Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:00:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080952.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_SRR3080952 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080952.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:00:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080952.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,342,098
Mapped reads	2,974,027 / 88.99%
Unmapped reads	368,071 / 11.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,581 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	141,166 / 4.22%
Duplication rate	3.59%
Clipped reads	1,300,097 / 38.9%

2.2. ACGT Content

Number/percentage of A's	56,099,294 / 28.17%
Number/percentage of C's	34,359,138 / 17.25%
Number/percentage of T's	64,487,083 / 32.38%
Number/percentage of G's	43,297,298 / 21.74%
Number/percentage of N's	922,127 / 0.46%
GC Percentage	38.99%

2.3. Coverage

Mean	0.0644

Standard Deviation	0.502

2.4. Mapping Quality

Mean Mapping Quality	47.03

2.5. Mismatches and indels

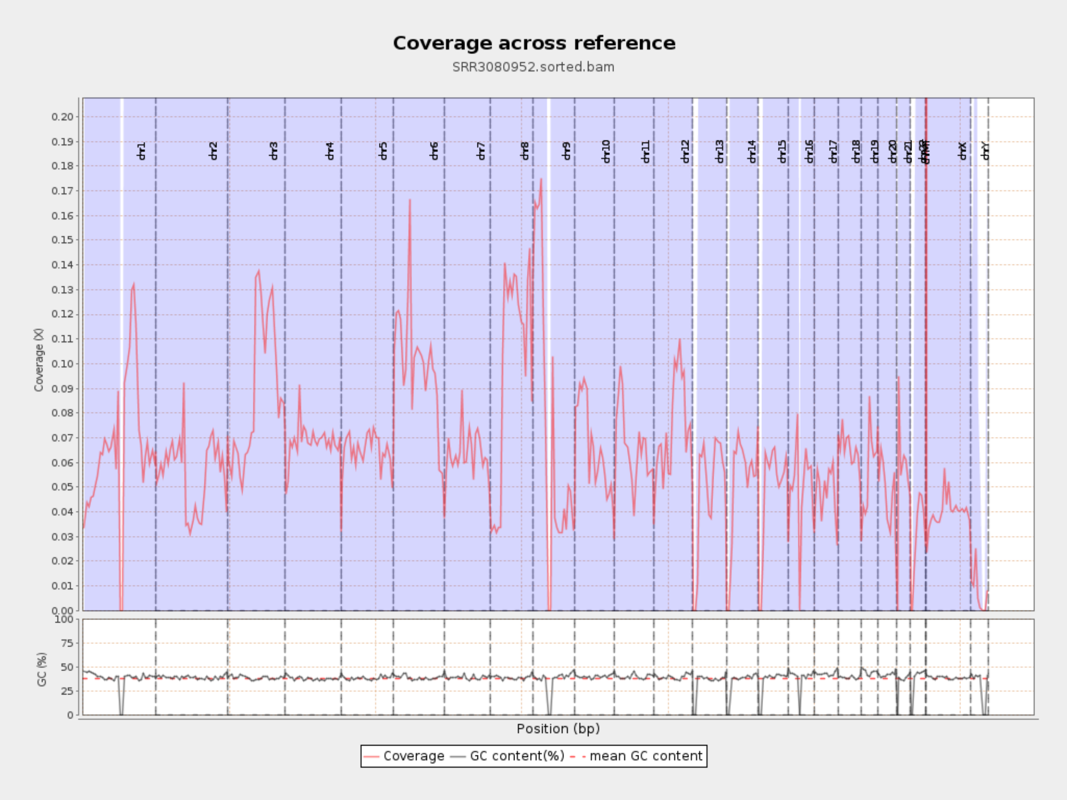
General error rate	1.12%
Mismatches	2,204,385
Insertions	15,724
Mapped reads with at least one insertion	0.53%
Deletions	44,462
Mapped reads with at least one deletion	1.48%
Homopolymer indels	49.09%

2.6. Chromosome stats

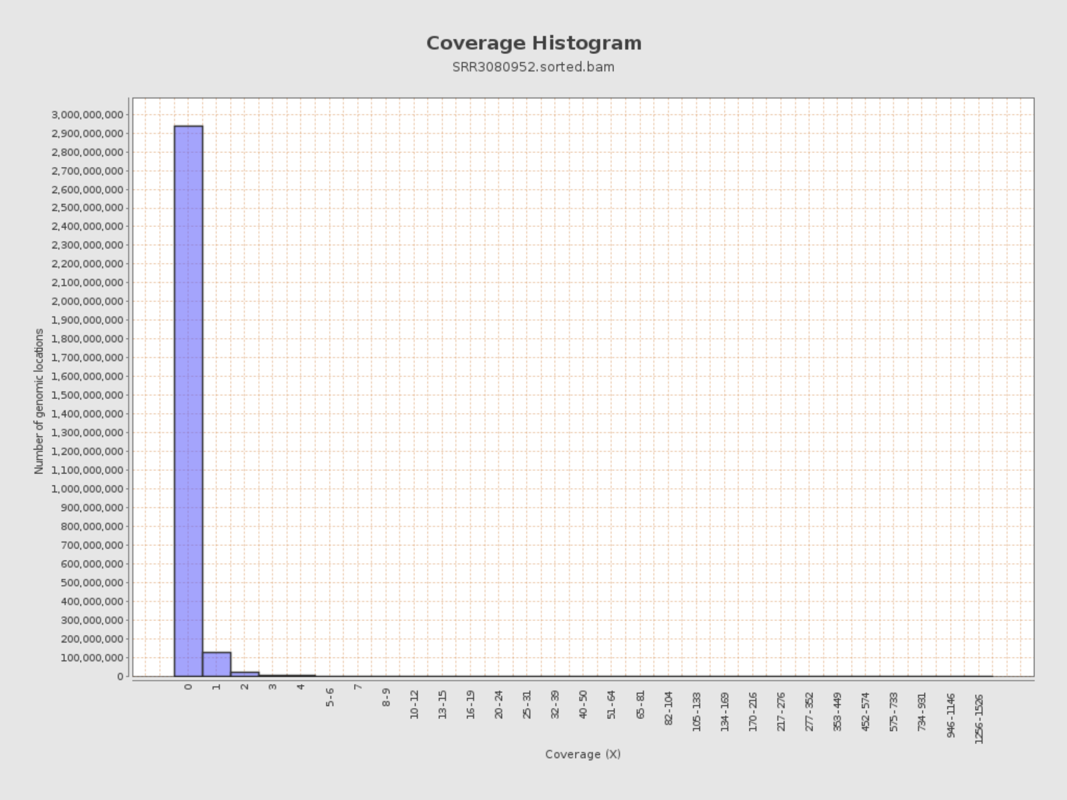
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16477269	0.0661	0.7423
chr2	243199373	13573133	0.0558	0.4594
chr3	198022430	17454355	0.0881	0.3621
chr4	191154276	13067630	0.0684	0.3332
chr5	180915260	11704002	0.0647	0.3107
chr6	171115067	17236710	0.1007	0.5544
chr7	159138663	10098903	0.0635	0.5273

chr8	146364022	14539541	0.0993	0.9972
chr9	141213431	10268083	0.0727	0.6006
chr10	135534747	9061726	0.0669	0.4305
chr11	135006516	8917256	0.0661	0.3836
chr12	133851895	9929147	0.0742	0.3457
chr13	115169878	5578242	0.0484	0.2642
chr14	107349540	5476532	0.051	0.3566
chr15	102531392	4934635	0.0481	0.2665
chr16	90354753	4389516	0.0486	0.3324
chr17	81195210	3964954	0.0488	0.2776
chr18	78077248	5126622	0.0657	1.0197
chr19	59128983	3378665	0.0571	0.5454
chr20	63025520	3090446	0.049	0.289
chr21	48129895	2750033	0.0571	0.3785
chr22	51304566	1534762	0.0299	0.2052
chrMT	16571	46086	2.7811	2.1928
chrX	155270560	6195662	0.0399	0.2727
chrY	59373566	444422	0.0075	0.1612

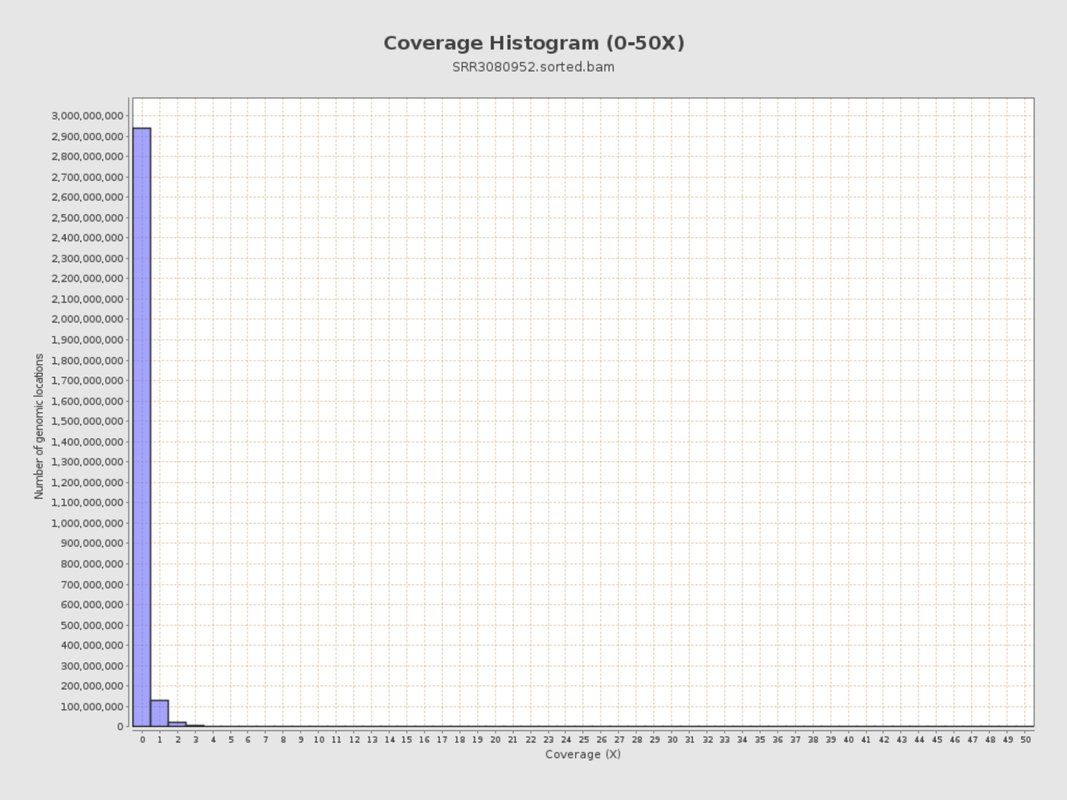
3. Results : Coverage across reference



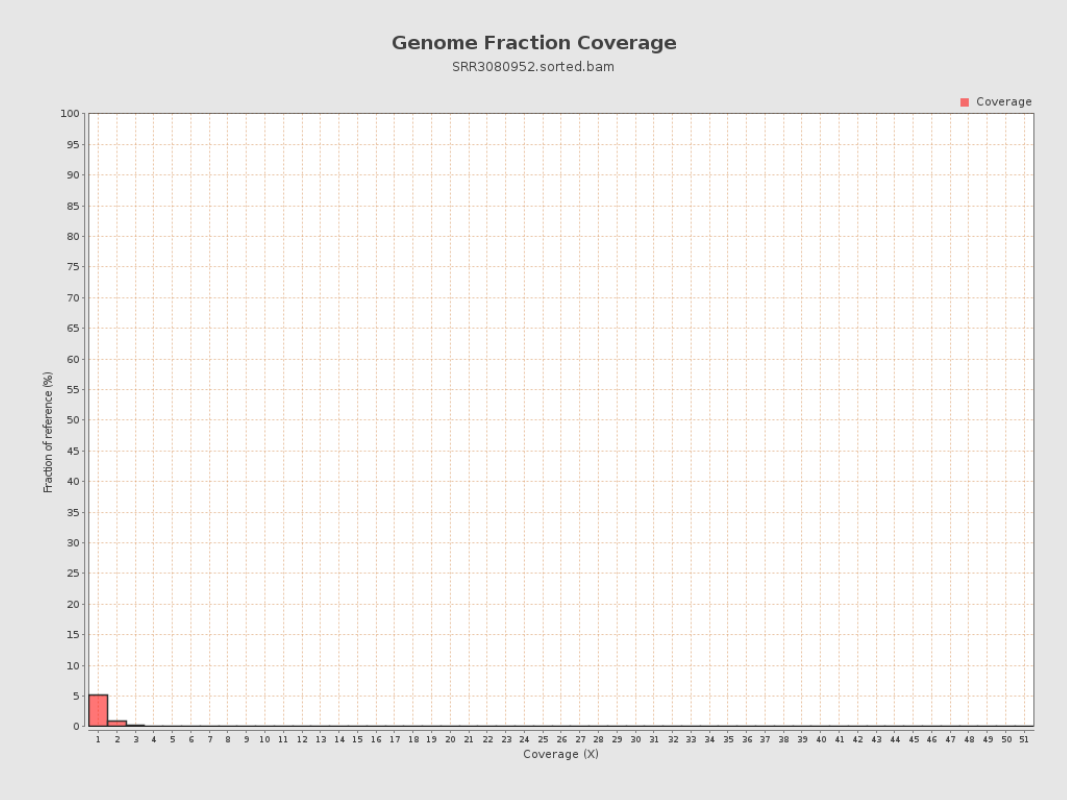
4. Results : Coverage Histogram



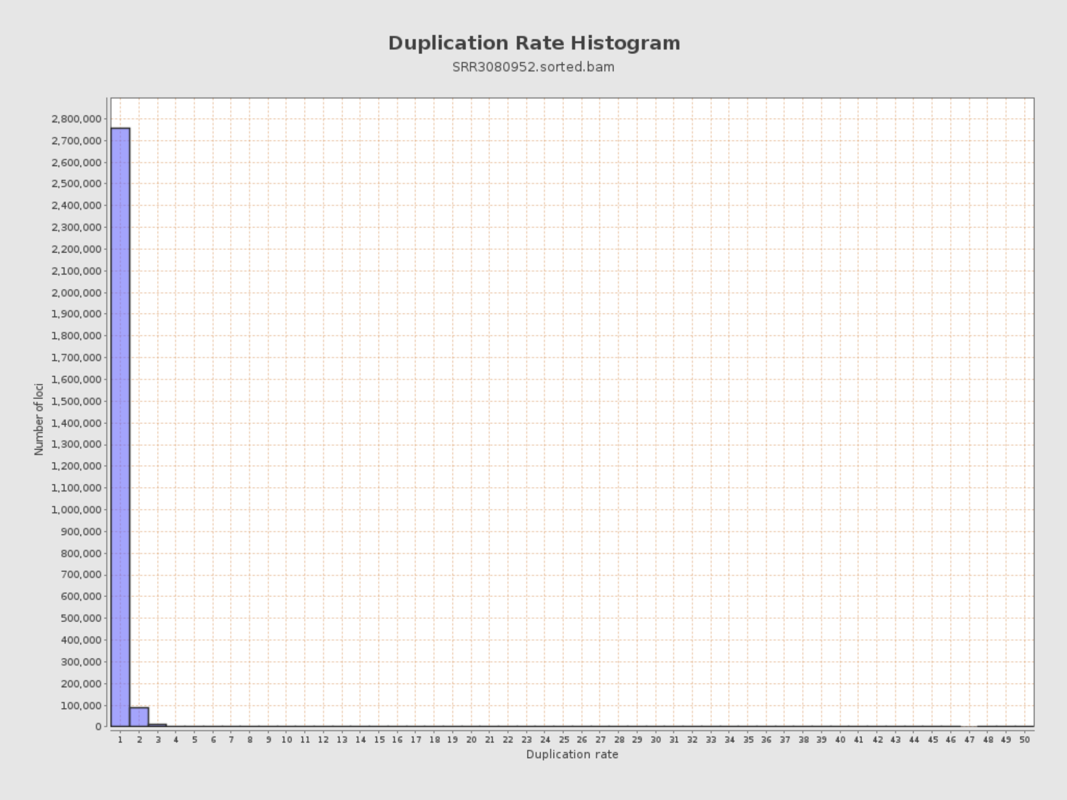
5. Results : Coverage Histogram (0-50X)



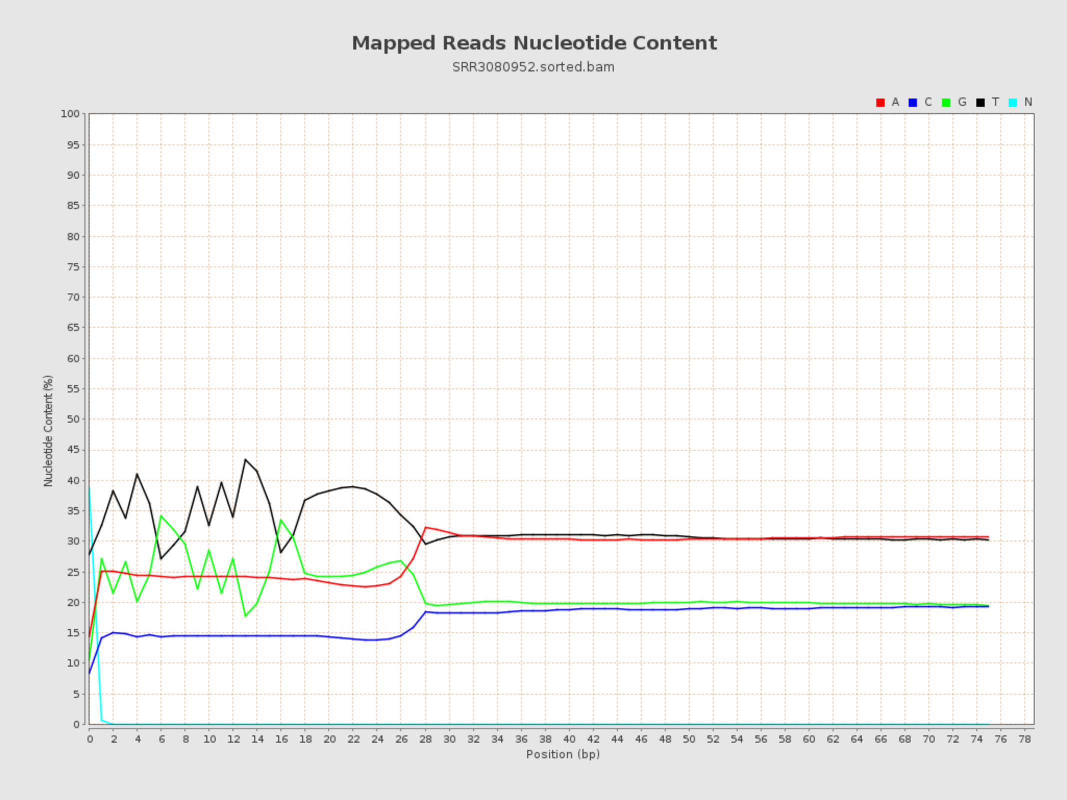
6. Results : Genome Fraction Coverage



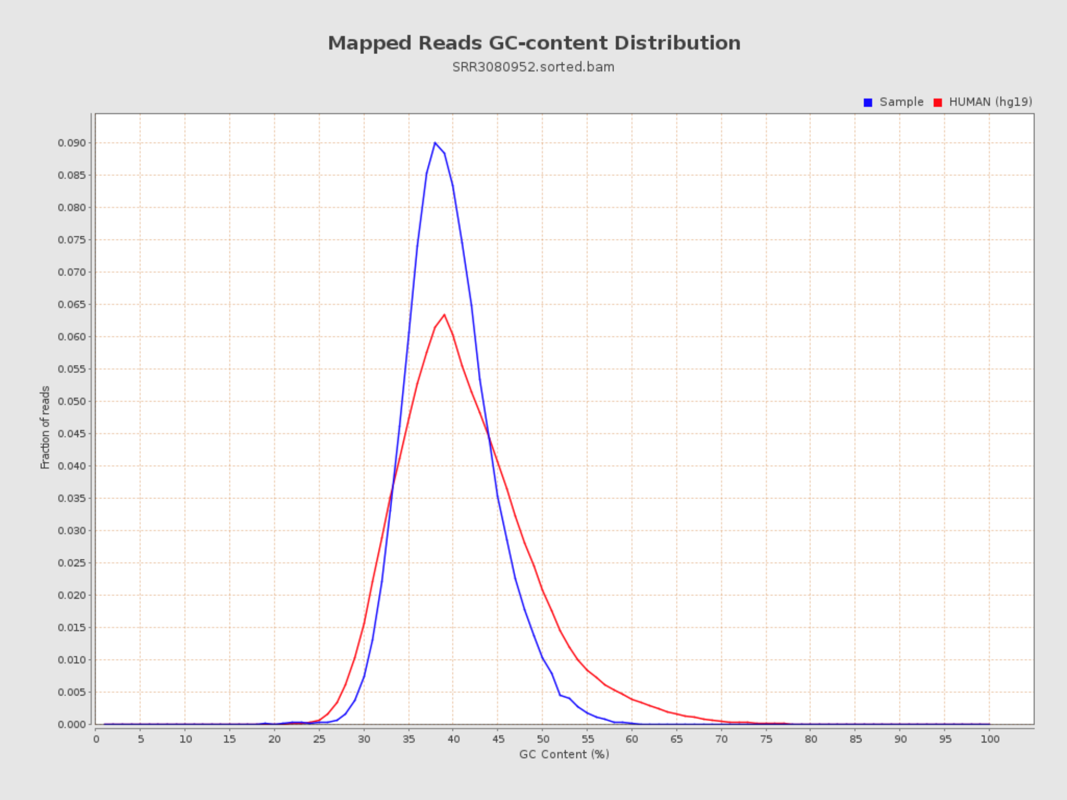
7. Results : Duplication Rate Histogram



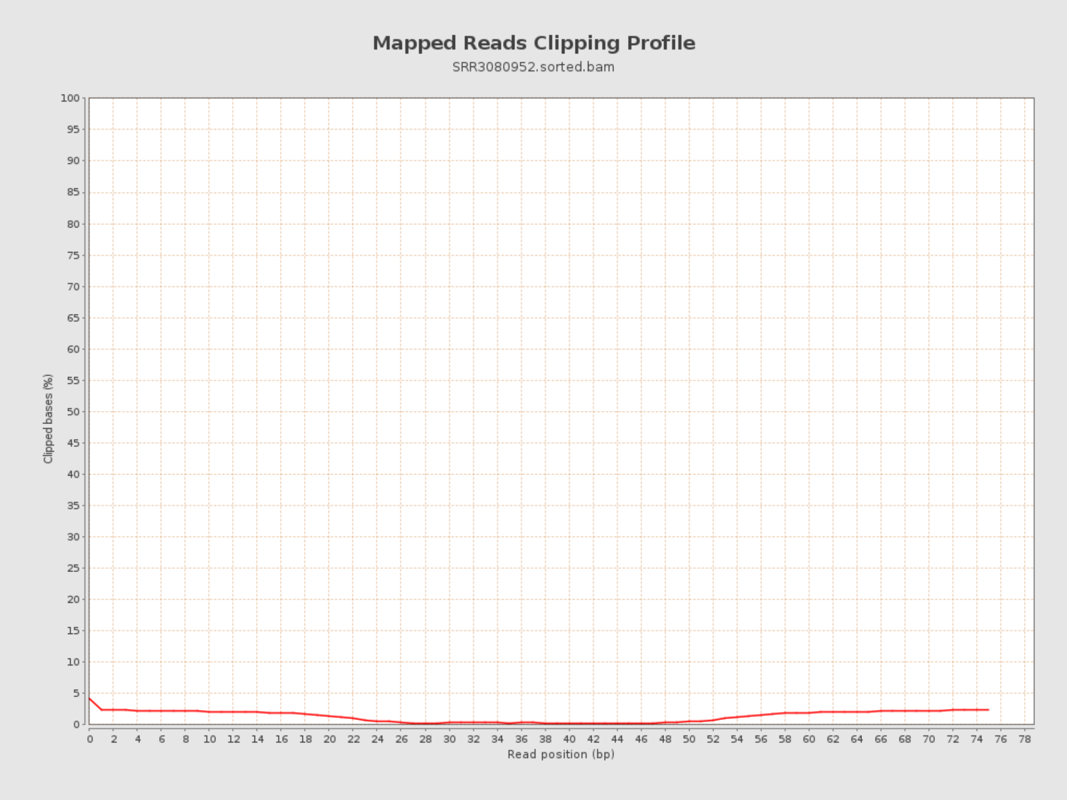
8. Results : Mapped Reads Nucleotide Content



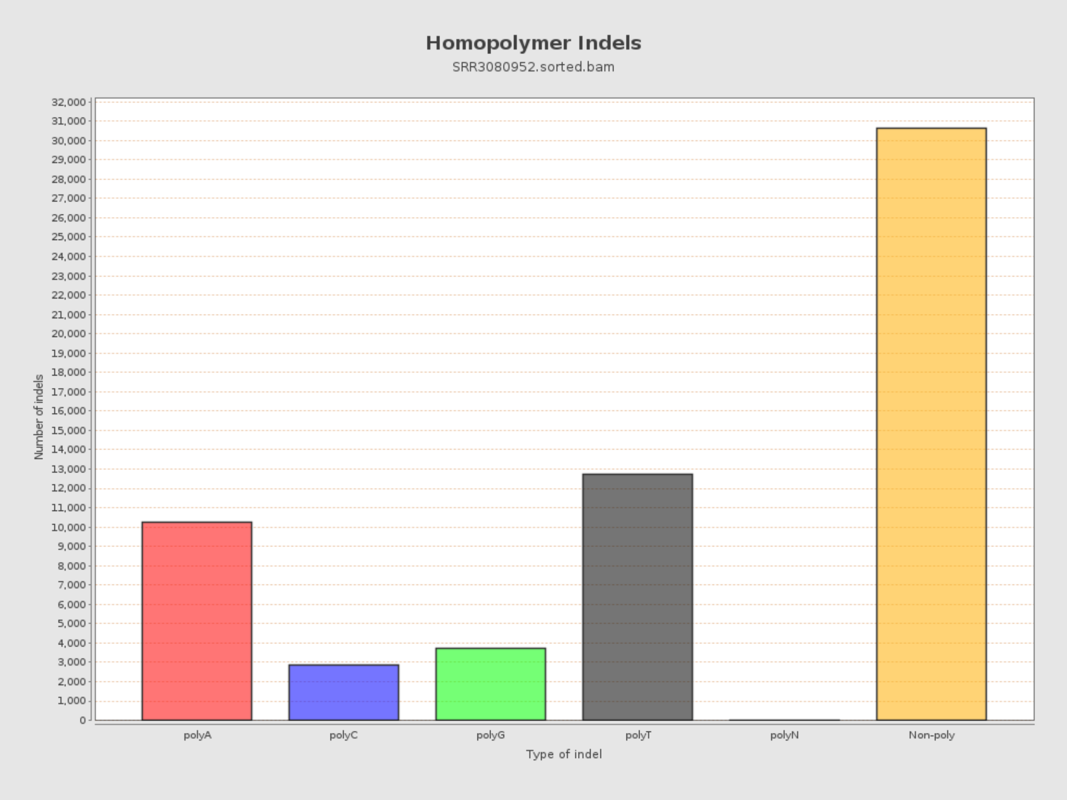
9. Results : Mapped Reads GC-content Distribution



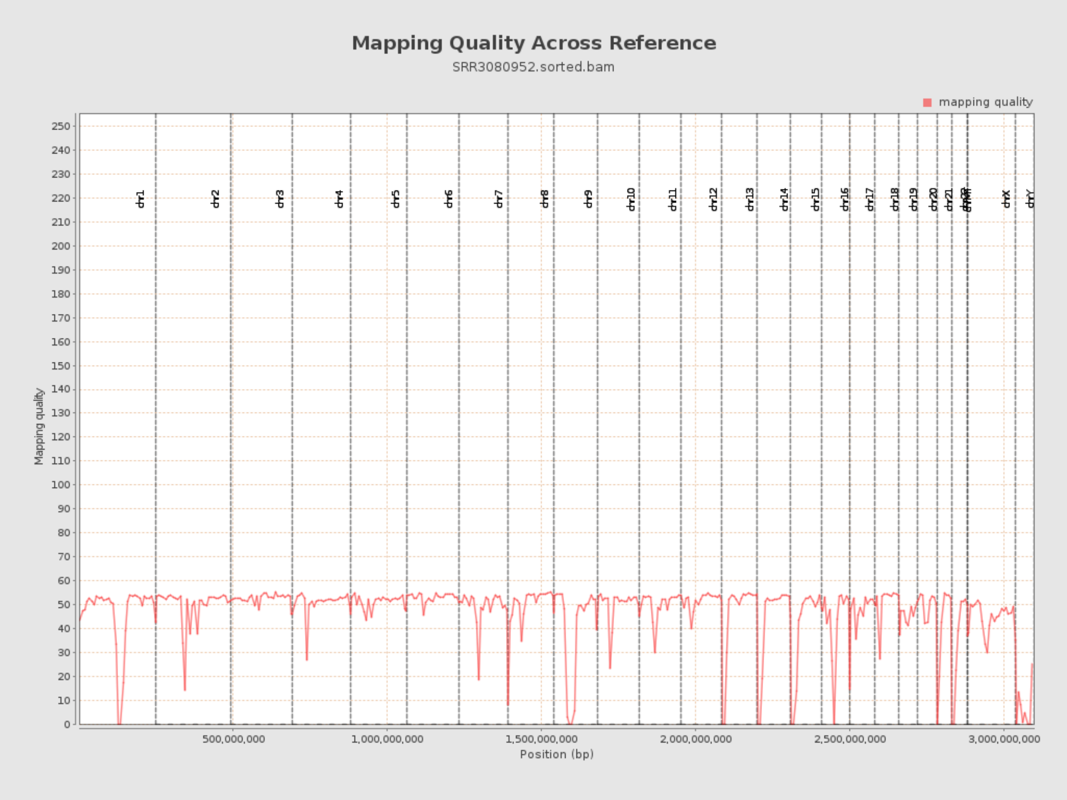
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram