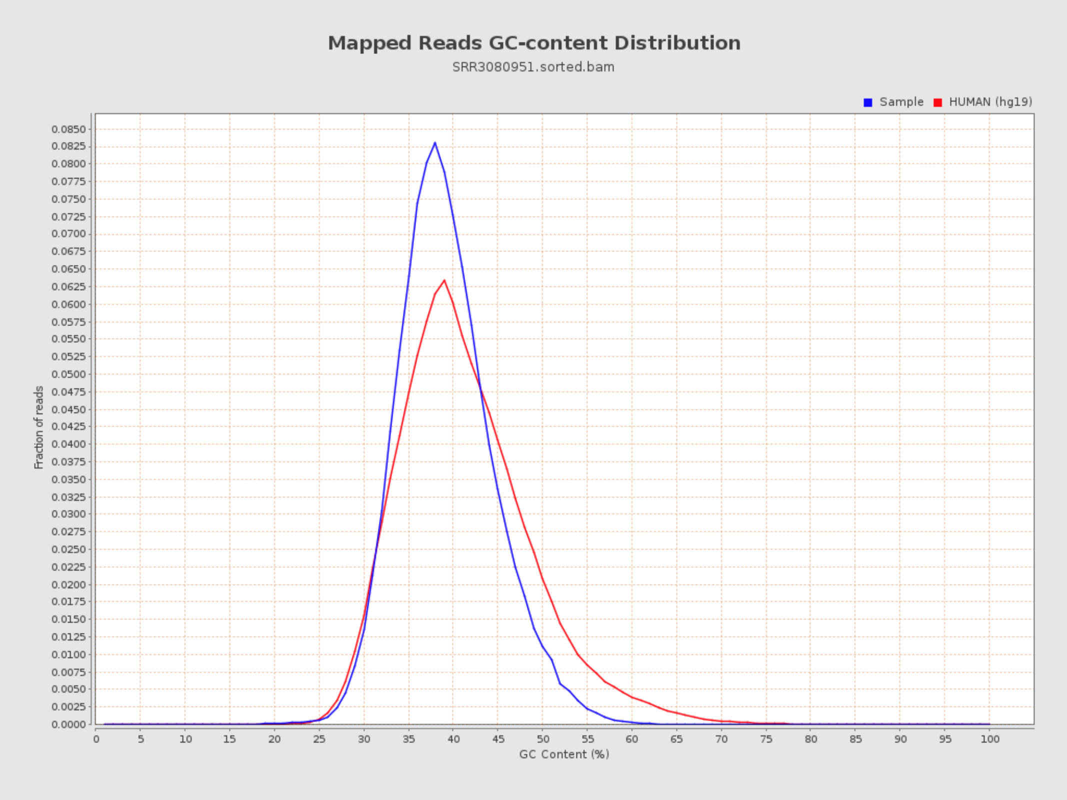
7. Results : Duplication Rate Histogram



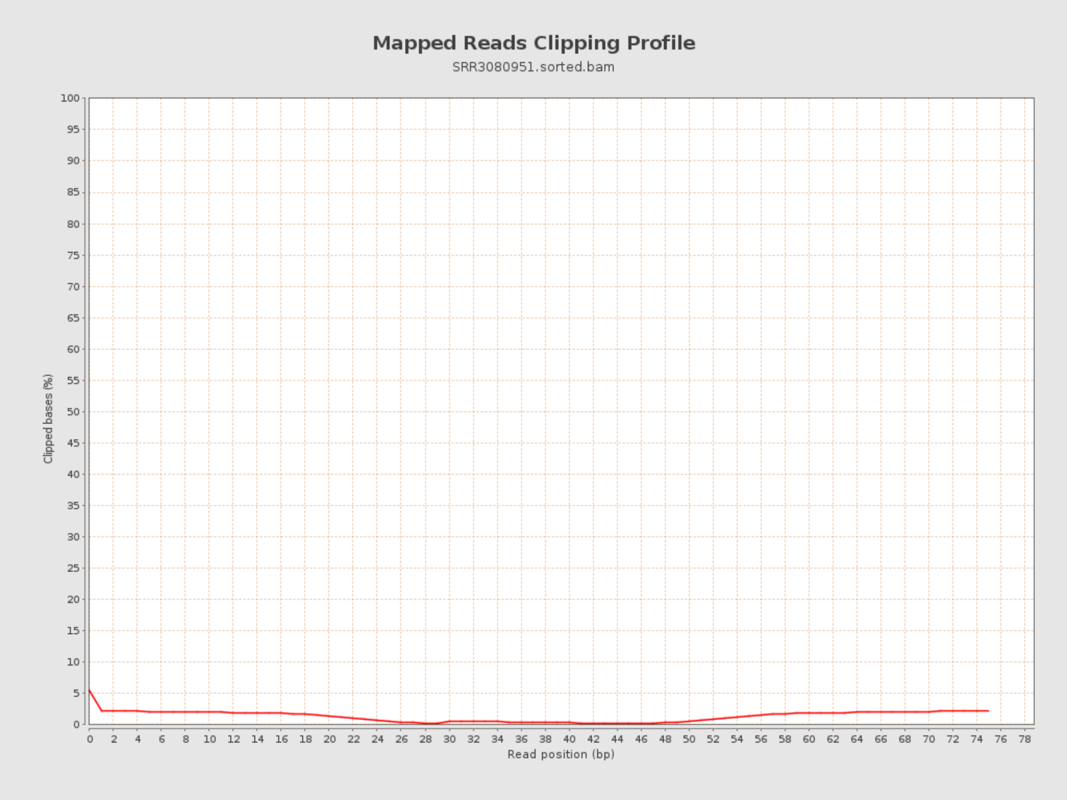
8. Results : Mapped Reads Nucleotide Content



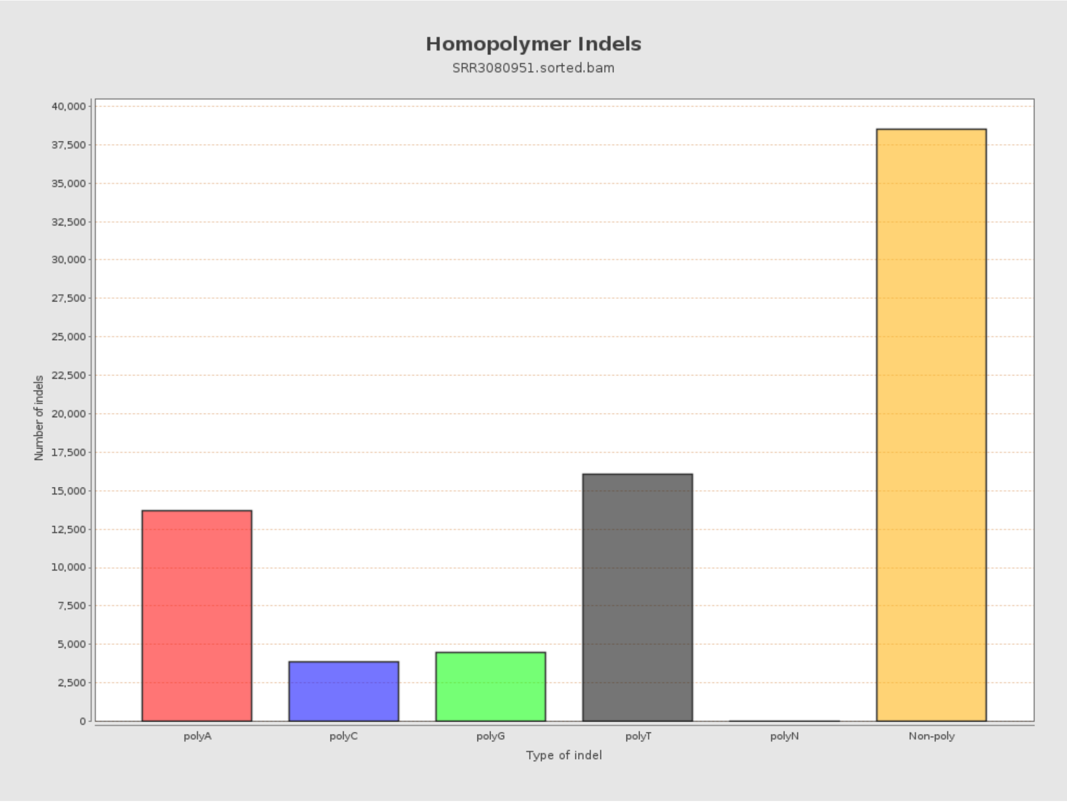
9. Results : Mapped Reads GC-content Distribution



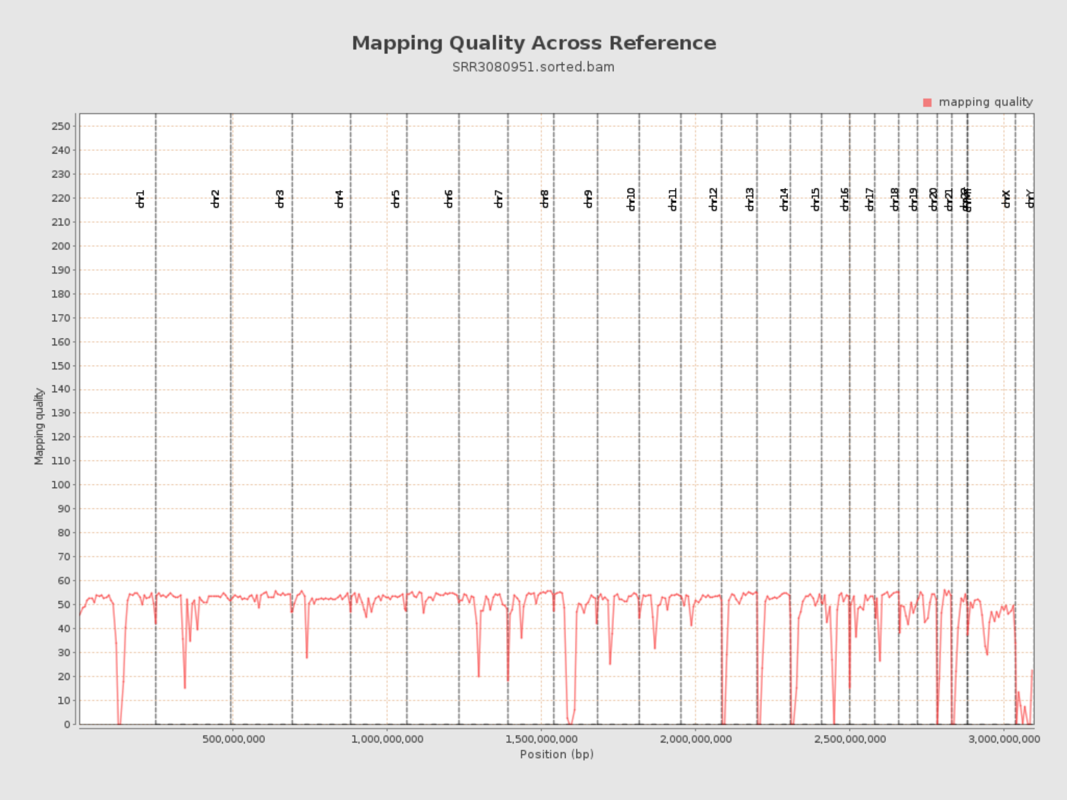
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram