Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:26:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080958.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_SRR3080958 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080958.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:26:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080958.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,372,743
Mapped reads	4,687,968 / 87.25%
Unmapped reads	684,775 / 12.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	48,982 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	363,340 / 6.76%
Duplication rate	5.93%
Clipped reads	2,084,702 / 38.8%

2.2. ACGT Content

Number/percentage of A's	87,680,846 / 27.97%
Number/percentage of C's	54,945,905 / 17.52%
Number/percentage of T's	102,420,409 / 32.67%
Number/percentage of G's	67,873,136 / 21.65%
Number/percentage of N's	614,782 / 0.2%
GC Percentage	39.17%

2.3. Coverage

Mean	0.1013

Standard Deviation	0.8761

2.4. Mapping Quality

Mean Mapping Quality	46.72

2.5. Mismatches and indels

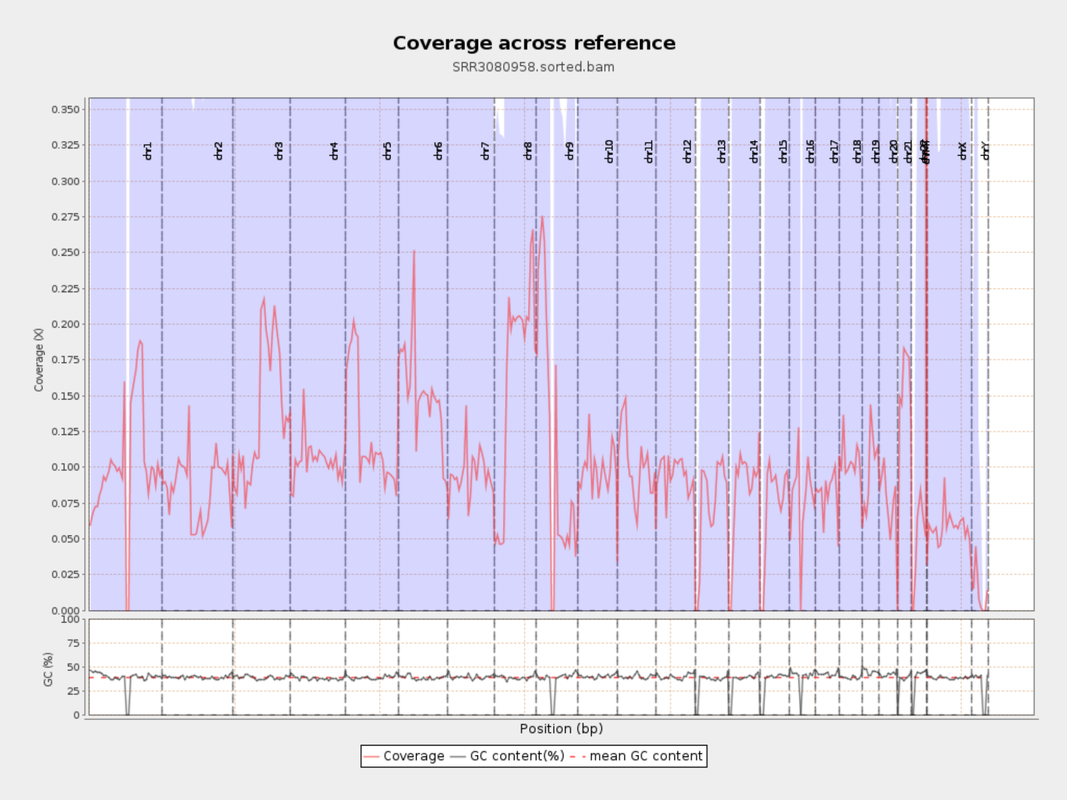
General error rate	1.04%
Mismatches	3,210,956
Insertions	25,909
Mapped reads with at least one insertion	0.55%
Deletions	71,117
Mapped reads with at least one deletion	1.5%
Homopolymer indels	49.04%

2.6. Chromosome stats

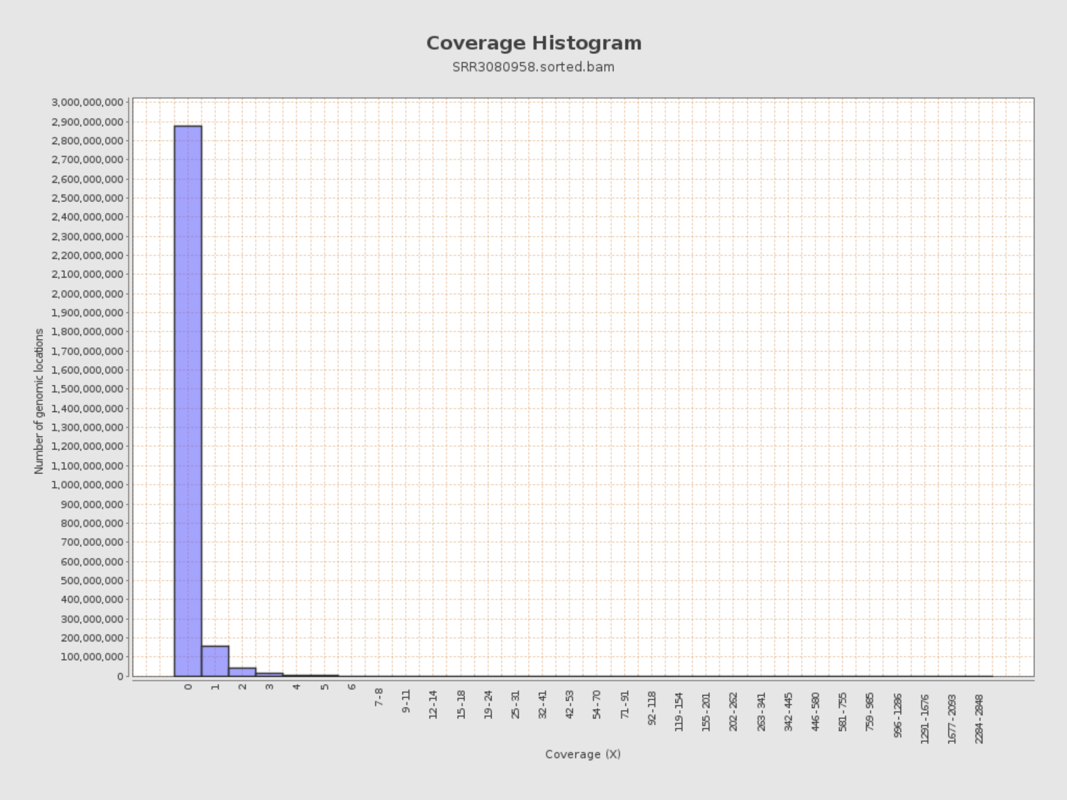
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25470073	0.1022	1.5856
chr2	243199373	20830232	0.0857	0.7233
chr3	198022430	27268485	0.1377	0.5003
chr4	191154276	19963466	0.1044	0.482
chr5	180915260	22304391	0.1233	0.4764
chr6	171115067	26137924	0.1528	0.8943
chr7	159138663	15218773	0.0956	0.8733

chr8	146364022	24236490	0.1656	1.8074
chr9	141213431	15931420	0.1128	0.9533
chr10	135534747	13421169	0.099	0.6884
chr11	135006516	13608631	0.1008	0.6014
chr12	133851895	12690212	0.0948	0.4454
chr13	115169878	8354207	0.0725	0.3564
chr14	107349540	8713512	0.0812	0.523
chr15	102531392	7450997	0.0727	0.3559
chr16	90354753	7195026	0.0796	0.5251
chr17	81195210	6579674	0.081	0.4044
chr18	78077248	8204850	0.1051	1.7731
chr19	59128983	5869750	0.0993	1.1151
chr20	63025520	4946729	0.0785	0.4416
chr21	48129895	7081174	0.1471	0.6447
chr22	51304566	2421893	0.0472	0.2819
chrMT	16571	87368	5.2723	3.8398
chrX	155270560	8933239	0.0575	0.3951
chrY	59373566	732655	0.0123	0.2845

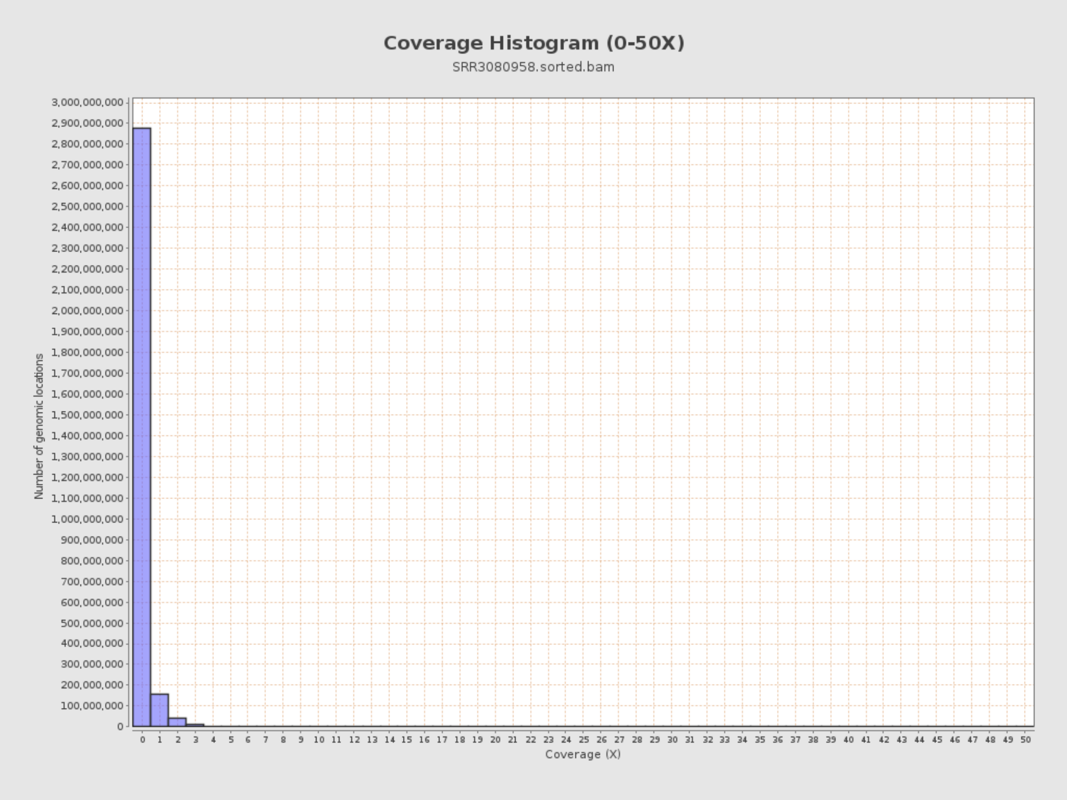
3. Results : Coverage across reference



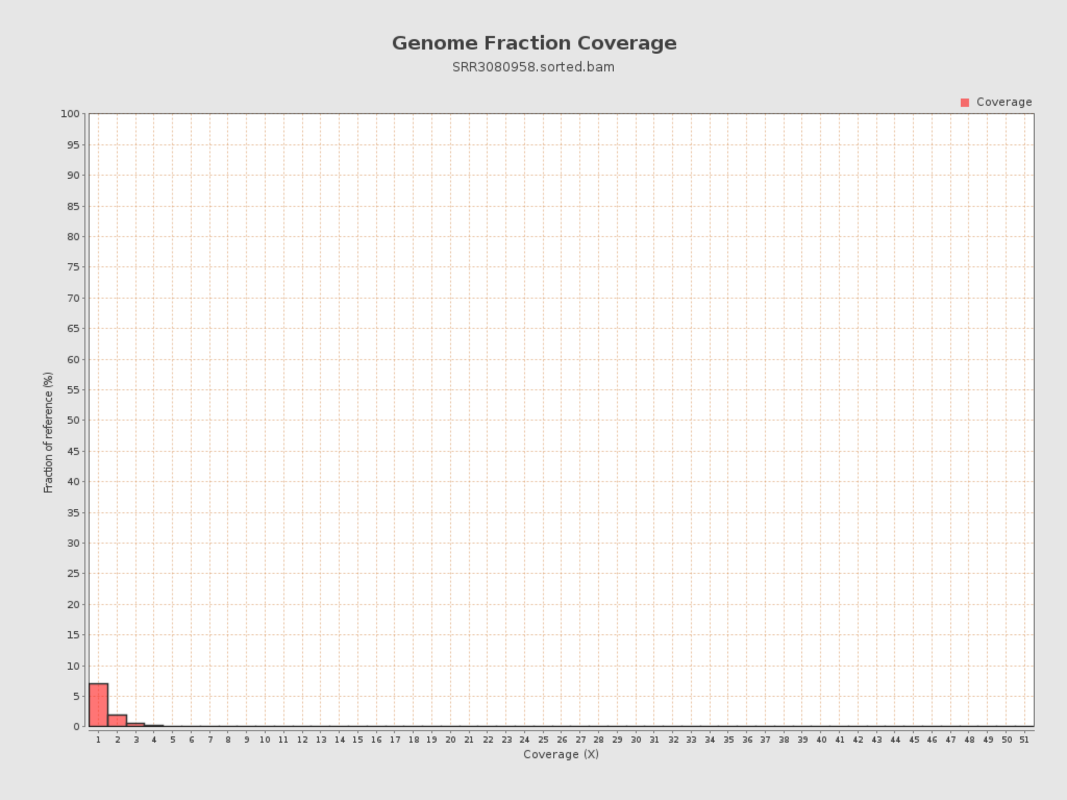
4. Results : Coverage Histogram



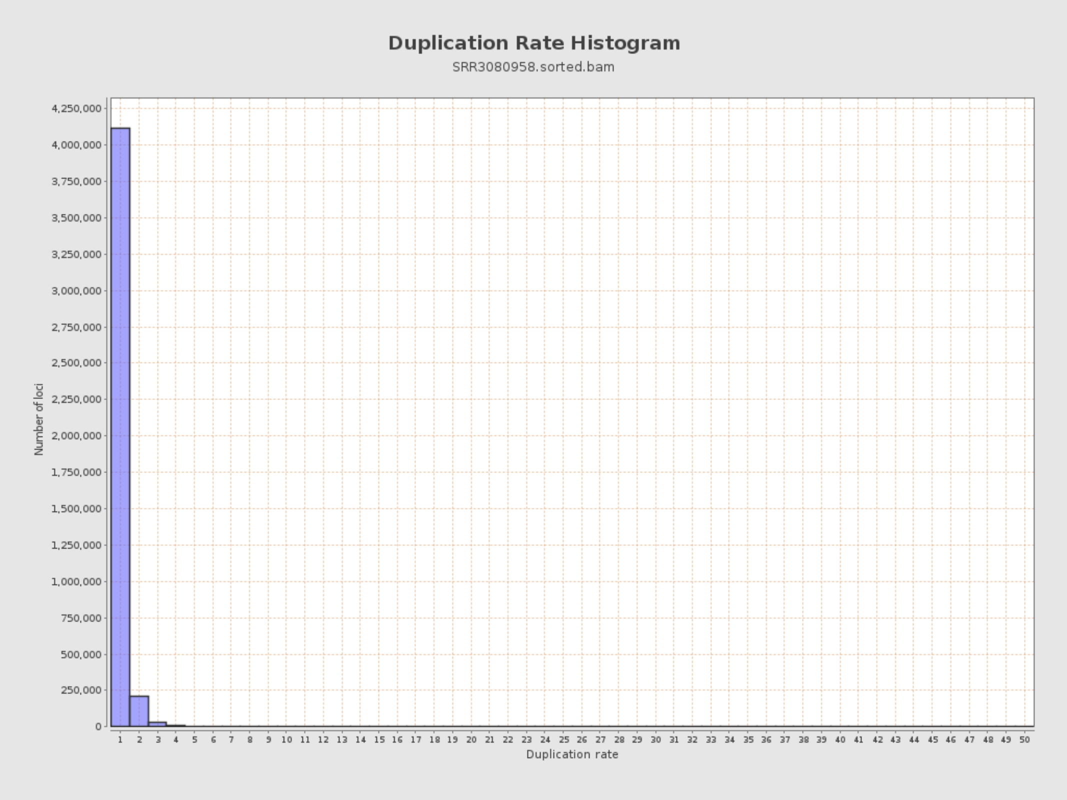
5. Results : Coverage Histogram (0-50X)



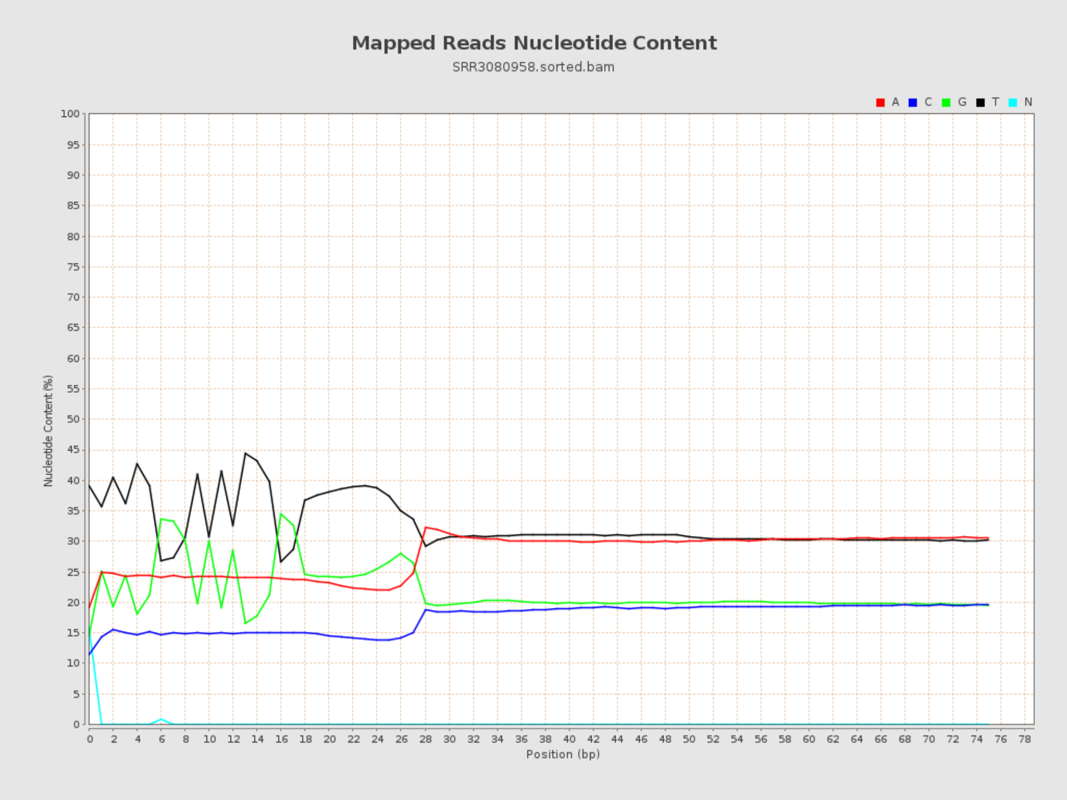
6. Results : Genome Fraction Coverage



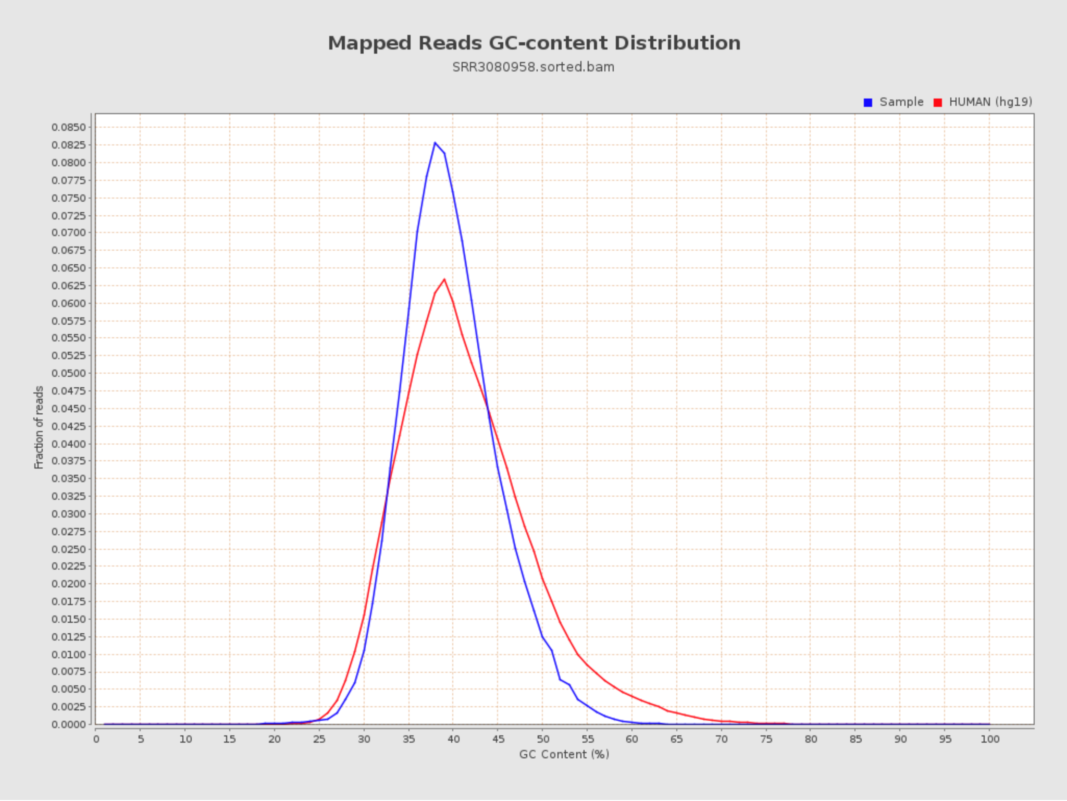
7. Results : Duplication Rate Histogram



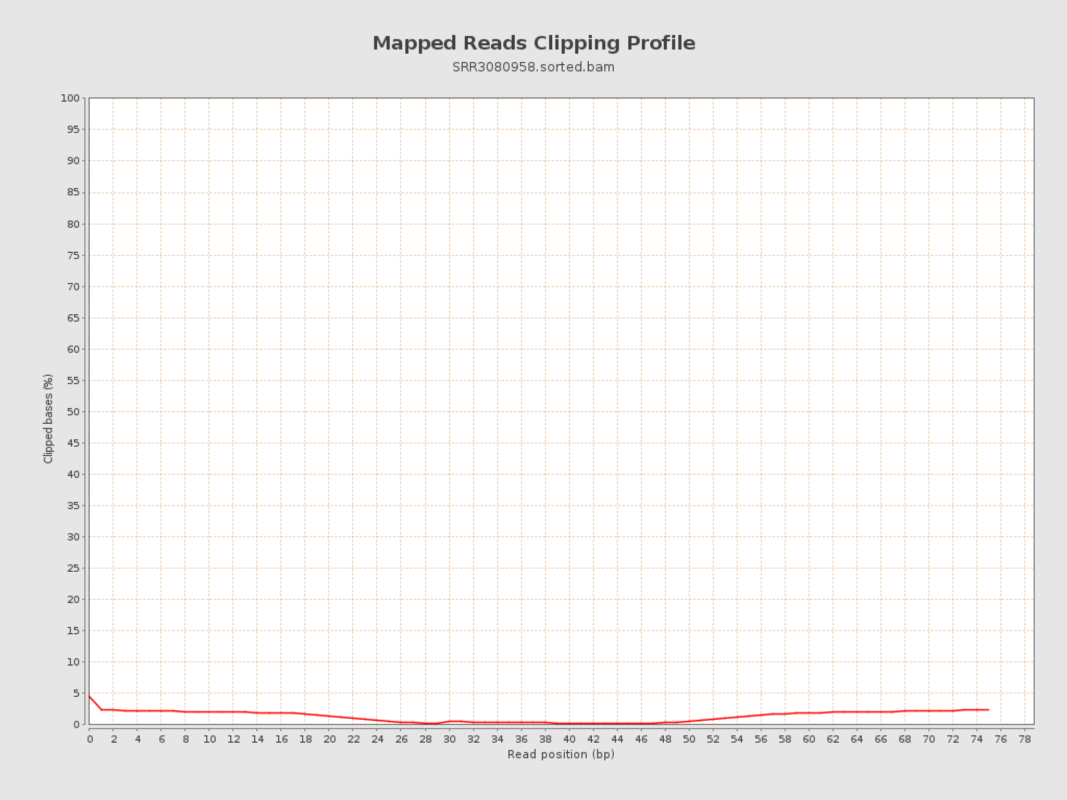
8. Results : Mapped Reads Nucleotide Content



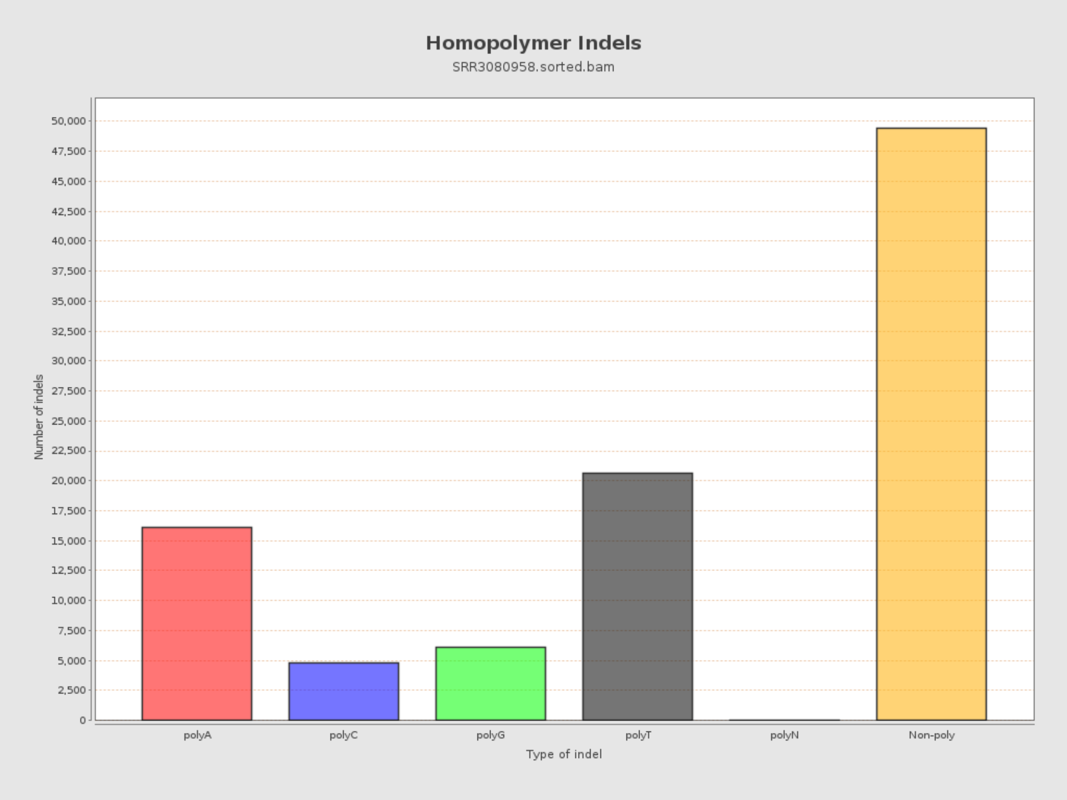
9. Results : Mapped Reads GC-content Distribution



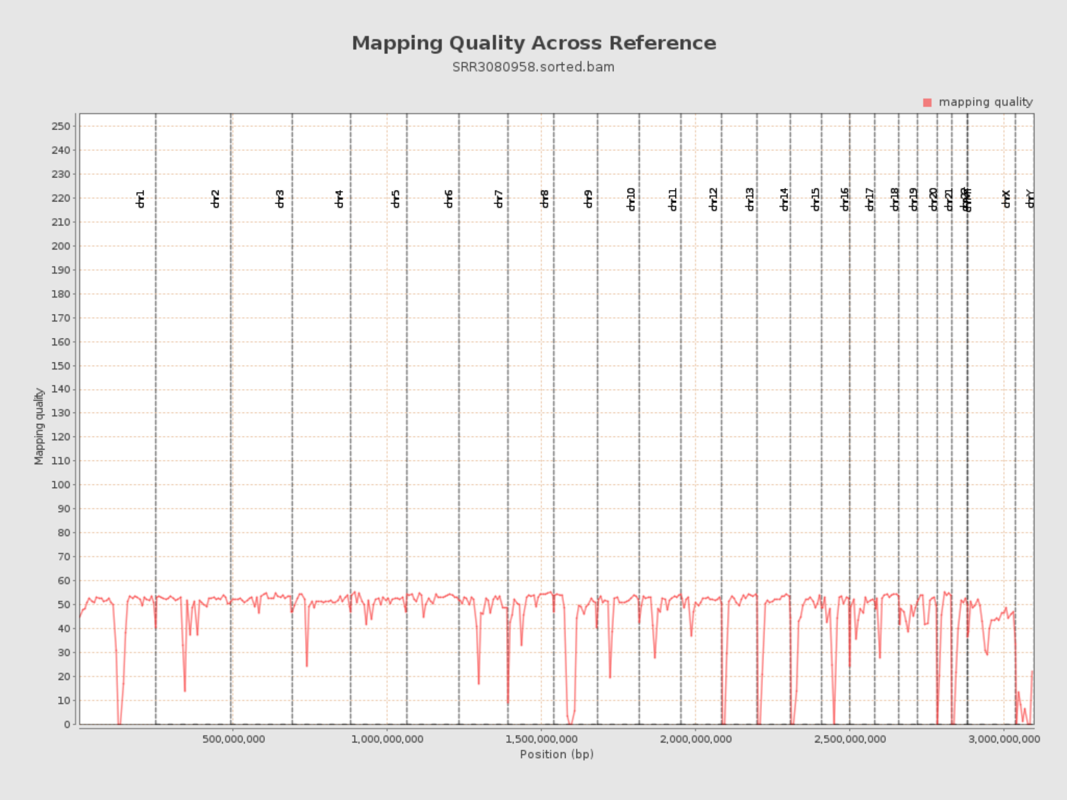
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram