Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:28:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080945.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_SRR3080945 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080945.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:28:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080945.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,677,099
Mapped reads	3,326,729 / 90.47%
Unmapped reads	350,370 / 9.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,387 / 1.1%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	141,278 / 3.84%
Duplication rate	3.5%
Clipped reads	1,127,540 / 30.66%

2.2. ACGT Content

Number/percentage of A's	67,277,379 / 29.2%
Number/percentage of C's	40,916,111 / 17.76%
Number/percentage of T's	73,821,614 / 32.05%
Number/percentage of G's	47,217,382 / 20.5%
Number/percentage of N's	1,136,061 / 0.49%
GC Percentage	38.26%

2.3. Coverage

Mean	0.0744

Standard Deviation	0.4637

2.4. Mapping Quality

Mean Mapping Quality	48.08

2.5. Mismatches and indels

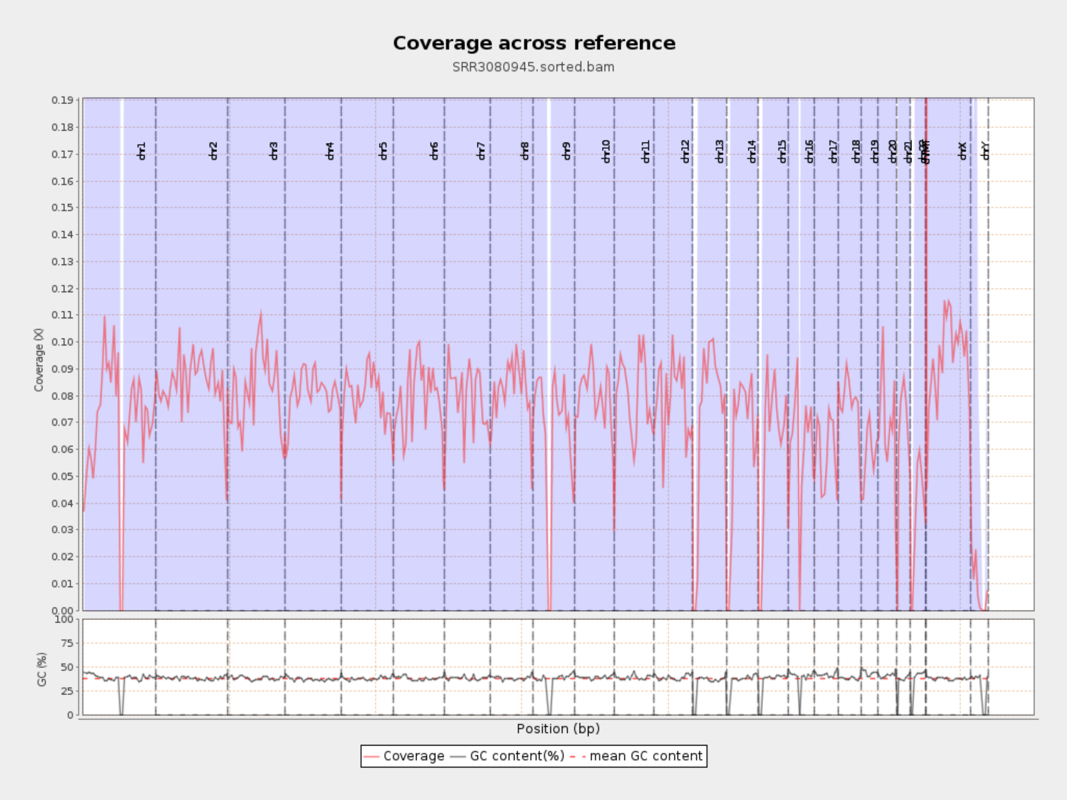
General error rate	1.18%
Mismatches	2,684,426
Insertions	17,604
Mapped reads with at least one insertion	0.53%
Deletions	51,227
Mapped reads with at least one deletion	1.52%
Homopolymer indels	50.01%

2.6. Chromosome stats

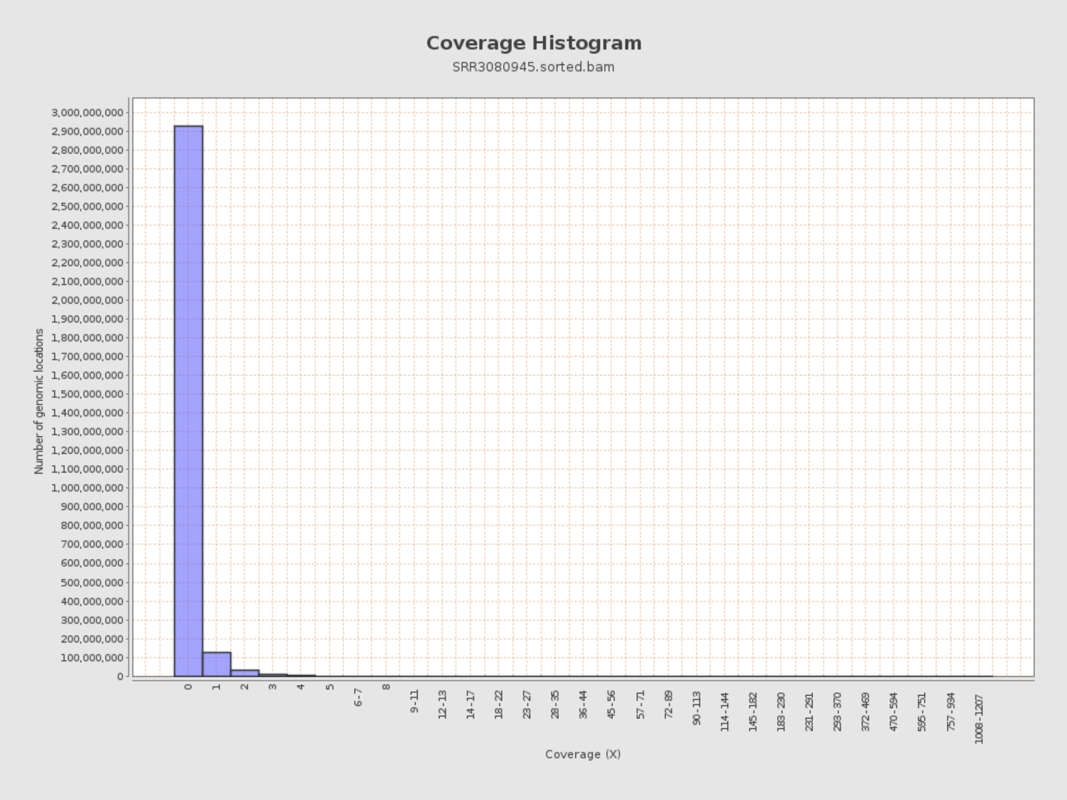
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17532749	0.0703	0.6877
chr2	243199373	20650374	0.0849	0.4595
chr3	198022430	16410943	0.0829	0.3754
chr4	191154276	15521814	0.0812	0.3785
chr5	180915260	14356145	0.0794	0.3693
chr6	171115067	13670945	0.0799	0.4051
chr7	159138663	12554607	0.0789	0.524

chr8	146364022	12058018	0.0824	0.8176
chr9	141213431	9433775	0.0668	0.4202
chr10	135534747	10945896	0.0808	0.4306
chr11	135006516	10805392	0.08	0.4404
chr12	133851895	10604514	0.0792	0.3687
chr13	115169878	8327658	0.0723	0.3509
chr14	107349540	6796399	0.0633	0.3422
chr15	102531392	6354056	0.062	0.3231
chr16	90354753	5379209	0.0595	0.3307
chr17	81195210	4865153	0.0599	0.3384
chr18	78077248	6133298	0.0786	0.6803
chr19	59128983	3457520	0.0585	0.4865
chr20	63025520	4582586	0.0727	0.3565
chr21	48129895	3110214	0.0646	0.3456
chr22	51304566	1833141	0.0357	0.2428
chrMT	16571	39619	2.3909	2.1508
chrX	155270560	14532449	0.0936	0.4153
chrY	59373566	497084	0.0084	0.1429

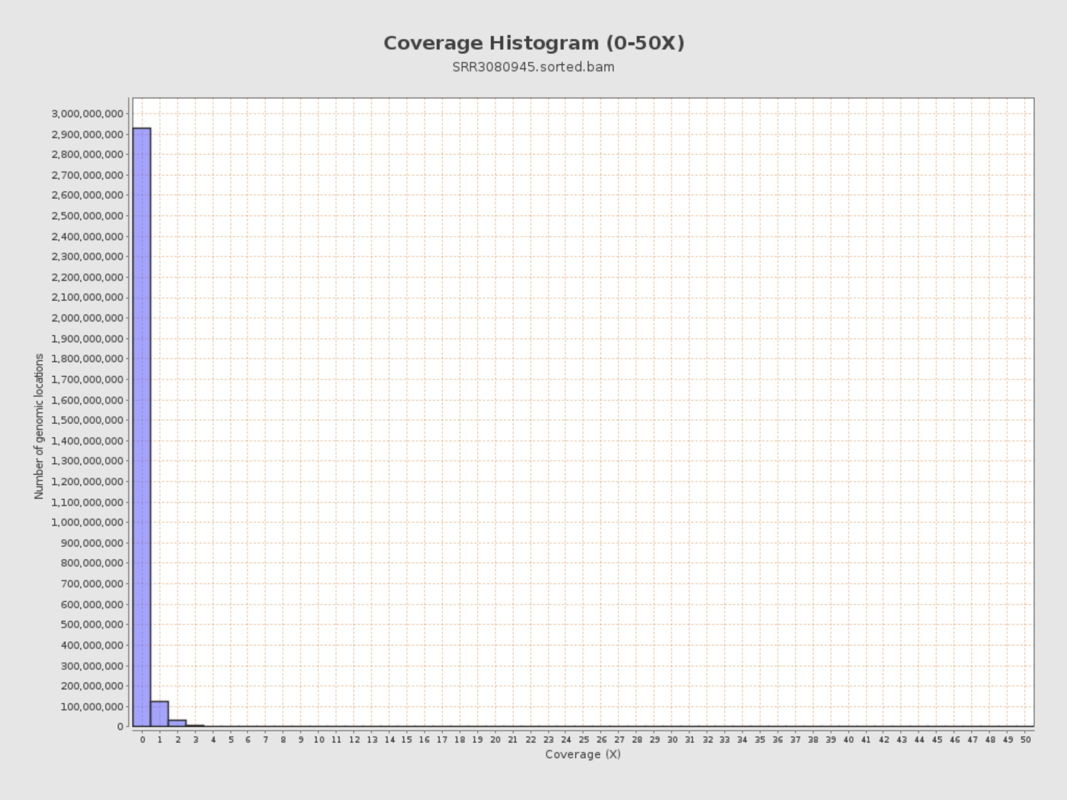
3. Results : Coverage across reference



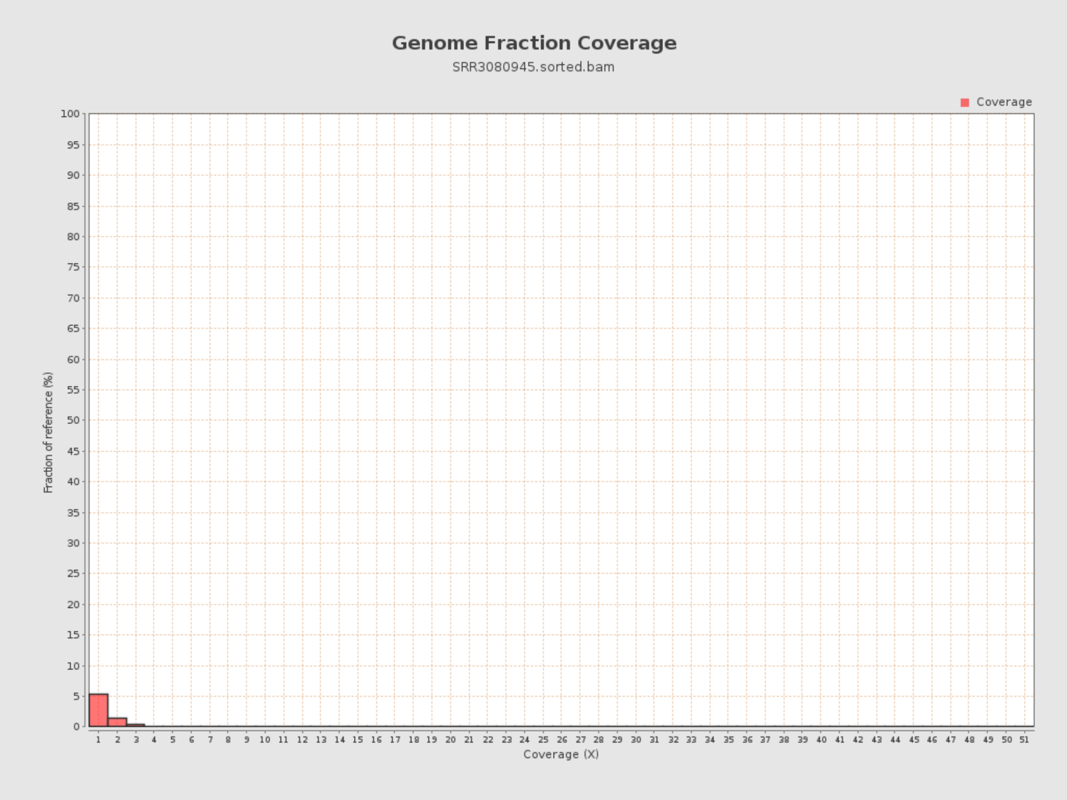
4. Results : Coverage Histogram



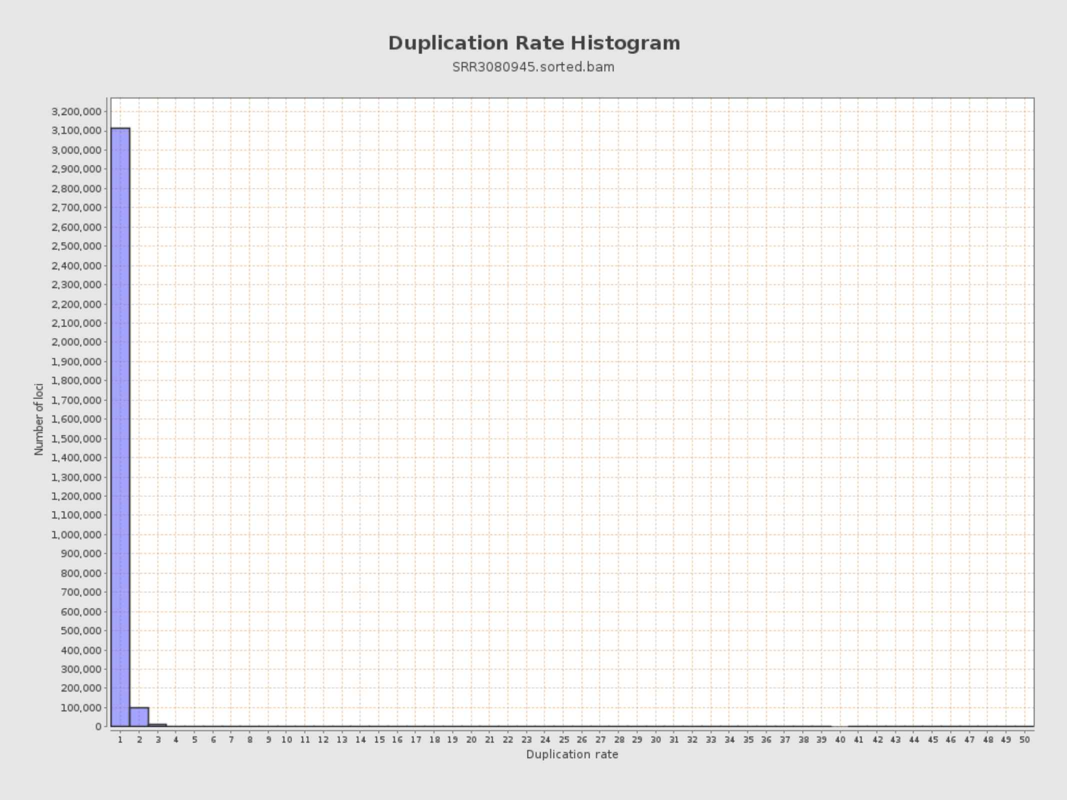
5. Results : Coverage Histogram (0-50X)



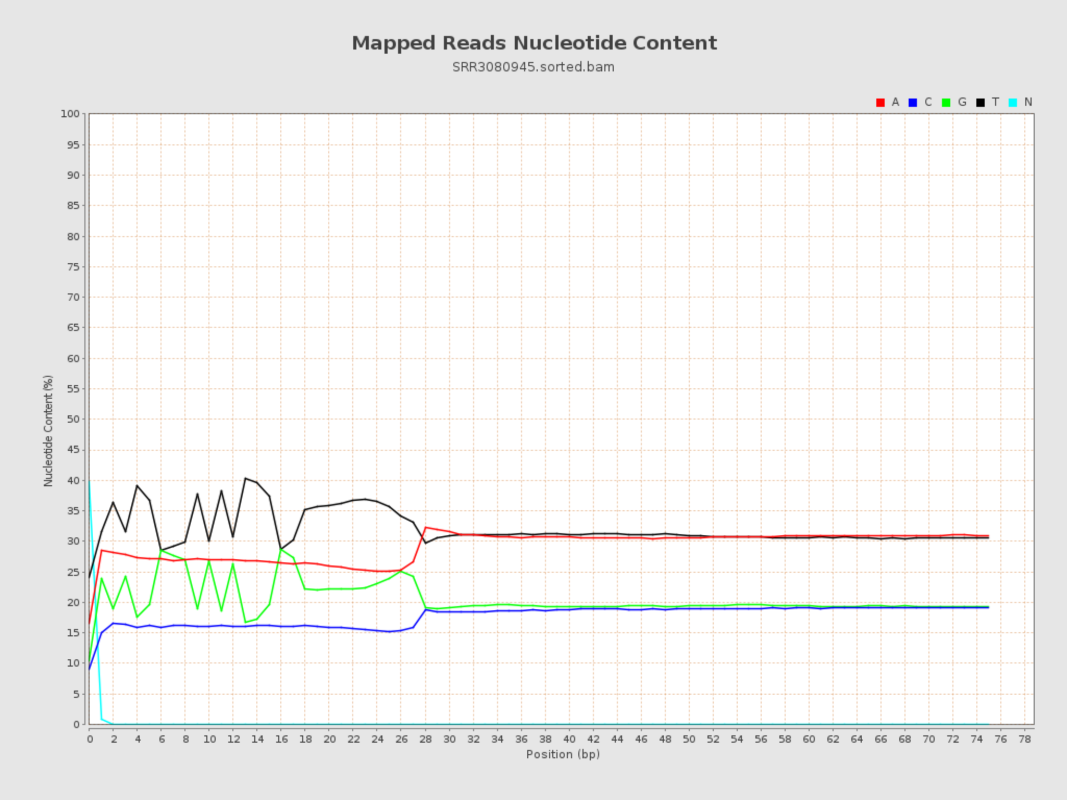
6. Results : Genome Fraction Coverage



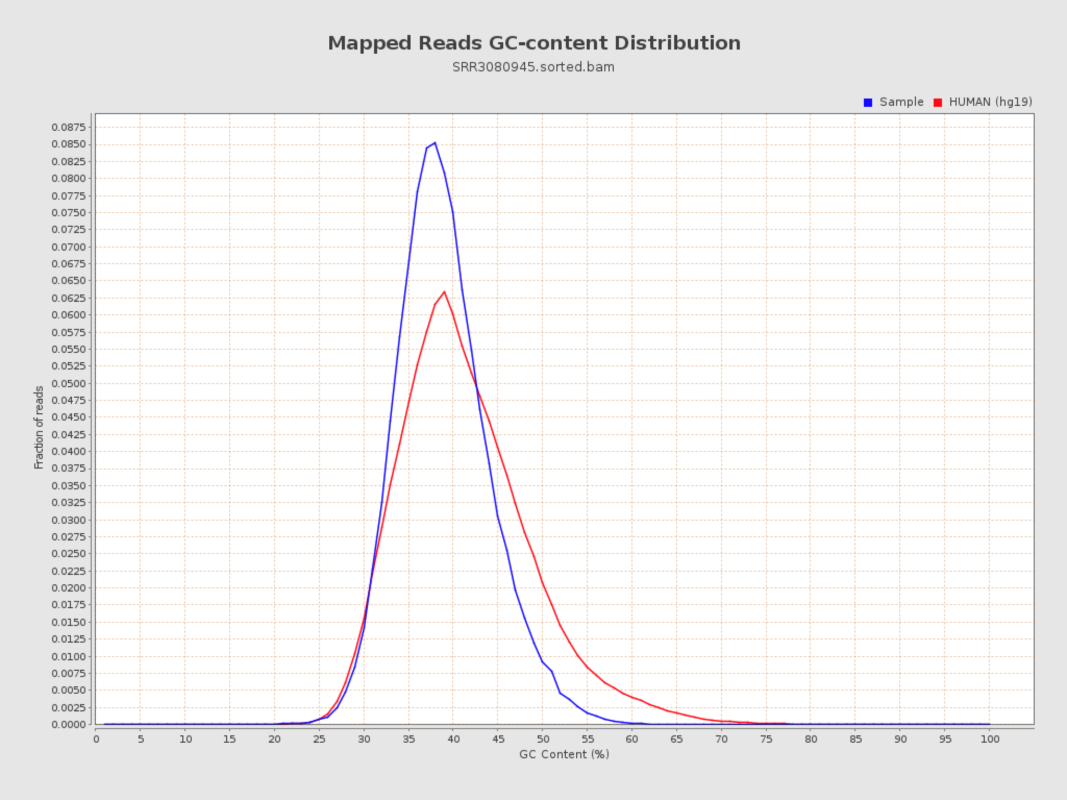
7. Results : Duplication Rate Histogram



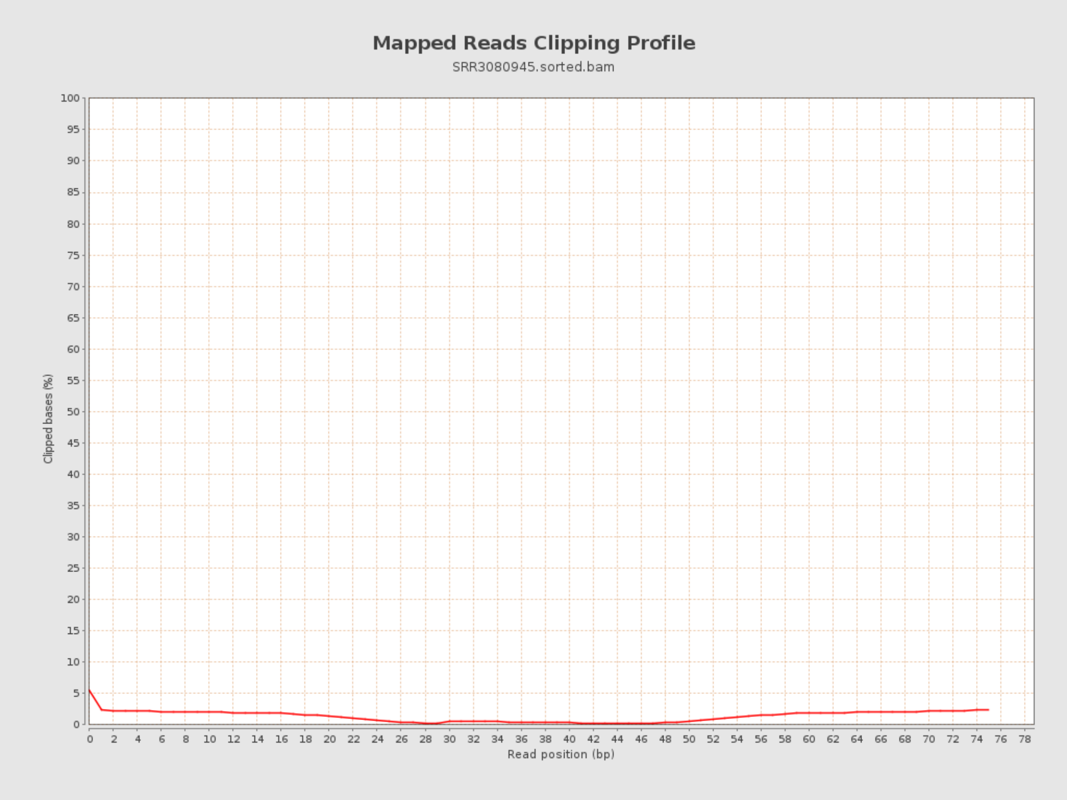
8. Results : Mapped Reads Nucleotide Content



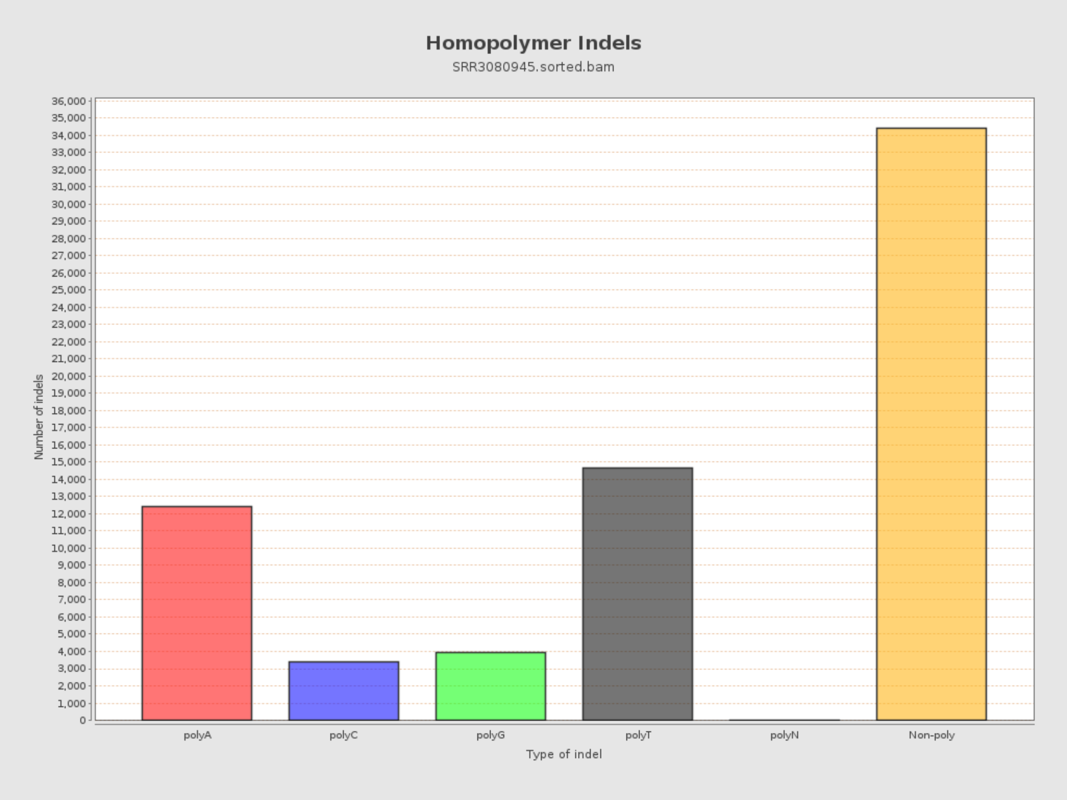
9. Results : Mapped Reads GC-content Distribution



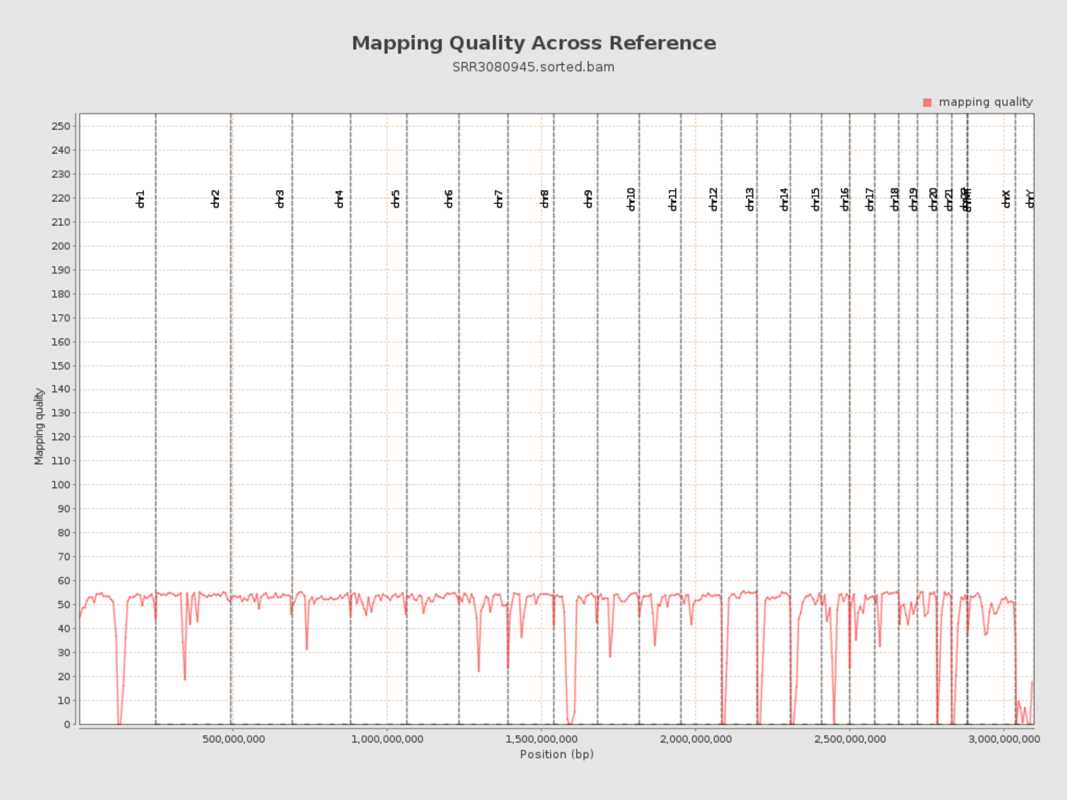
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram