Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:16:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085038.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_SRR3085038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085038.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:16:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,177,721
Mapped reads	2,848,556 / 89.64%
Unmapped reads	329,165 / 10.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,801 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	122,198 / 3.85%
Duplication rate	3.16%
Clipped reads	1,384,758 / 43.58%

2.2. ACGT Content

Number/percentage of A's	53,395,538 / 28.41%
Number/percentage of C's	35,298,218 / 18.78%
Number/percentage of T's	57,665,553 / 30.68%
Number/percentage of G's	41,590,118 / 22.13%
Number/percentage of N's	25,753 / 0.01%
GC Percentage	40.9%

2.3. Coverage

Mean	0.0607

Standard Deviation	0.5199

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

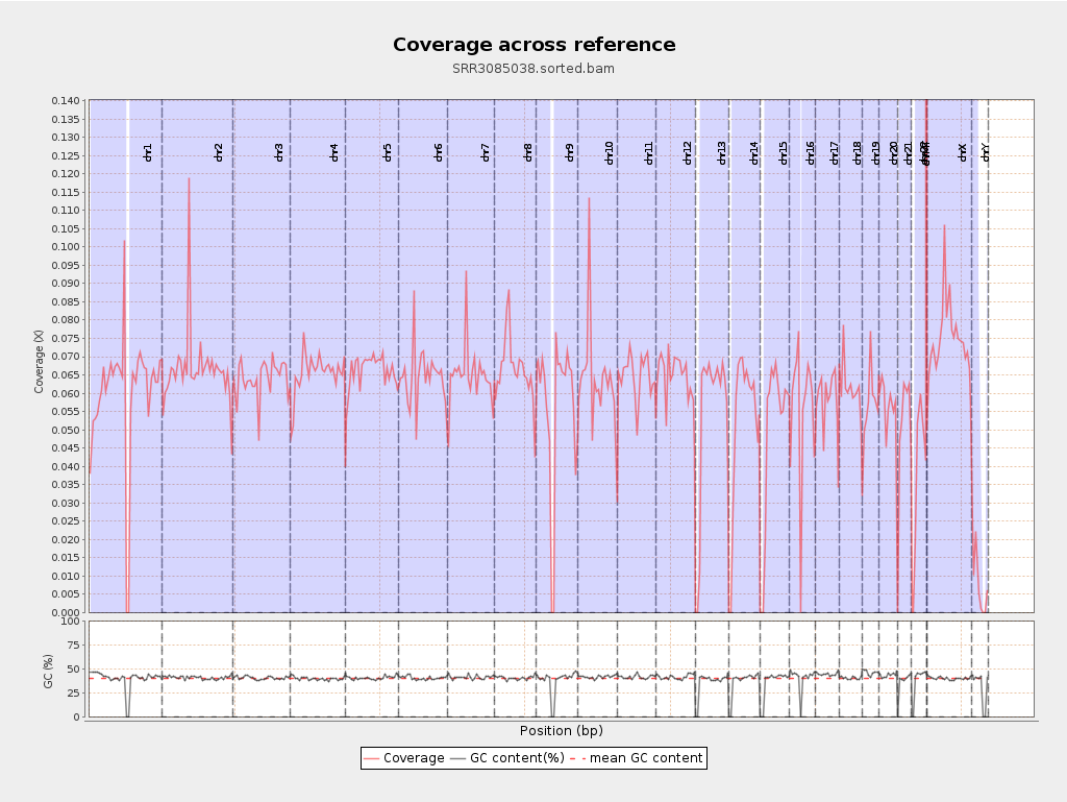
General error rate	0.87%
Mismatches	1,612,867
Insertions	15,446
Mapped reads with at least one insertion	0.54%
Deletions	47,094
Mapped reads with at least one deletion	1.64%
Homopolymer indels	46.46%

2.6. Chromosome stats

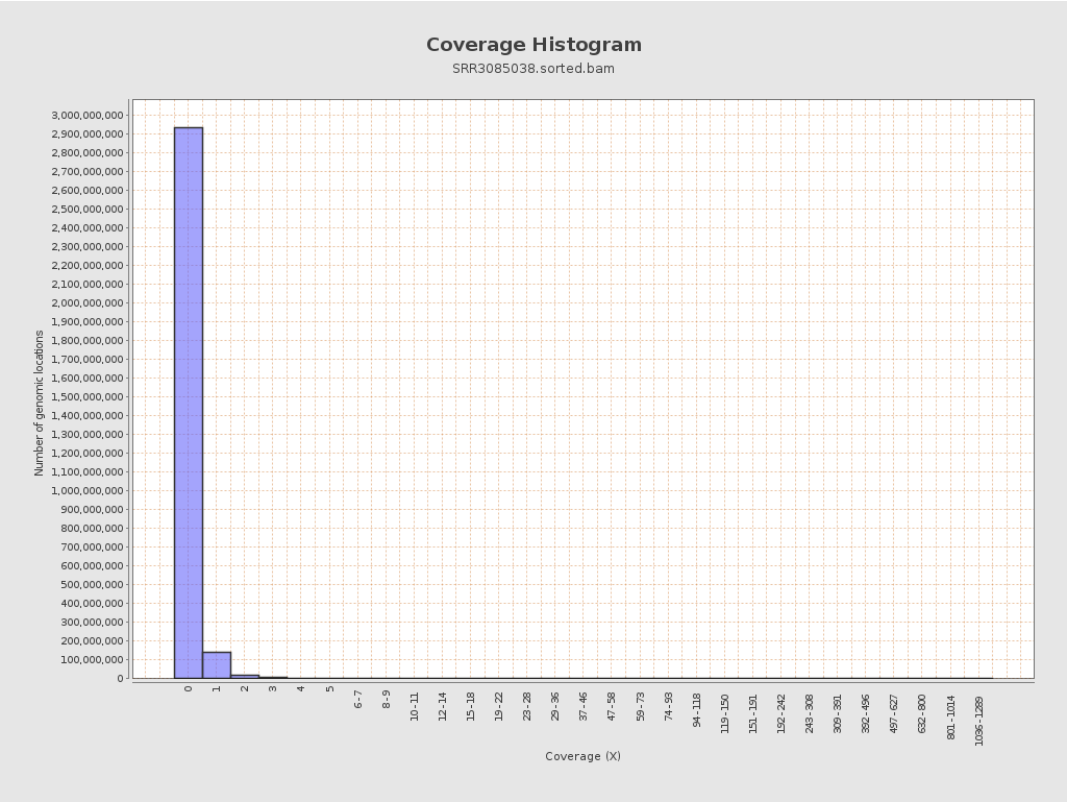
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14936569	0.0599	0.9496
chr2	243199373	16226077	0.0667	0.609
chr3	198022430	12686885	0.0641	0.2954
chr4	191154276	12537197	0.0656	0.3067
chr5	180915260	11988197	0.0663	0.2956
chr6	171115067	11016084	0.0644	0.4043
chr7	159138663	10378672	0.0652	0.4991

chr8	146364022	9688176	0.0662	0.8385
chr9	141213431	7940708	0.0562	0.4806
chr10	135534747	8693513	0.0641	0.5766
chr11	135006516	8663046	0.0642	0.5304
chr12	133851895	8661055	0.0647	0.2985
chr13	115169878	6182094	0.0537	0.2612
chr14	107349540	5554991	0.0517	0.3108
chr15	102531392	5046340	0.0492	0.2588
chr16	90354753	5039145	0.0558	0.3235
chr17	81195210	4687013	0.0577	0.3417
chr18	78077248	4830123	0.0619	0.925
chr19	59128983	3405174	0.0576	0.6735
chr20	63025520	3529386	0.056	0.2864
chr21	48129895	2418800	0.0503	0.281
chr22	51304566	1864419	0.0363	0.2151
chrMT	16571	30777	1.8573	1.7731
chrX	155270560	11578192	0.0746	0.3765
chrY	59373566	468895	0.0079	0.1464

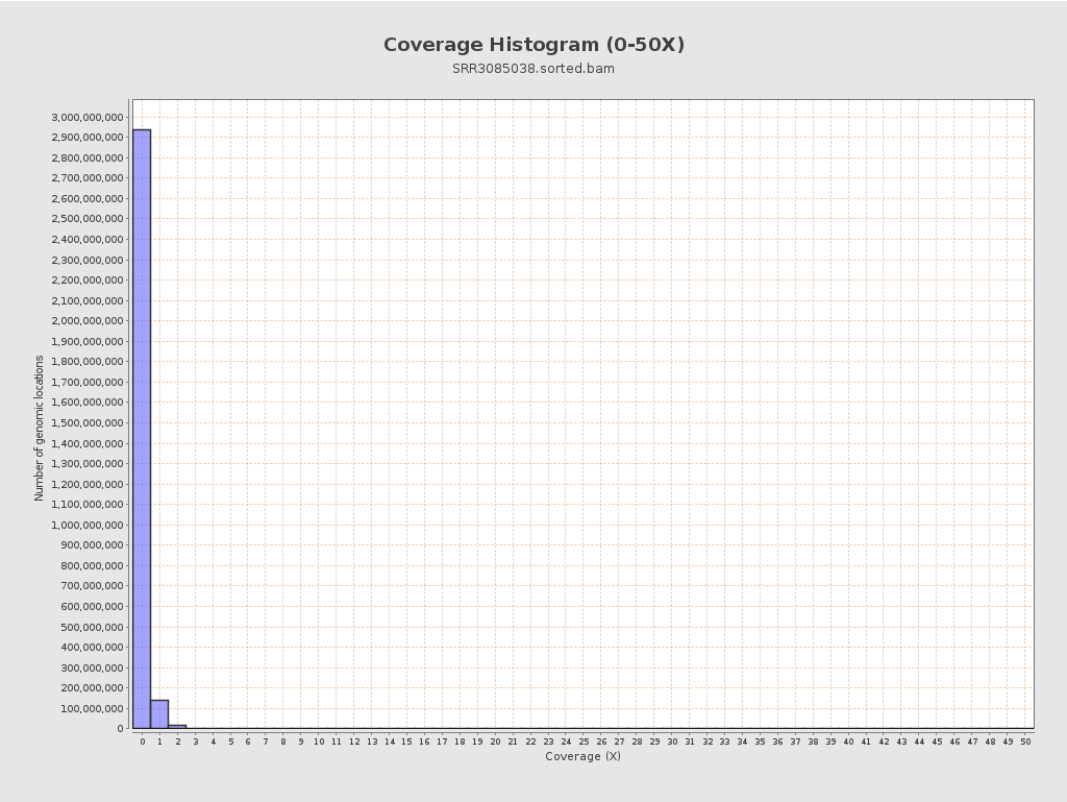
3. Results : Coverage across reference



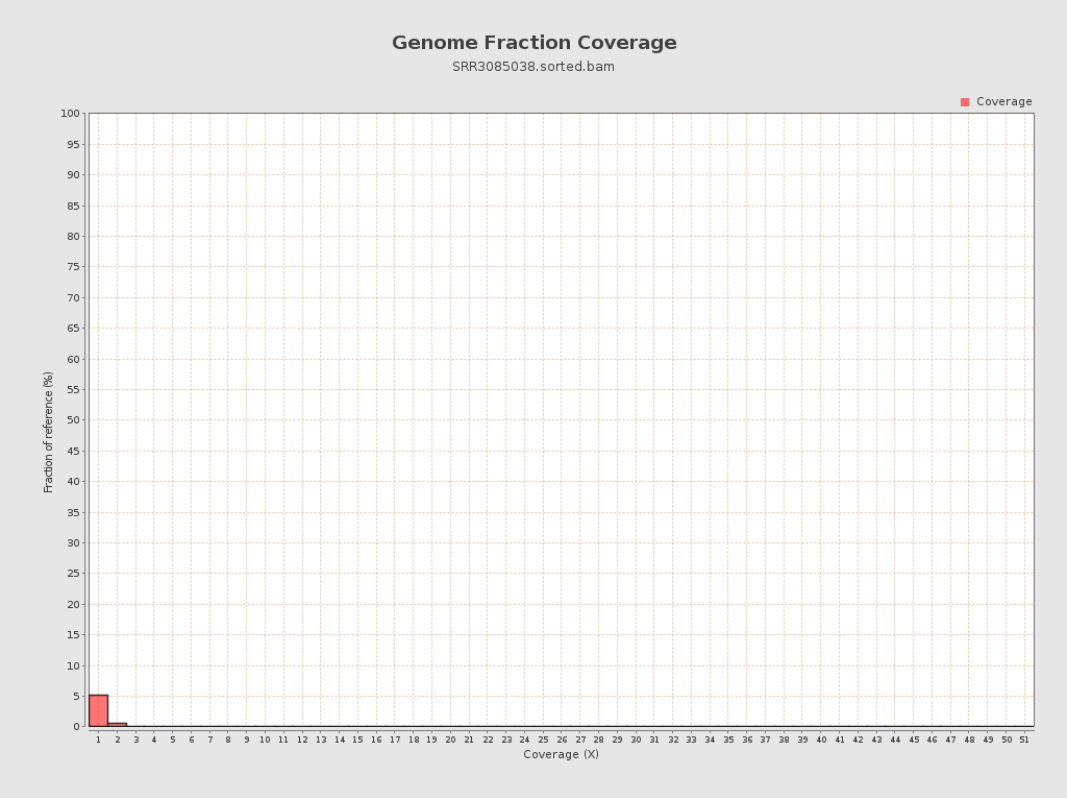
4. Results : Coverage Histogram



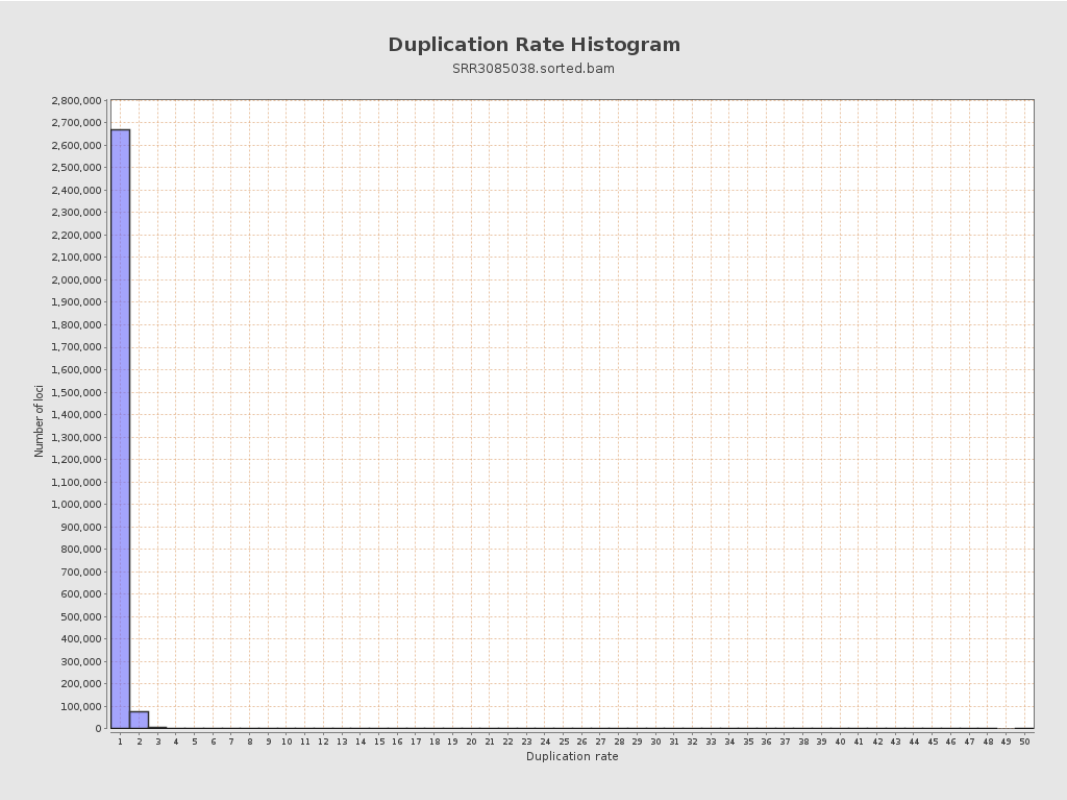
5. Results : Coverage Histogram (0-50X)



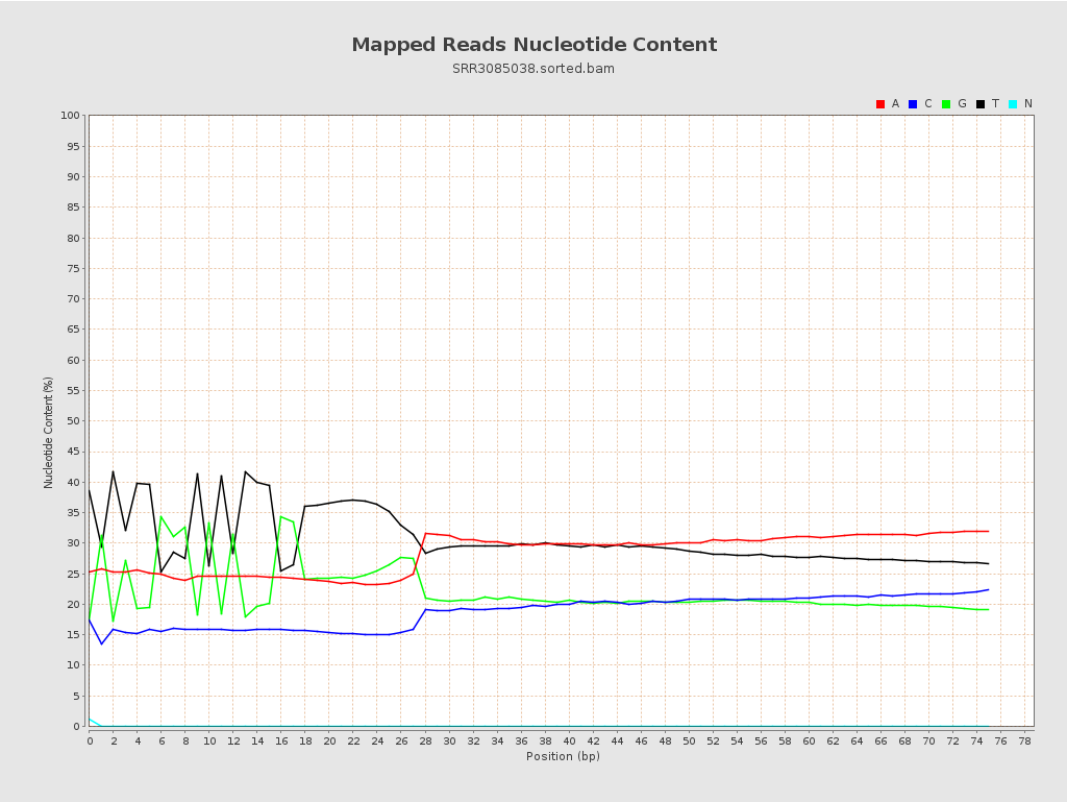
6. Results : Genome Fraction Coverage



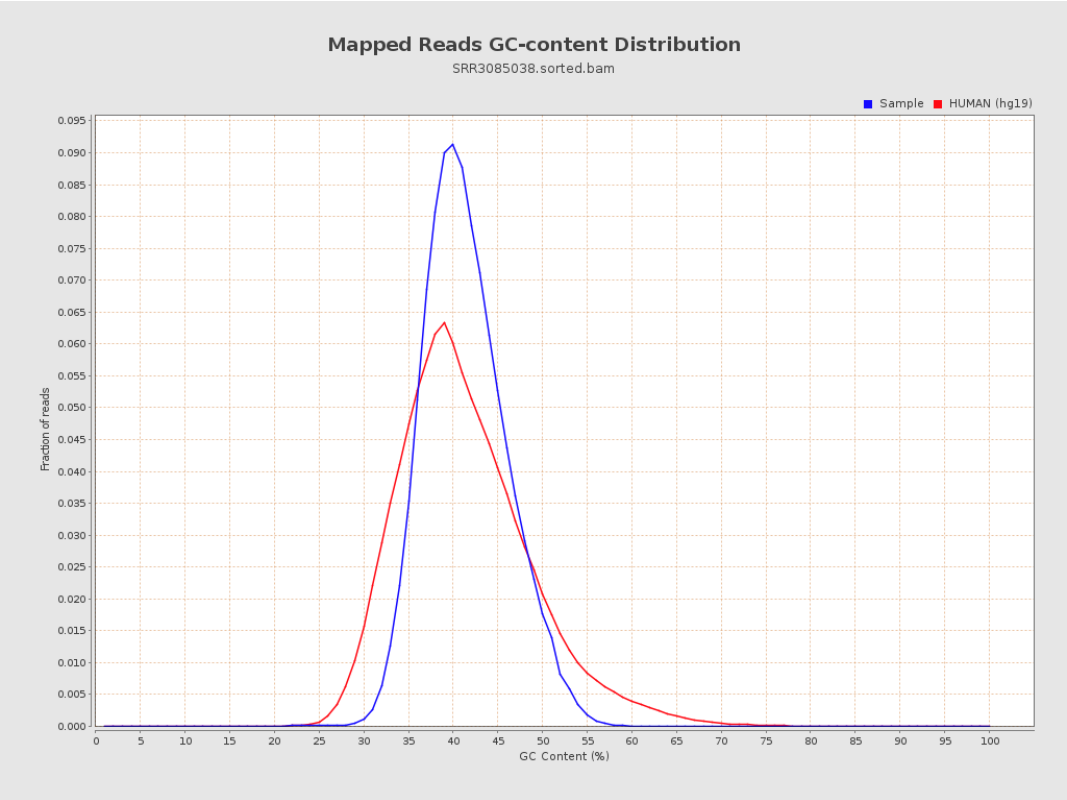
7. Results : Duplication Rate Histogram



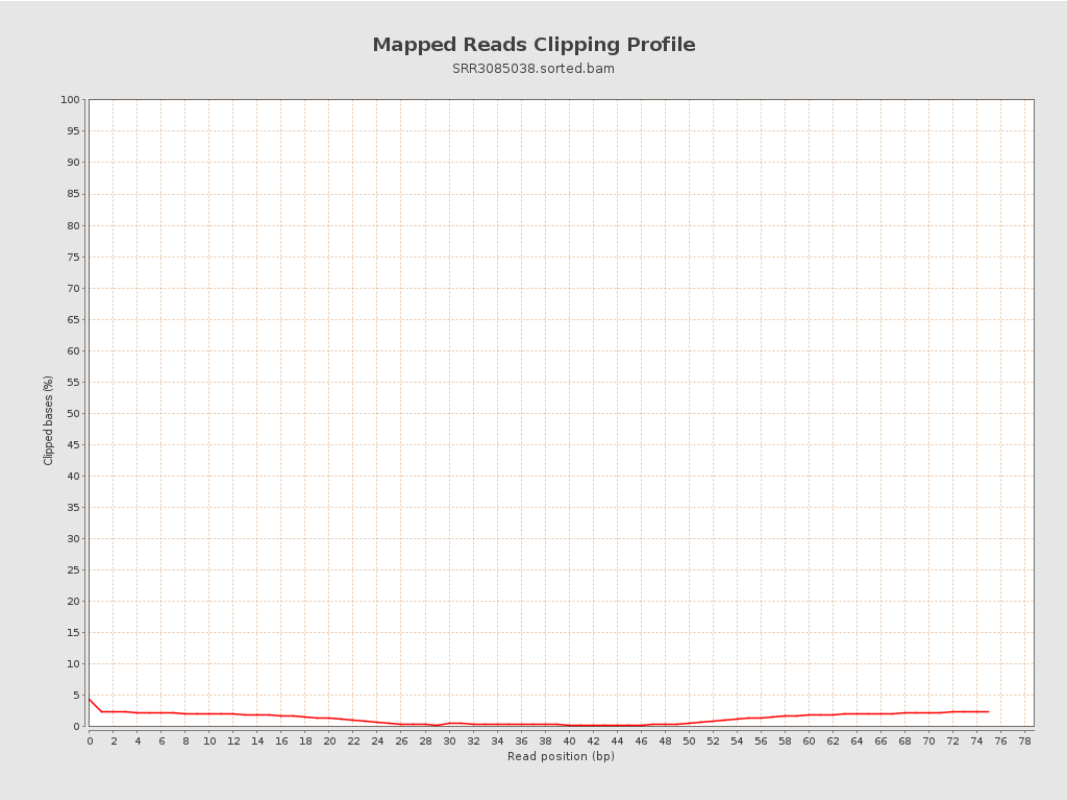
8. Results : Mapped Reads Nucleotide Content



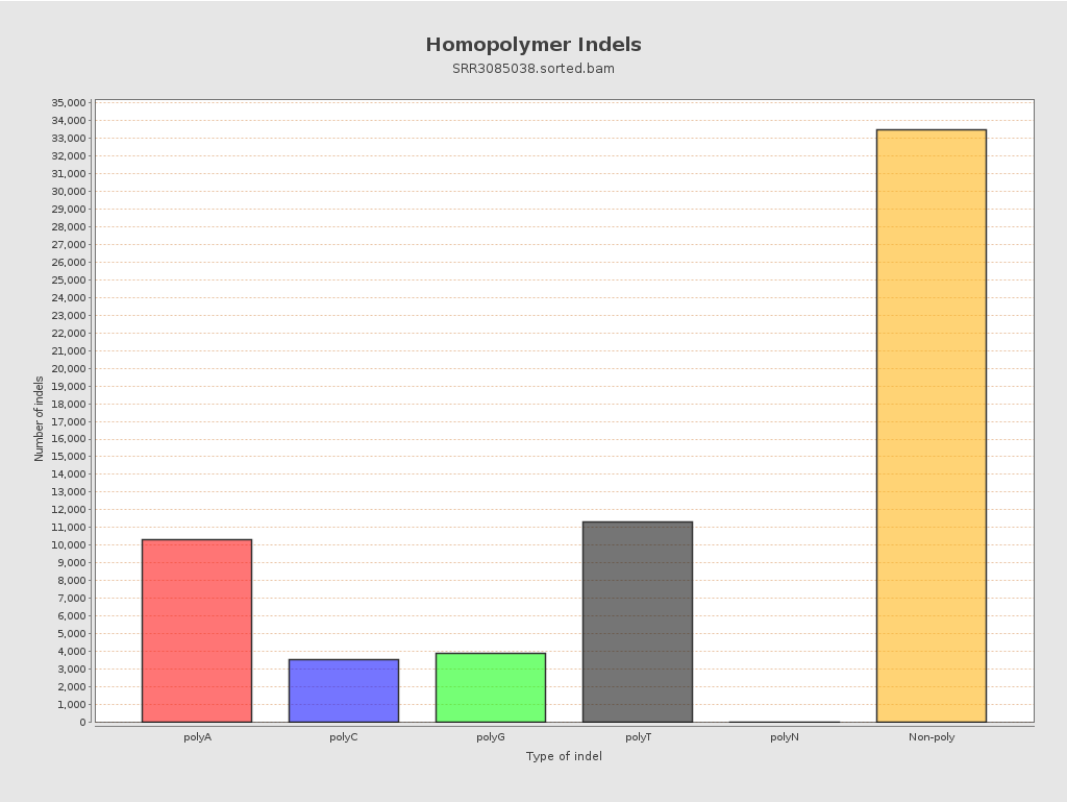
9. Results : Mapped Reads GC-content Distribution



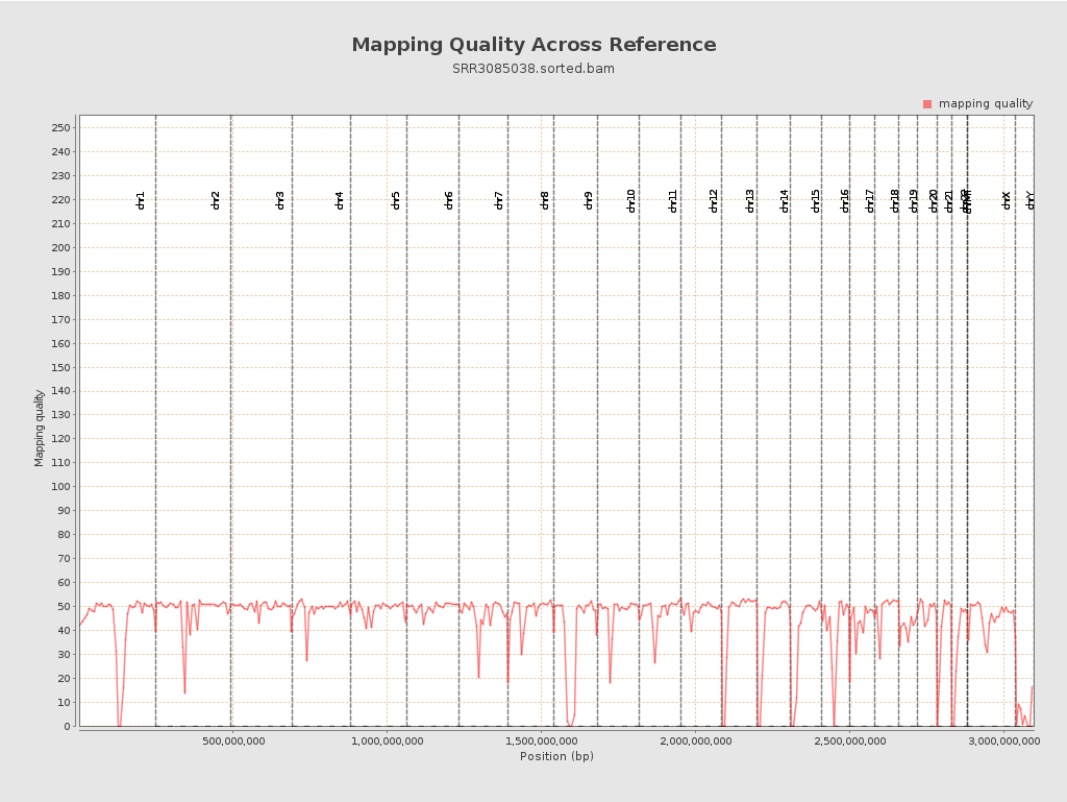
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram