Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:06:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080901.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_SRR3080901 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080901.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:06:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080901.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,072,937
Mapped reads	4,606,032 / 90.8%
Unmapped reads	466,905 / 9.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	41,350 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	247,592 / 4.88%
Duplication rate	4.27%
Clipped reads	1,737,784 / 34.26%

2.2. ACGT Content

Number/percentage of A's	90,063,996 / 28.62%
Number/percentage of C's	55,349,860 / 17.59%
Number/percentage of T's	101,285,353 / 32.19%
Number/percentage of G's	66,456,500 / 21.12%
Number/percentage of N's	1,529,896 / 0.49%
GC Percentage	38.71%

2.3. Coverage

Mean	0.1017

Standard Deviation	0.6333

2.4. Mapping Quality

Mean Mapping Quality	47.93

2.5. Mismatches and indels

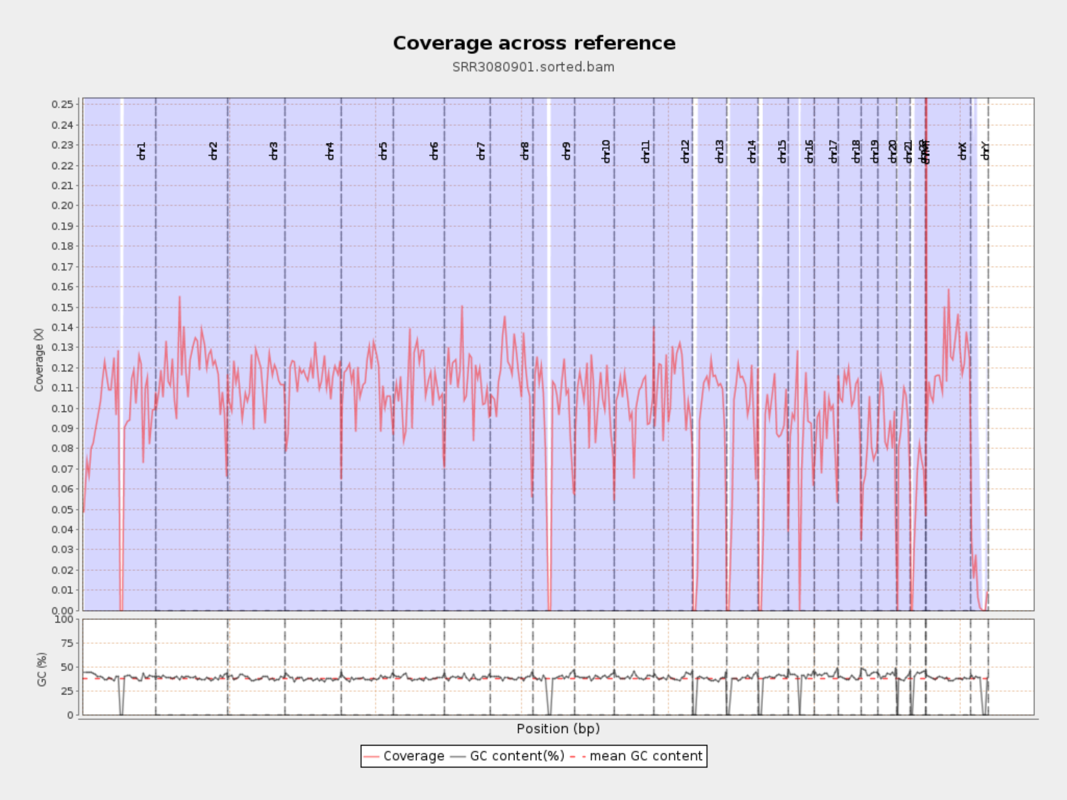
General error rate	1.16%
Mismatches	3,598,368
Insertions	24,091
Mapped reads with at least one insertion	0.52%
Deletions	69,908
Mapped reads with at least one deletion	1.5%
Homopolymer indels	50.2%

2.6. Chromosome stats

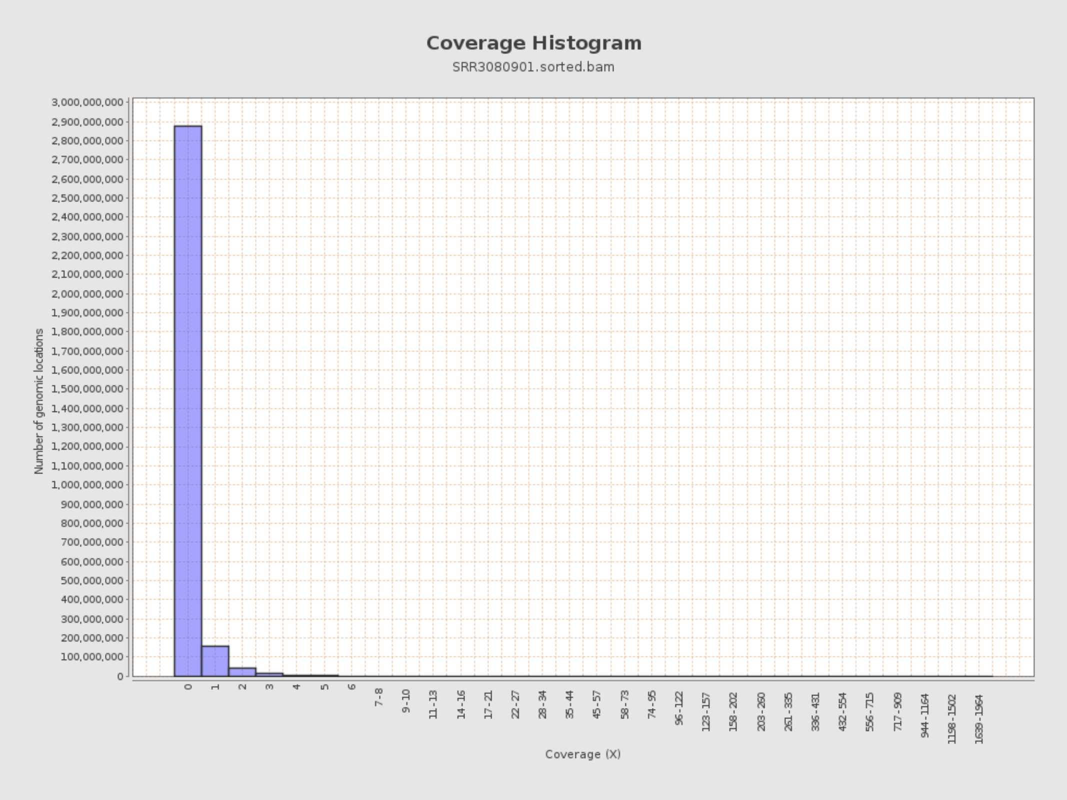
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23413881	0.0939	0.8501
chr2	243199373	28790620	0.1184	0.6385
chr3	198022430	22167802	0.1119	0.4513
chr4	191154276	22035691	0.1153	0.4746
chr5	180915260	20295319	0.1122	0.4549
chr6	171115067	19113085	0.1117	0.5674
chr7	159138663	18045098	0.1134	0.8762

chr8	146364022	17004221	0.1162	1.2606
chr9	141213431	13192163	0.0934	0.5977
chr10	135534747	14153142	0.1044	0.546
chr11	135006516	13798403	0.1022	0.5847
chr12	133851895	14710681	0.1099	0.4558
chr13	115169878	10422510	0.0905	0.4086
chr14	107349540	9446561	0.088	0.433
chr15	102531392	8195542	0.0799	0.3824
chr16	90354753	7470770	0.0827	0.4183
chr17	81195210	7300424	0.0899	0.4561
chr18	78077248	8482057	0.1086	1.0744
chr19	59128983	4549516	0.0769	0.5969
chr20	63025520	5829325	0.0925	0.4308
chr21	48129895	4015413	0.0834	0.4293
chr22	51304566	2643362	0.0515	0.3024
chrMT	16571	45914	2.7707	2.7908
chrX	155270560	19026998	0.1225	0.5081
chrY	59373566	651617	0.011	0.1794

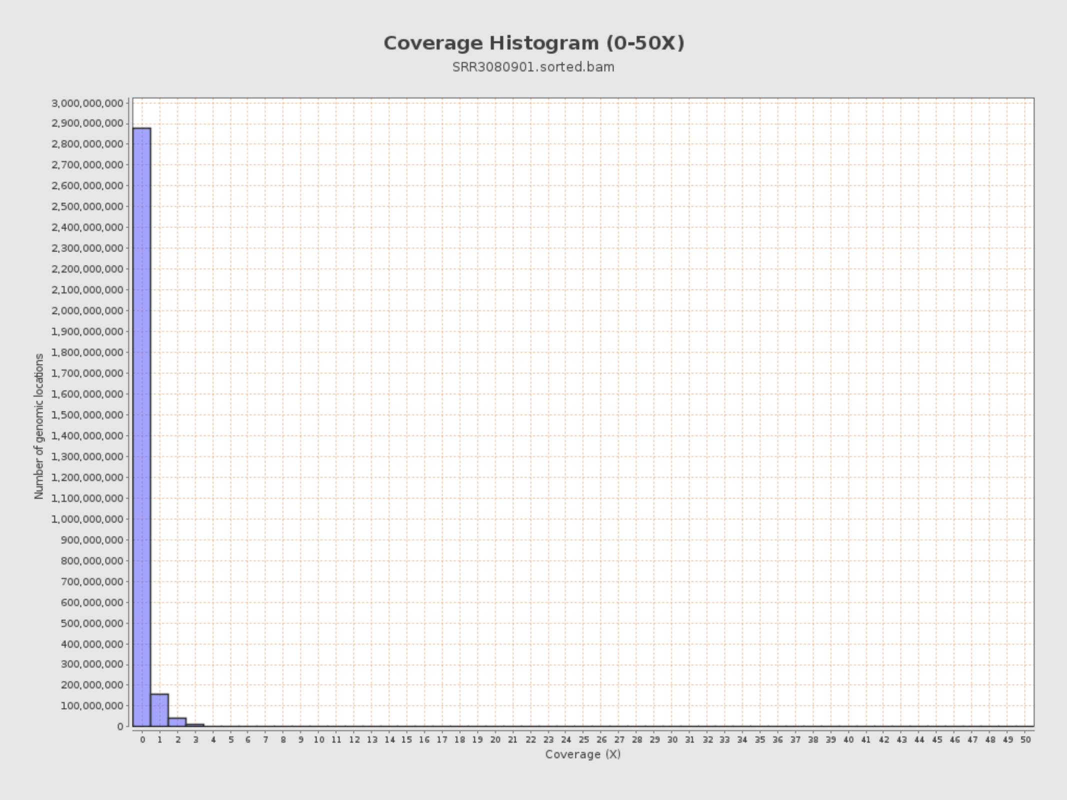
3. Results : Coverage across reference



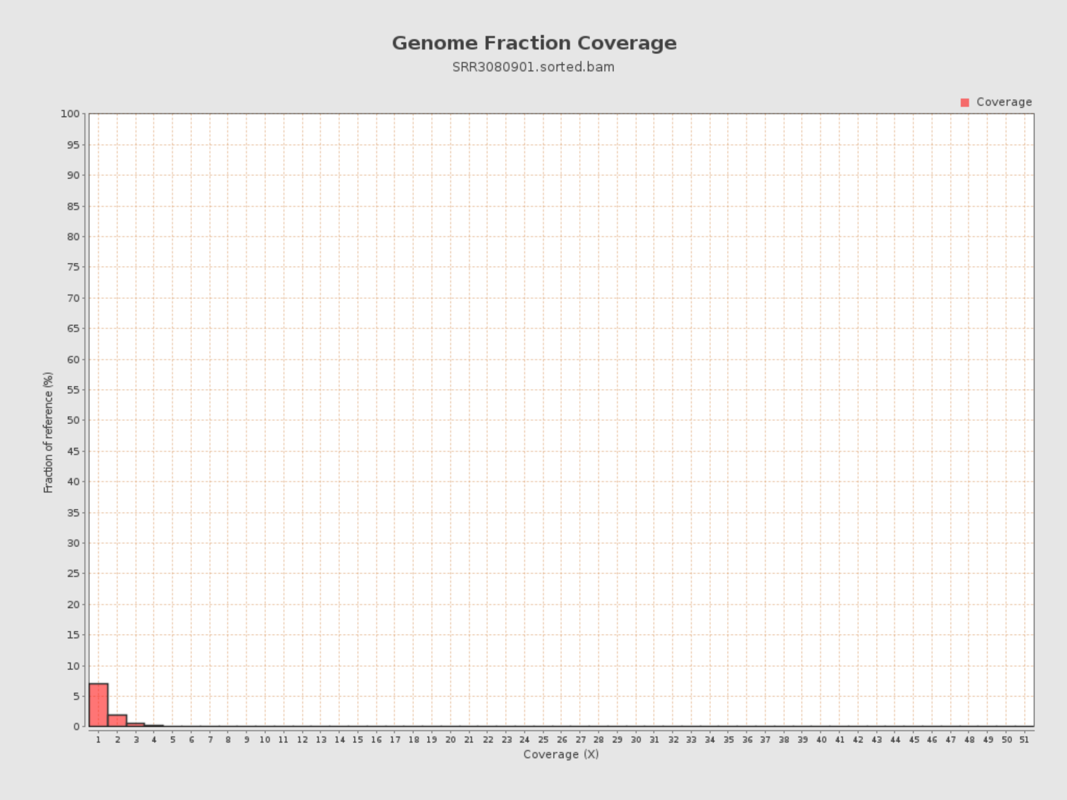
4. Results : Coverage Histogram



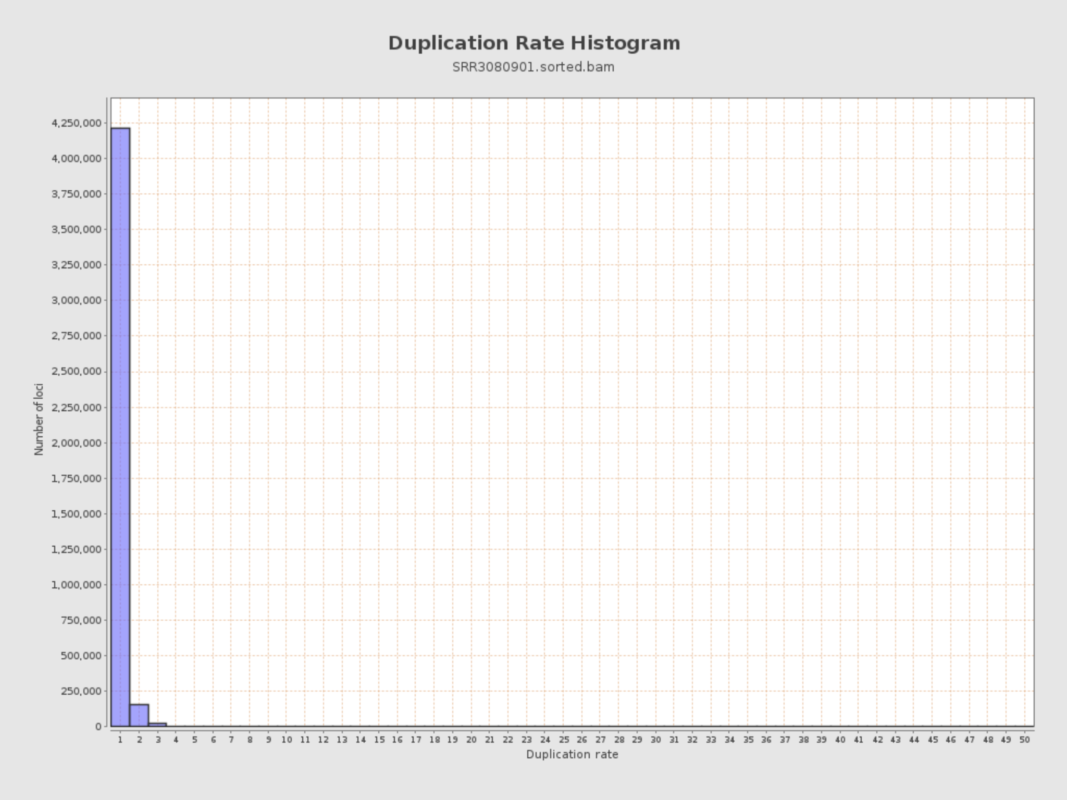
5. Results : Coverage Histogram (0-50X)



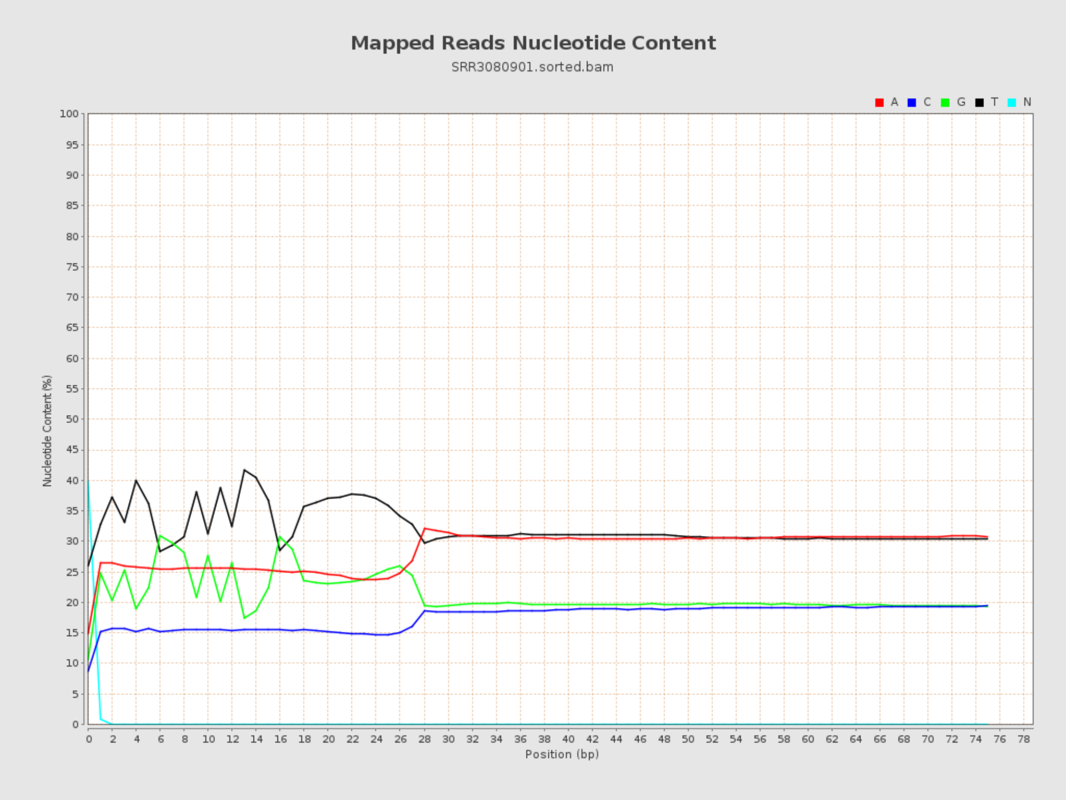
6. Results : Genome Fraction Coverage



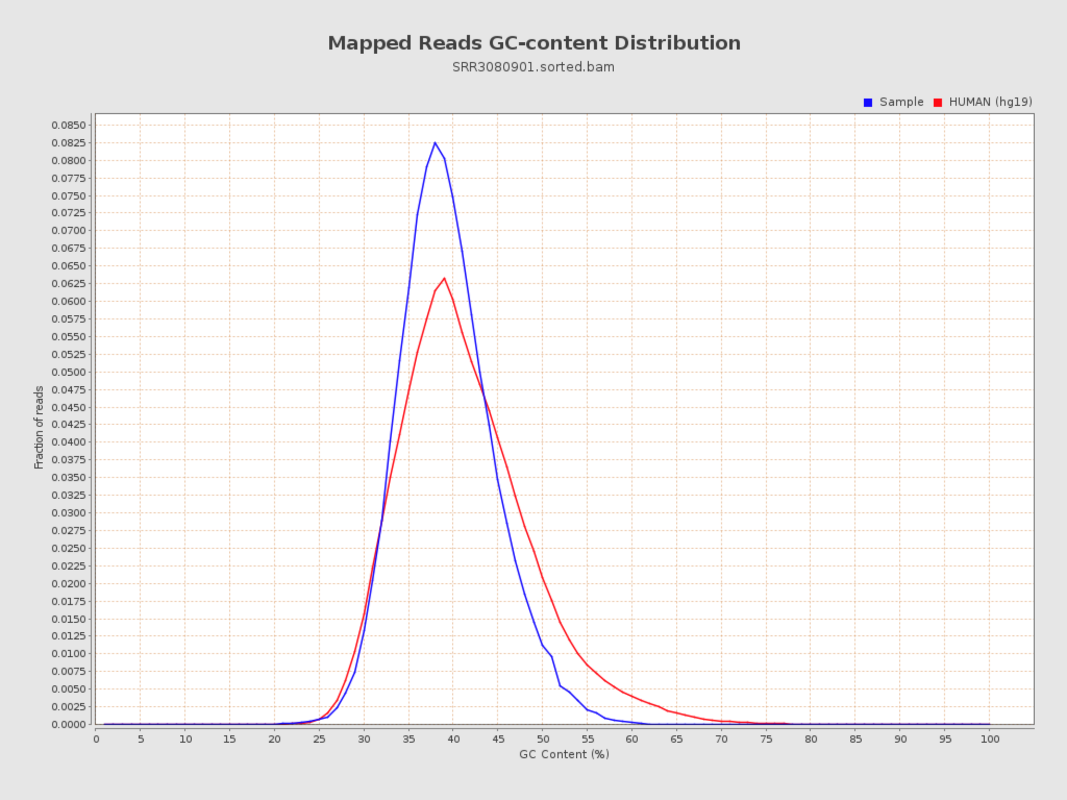
7. Results : Duplication Rate Histogram



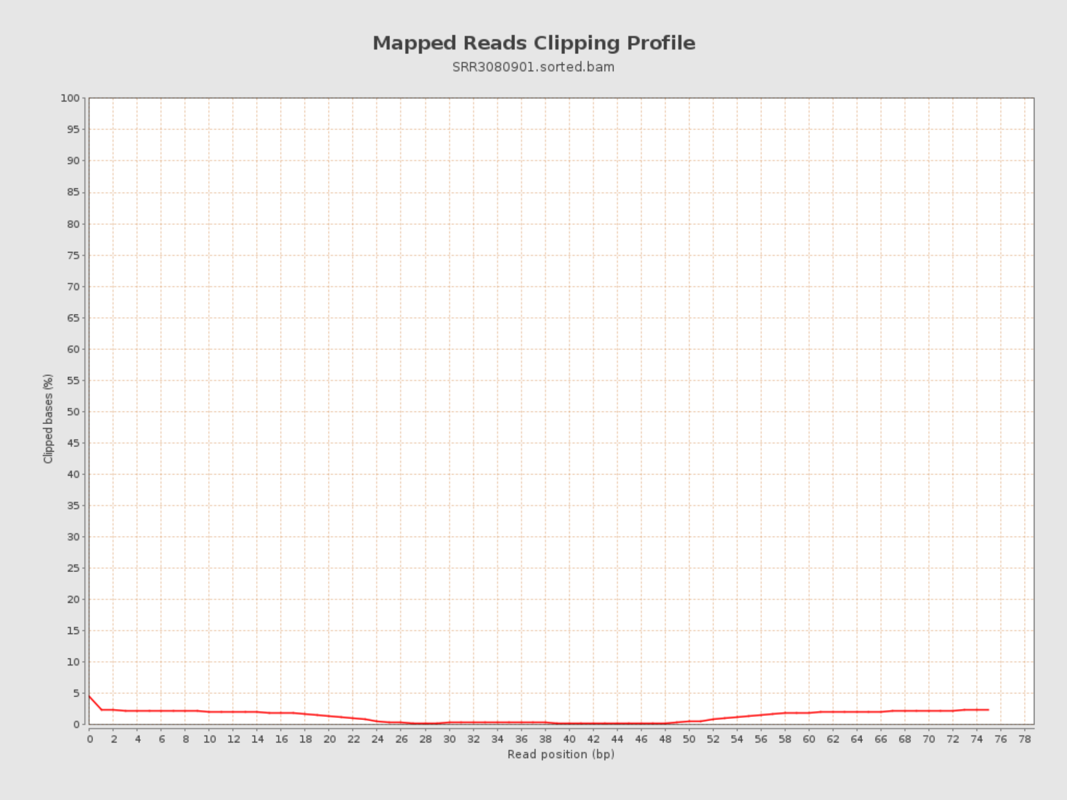
8. Results : Mapped Reads Nucleotide Content



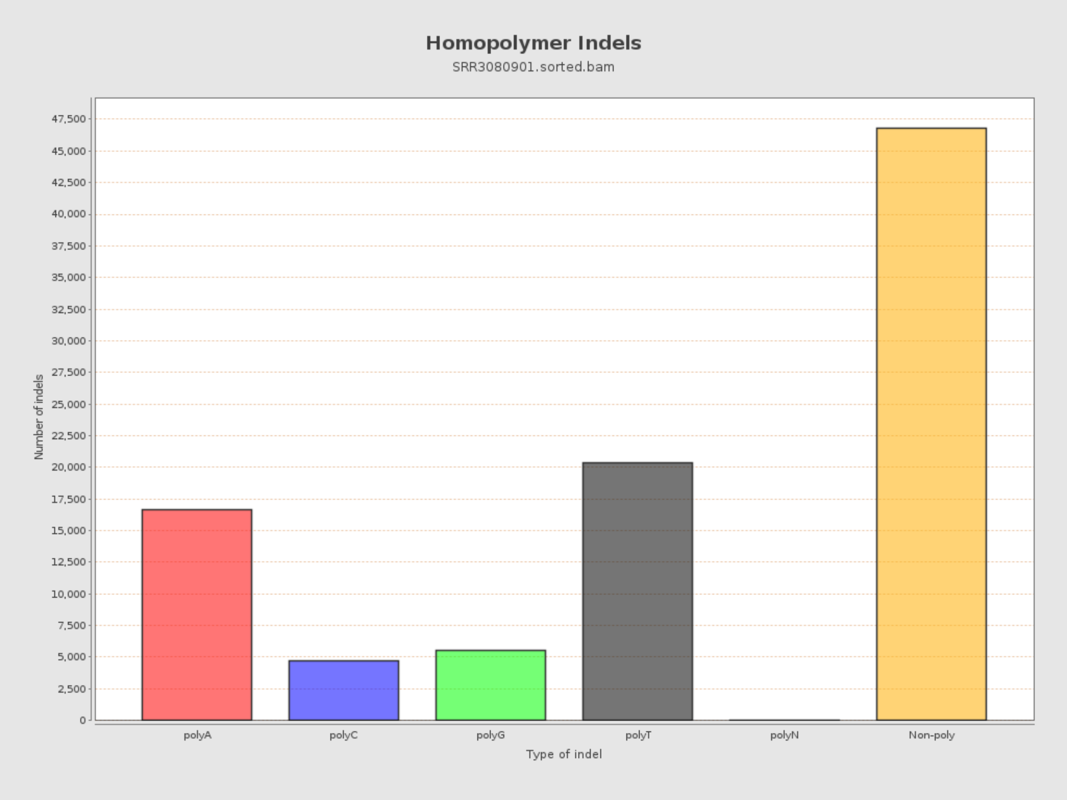
9. Results : Mapped Reads GC-content Distribution



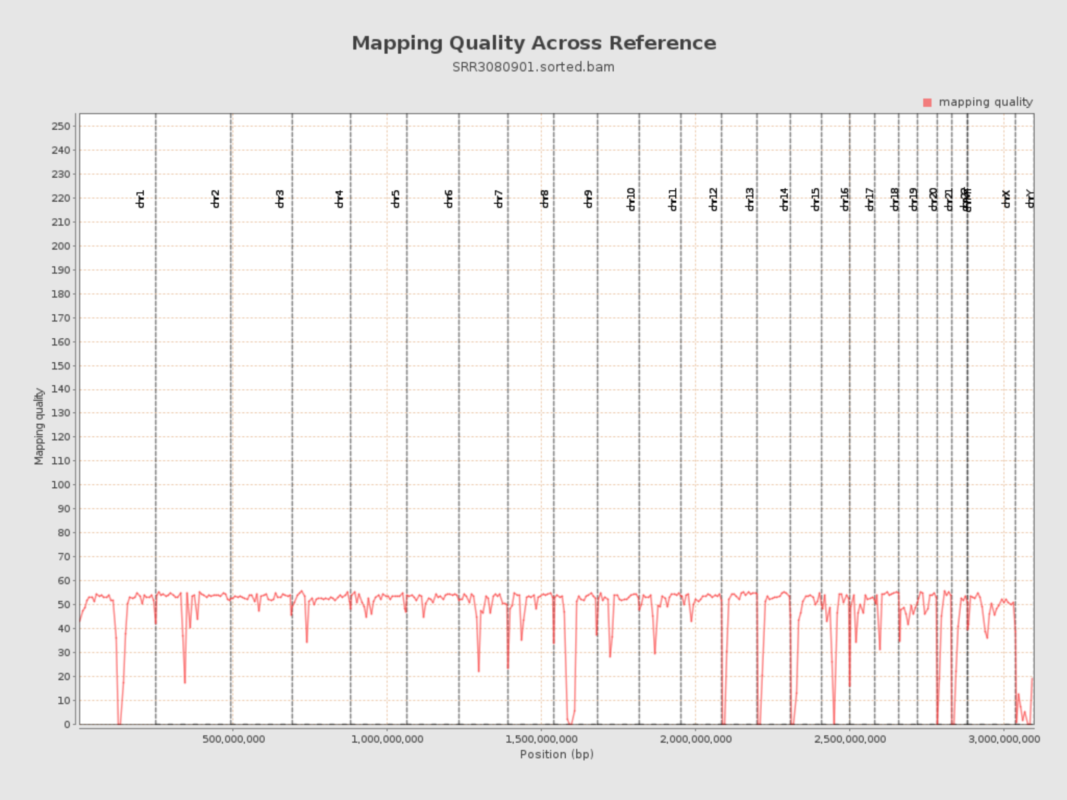
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram