Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:05:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080720.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_SRR3080720 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080720.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:05:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080720.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,364,986
Mapped reads	2,120,525 / 89.66%
Unmapped reads	244,461 / 10.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,276 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	121,388 / 5.13%
Duplication rate	4.86%
Clipped reads	899,681 / 38.04%

2.2. ACGT Content

Number/percentage of A's	39,434,854 / 27.72%
Number/percentage of C's	26,158,488 / 18.38%
Number/percentage of T's	45,477,519 / 31.96%
Number/percentage of G's	31,211,203 / 21.94%
Number/percentage of N's	2,044 / 0%
GC Percentage	40.32%

2.3. Coverage

Mean	0.046

Standard Deviation	0.3801

2.4. Mapping Quality

Mean Mapping Quality	46.07

2.5. Mismatches and indels

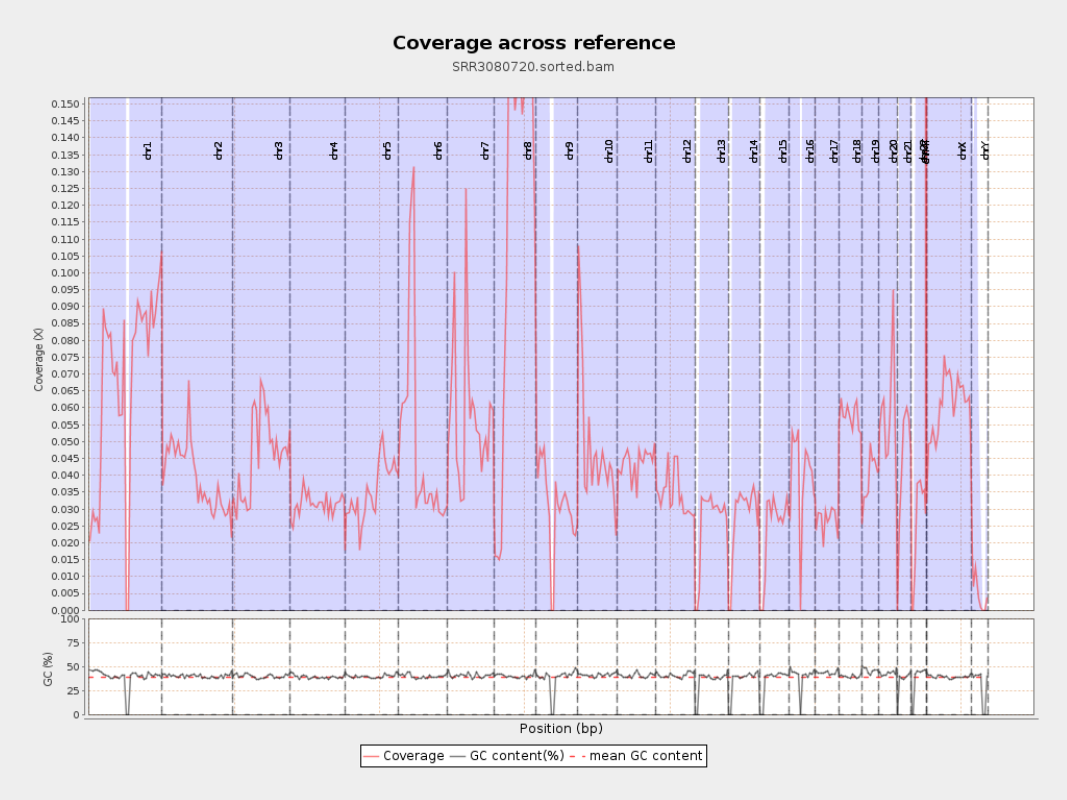
General error rate	0.84%
Mismatches	1,171,931
Insertions	10,170
Mapped reads with at least one insertion	0.48%
Deletions	29,300
Mapped reads with at least one deletion	1.37%
Homopolymer indels	48.36%

2.6. Chromosome stats

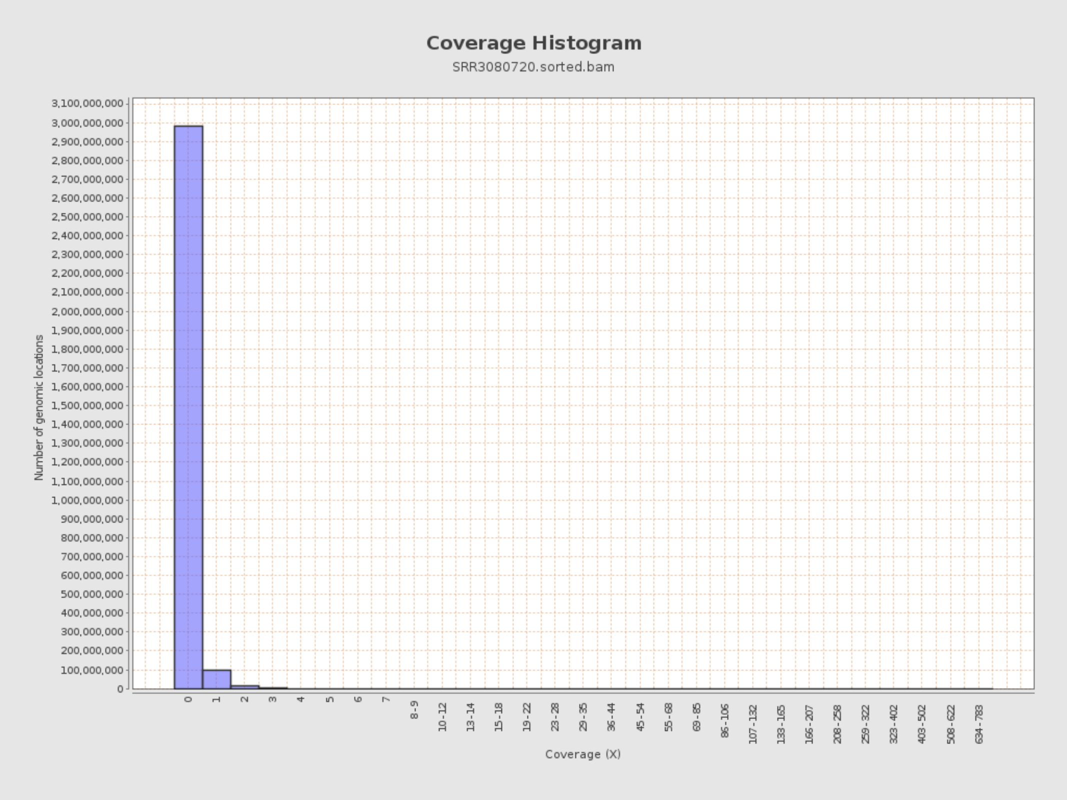
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16632877	0.0667	0.4945
chr2	243199373	9602844	0.0395	0.3921
chr3	198022430	9167572	0.0463	0.2503
chr4	191154276	6003918	0.0314	0.2111
chr5	180915260	6451343	0.0357	0.219
chr6	171115067	8560729	0.05	0.3749
chr7	159138663	9313584	0.0585	0.9544

chr8	146364022	17397737	0.1189	0.524
chr9	141213431	4307172	0.0305	0.2754
chr10	135534747	6665448	0.0492	0.3291
chr11	135006516	5891088	0.0436	0.2807
chr12	133851895	4578666	0.0342	0.2182
chr13	115169878	2979717	0.0259	0.1885
chr14	107349540	2934309	0.0273	0.2034
chr15	102531392	2467081	0.0241	0.1823
chr16	90354753	3640076	0.0403	0.251
chr17	81195210	2149802	0.0265	0.1986
chr18	78077248	4507233	0.0577	0.4182
chr19	59128983	2340809	0.0396	0.3438
chr20	63025520	3661276	0.0581	0.2874
chr21	48129895	2088471	0.0434	0.2518
chr22	51304566	1296303	0.0253	0.1833
chrMT	16571	29663	1.7901	1.77
chrX	155270560	9366851	0.0603	0.302
chrY	59373566	300790	0.0051	0.1014

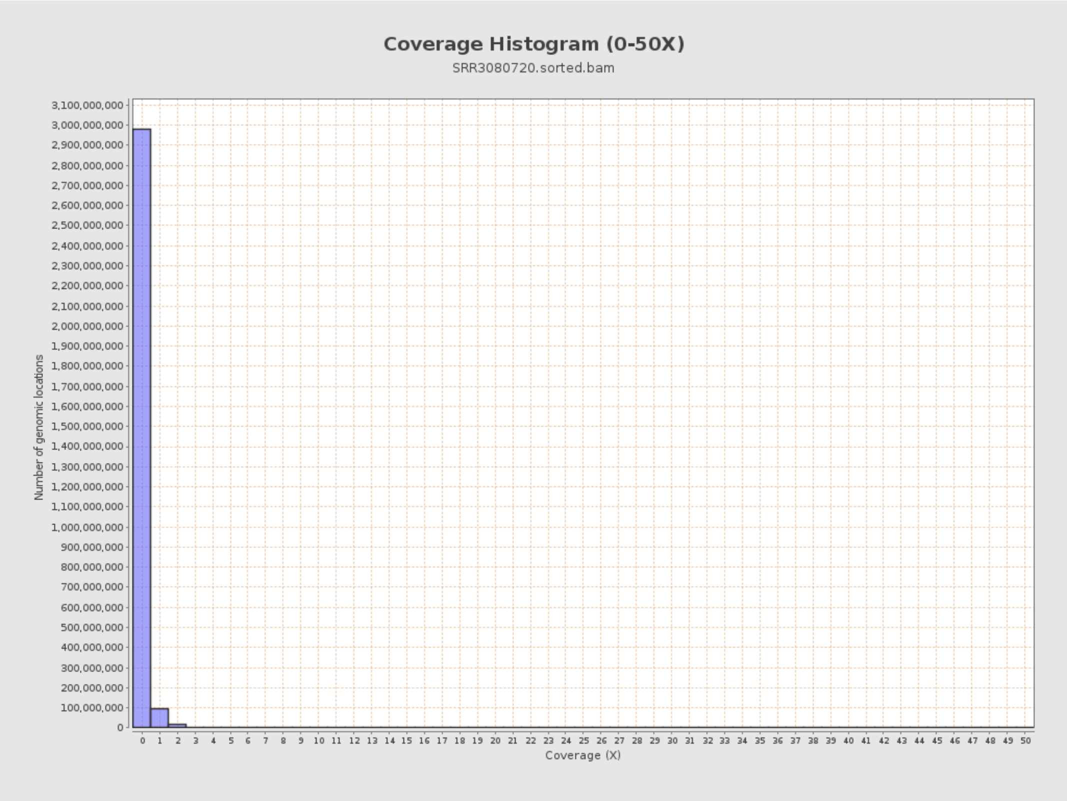
3. Results : Coverage across reference



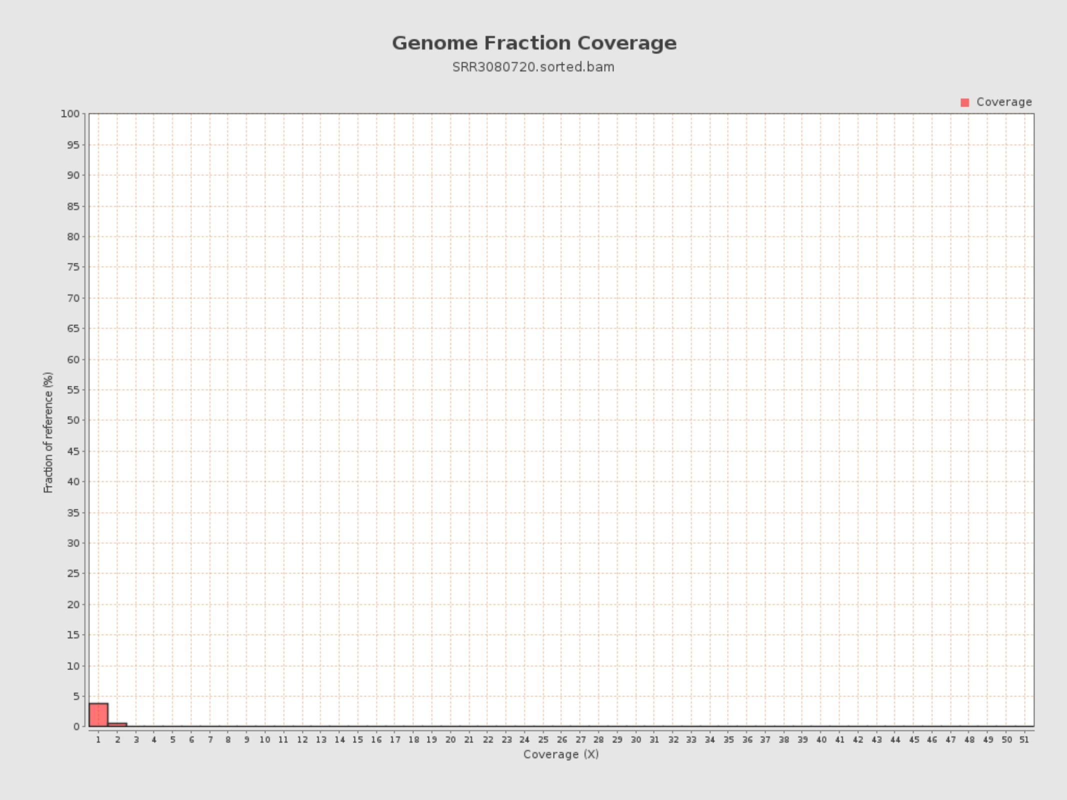
4. Results : Coverage Histogram



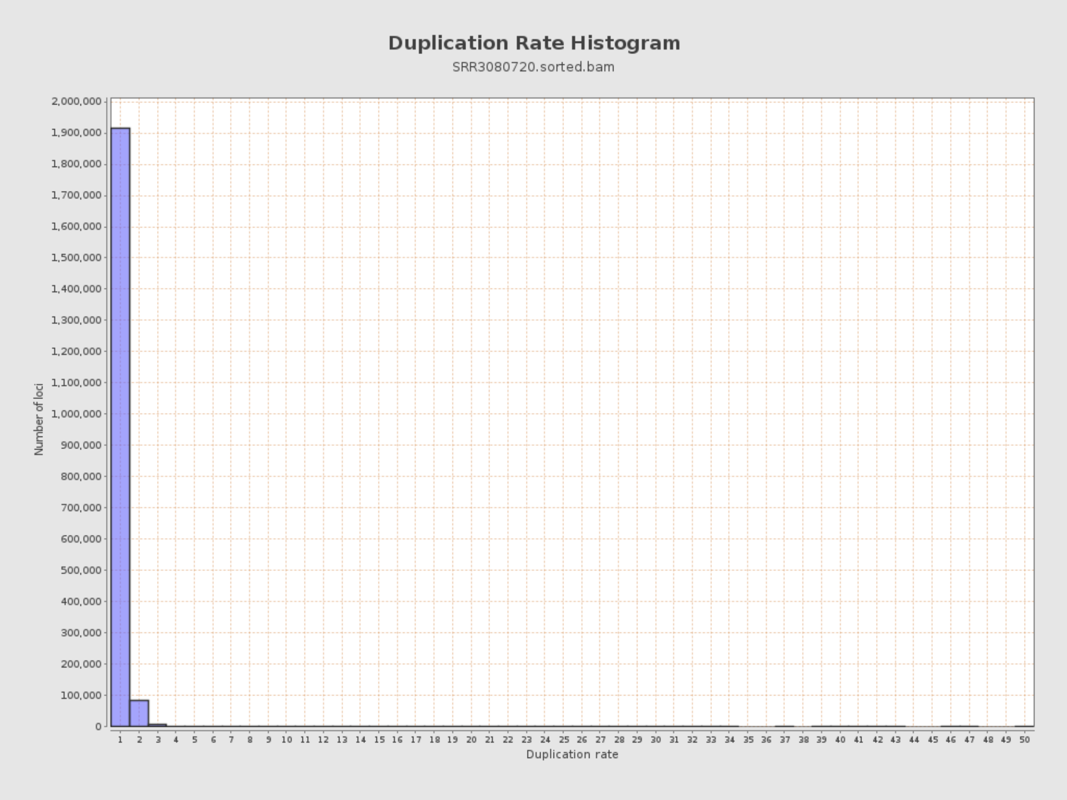
5. Results : Coverage Histogram (0-50X)



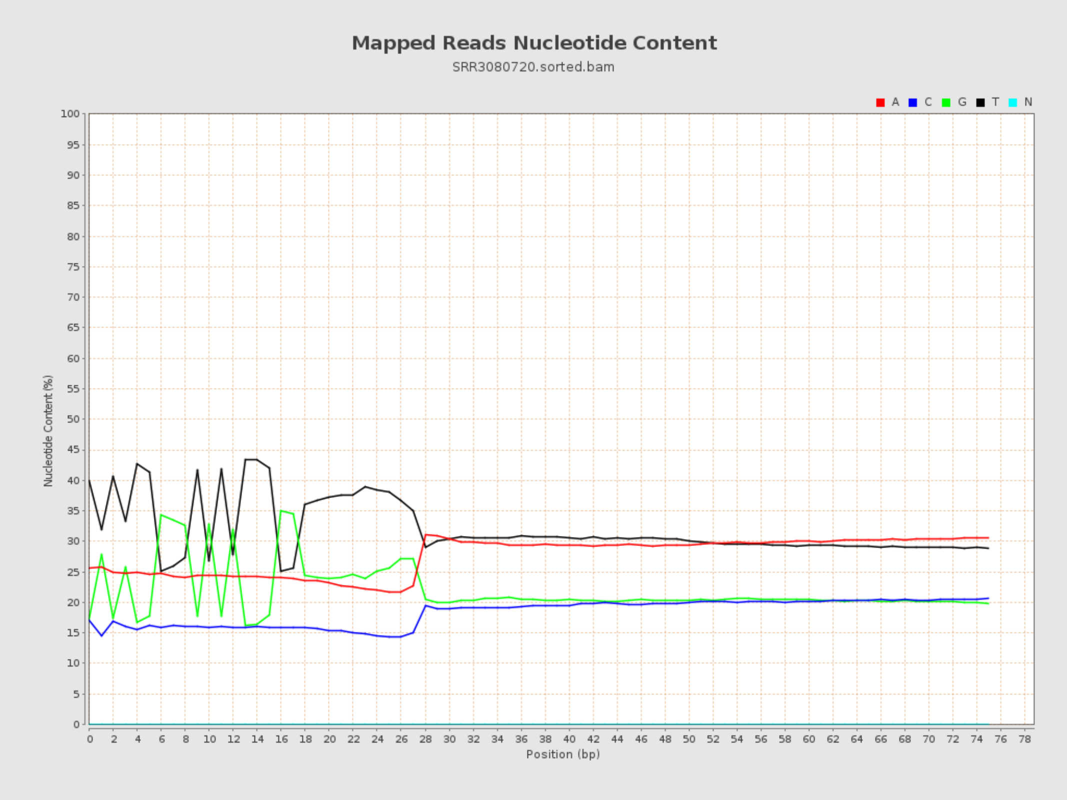
6. Results : Genome Fraction Coverage



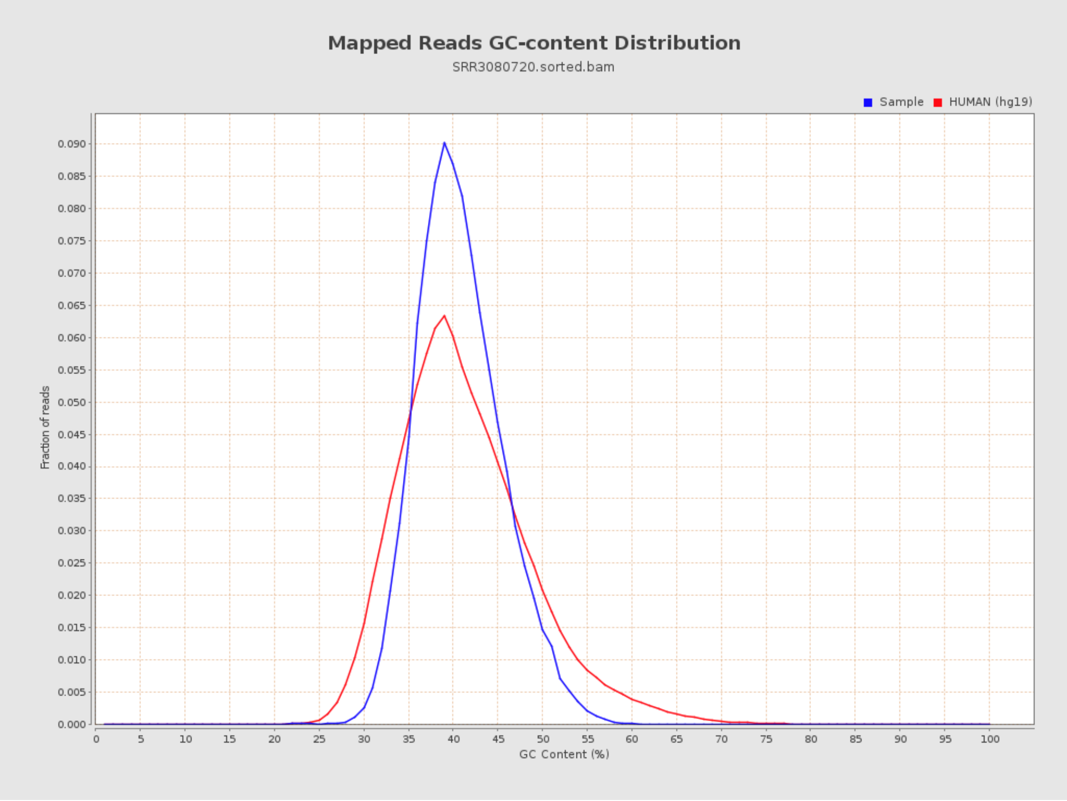
7. Results : Duplication Rate Histogram



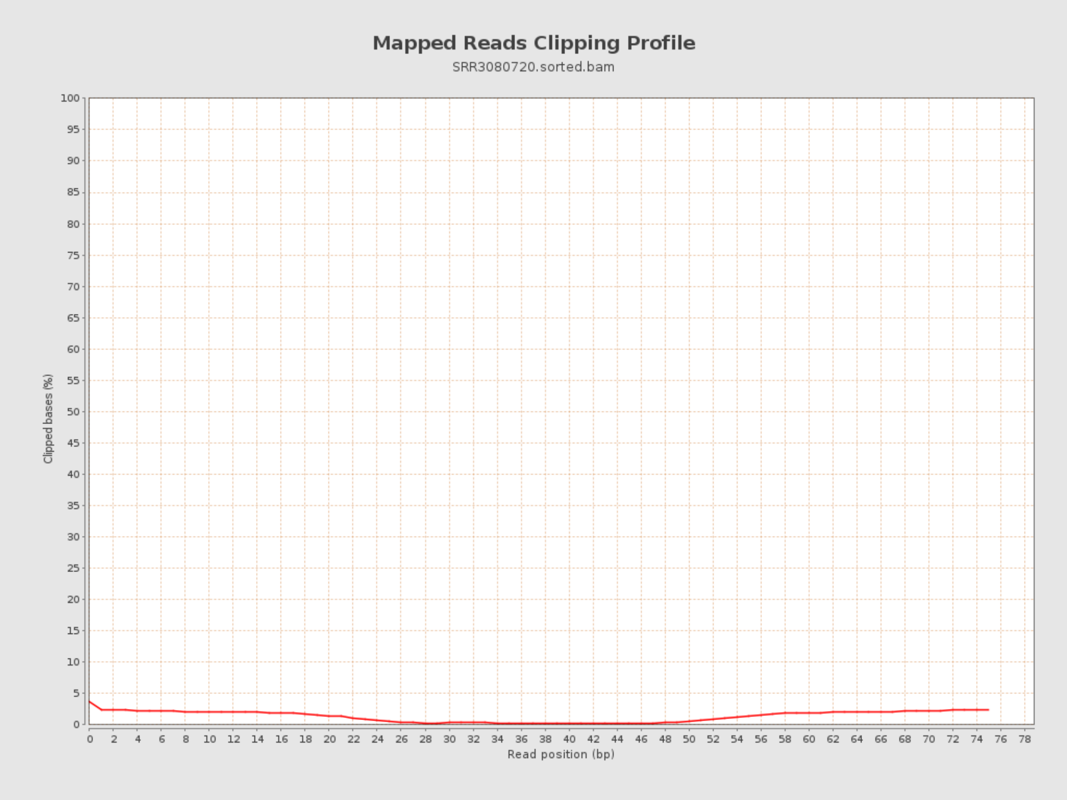
8. Results : Mapped Reads Nucleotide Content



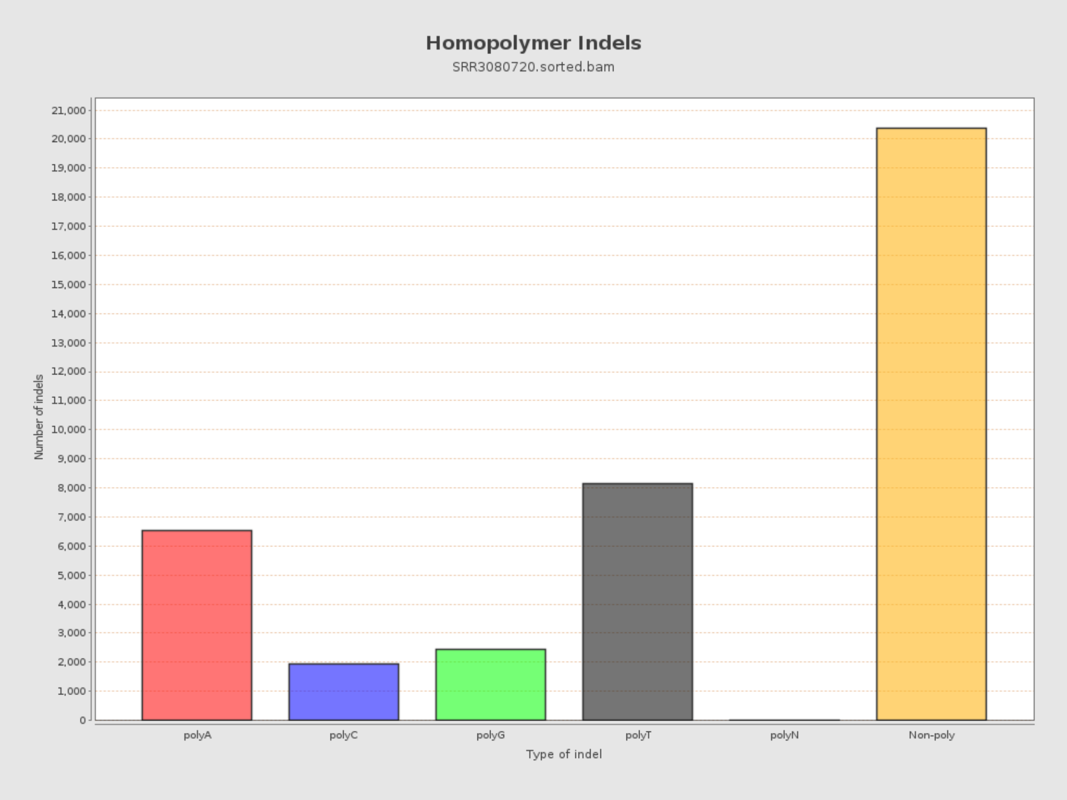
9. Results : Mapped Reads GC-content Distribution



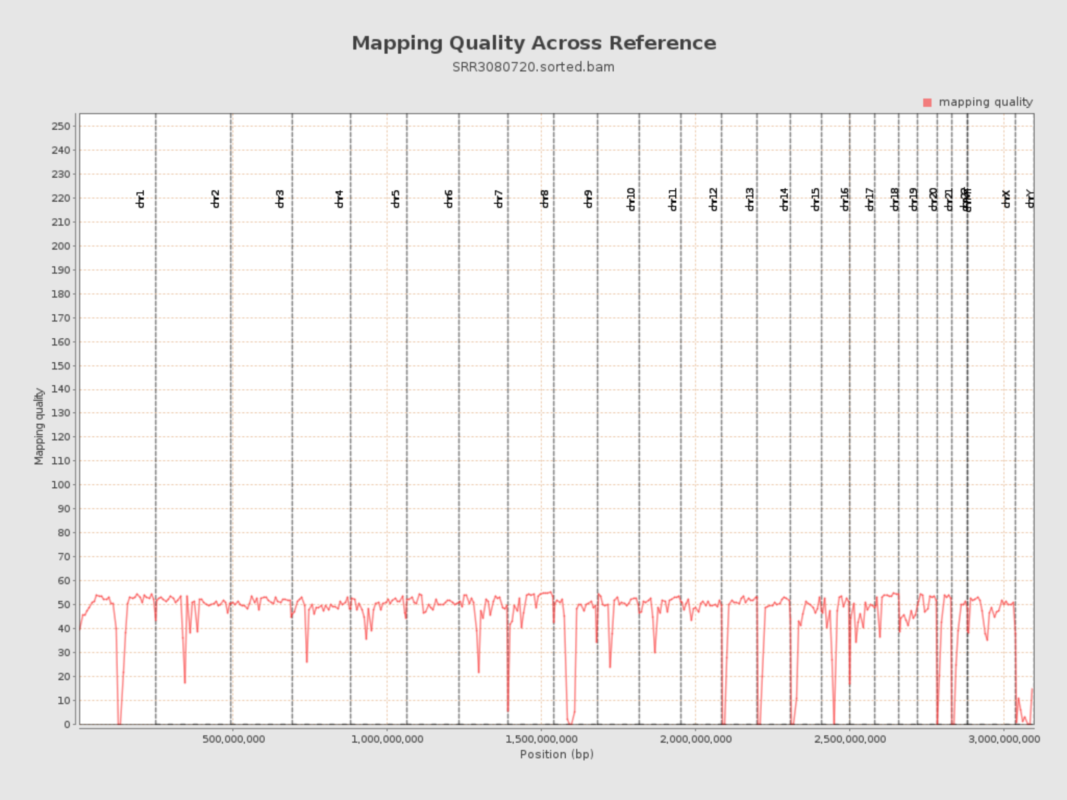
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram