Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 17:36:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080691.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_SRR3080691 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080691.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 17:36:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080691.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,605,805
Mapped reads	2,311,597 / 88.71%
Unmapped reads	294,208 / 11.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,611 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	148,769 / 5.71%
Duplication rate	5.3%
Clipped reads	794,431 / 30.49%

2.2. ACGT Content

Number/percentage of A's	47,241,905 / 29.48%
Number/percentage of C's	29,344,306 / 18.31%
Number/percentage of T's	50,851,771 / 31.73%
Number/percentage of G's	32,809,544 / 20.47%
Number/percentage of N's	2,314 / 0%
GC Percentage	38.79%

2.3. Coverage

Mean	0.0518

Standard Deviation	0.4846

2.4. Mapping Quality

Mean Mapping Quality	47.62

2.5. Mismatches and indels

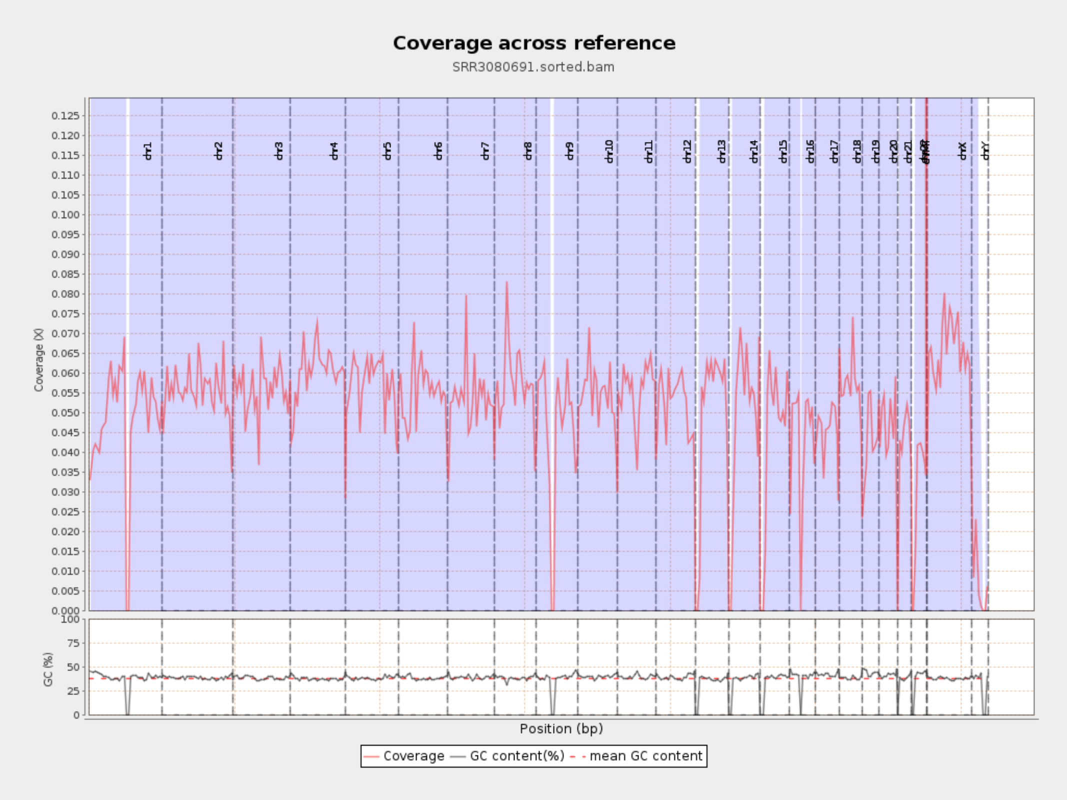
General error rate	0.82%
Mismatches	1,295,680
Insertions	12,392
Mapped reads with at least one insertion	0.53%
Deletions	34,128
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.18%

2.6. Chromosome stats

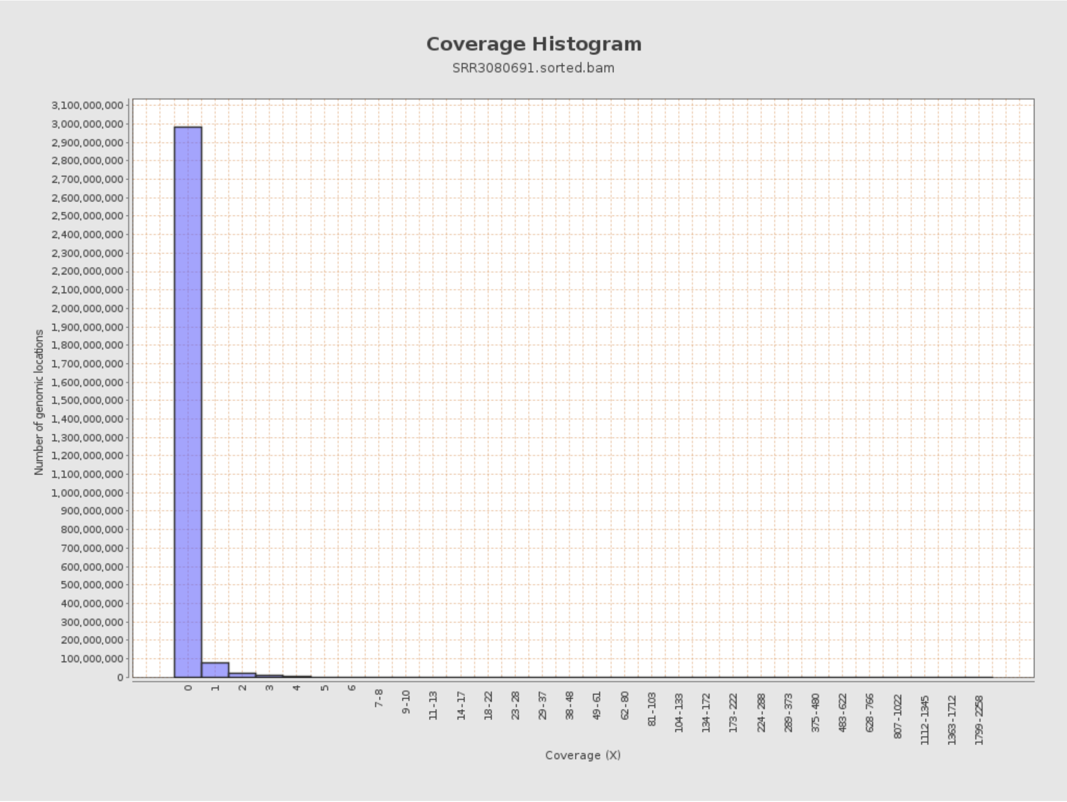
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12119663	0.0486	0.5824
chr2	243199373	13537945	0.0557	0.4155
chr3	198022430	11053097	0.0558	0.3175
chr4	191154276	11558723	0.0605	0.3472
chr5	180915260	10400597	0.0575	0.3228
chr6	171115067	9493951	0.0555	0.3375
chr7	159138663	8566799	0.0538	0.5347

chr8	146364022	8377658	0.0572	1.3994
chr9	141213431	6499496	0.046	0.3572
chr10	135534747	7452598	0.055	0.3848
chr11	135006516	7466731	0.0553	0.4153
chr12	133851895	7017484	0.0524	0.3088
chr13	115169878	5587598	0.0485	0.298
chr14	107349540	5121694	0.0477	0.302
chr15	102531392	4471935	0.0436	0.2788
chr16	90354753	3888628	0.043	0.2913
chr17	81195210	3657019	0.045	0.3093
chr18	78077248	4524708	0.058	0.5385
chr19	59128983	2525956	0.0427	0.447
chr20	63025520	2970782	0.0471	0.2952
chr21	48129895	1961898	0.0408	0.2849
chr22	51304566	1431619	0.0279	0.2171
chrMT	16571	73056	4.4087	3.7301
chrX	155270560	10130937	0.0652	0.3596
chrY	59373566	419508	0.0071	0.1939

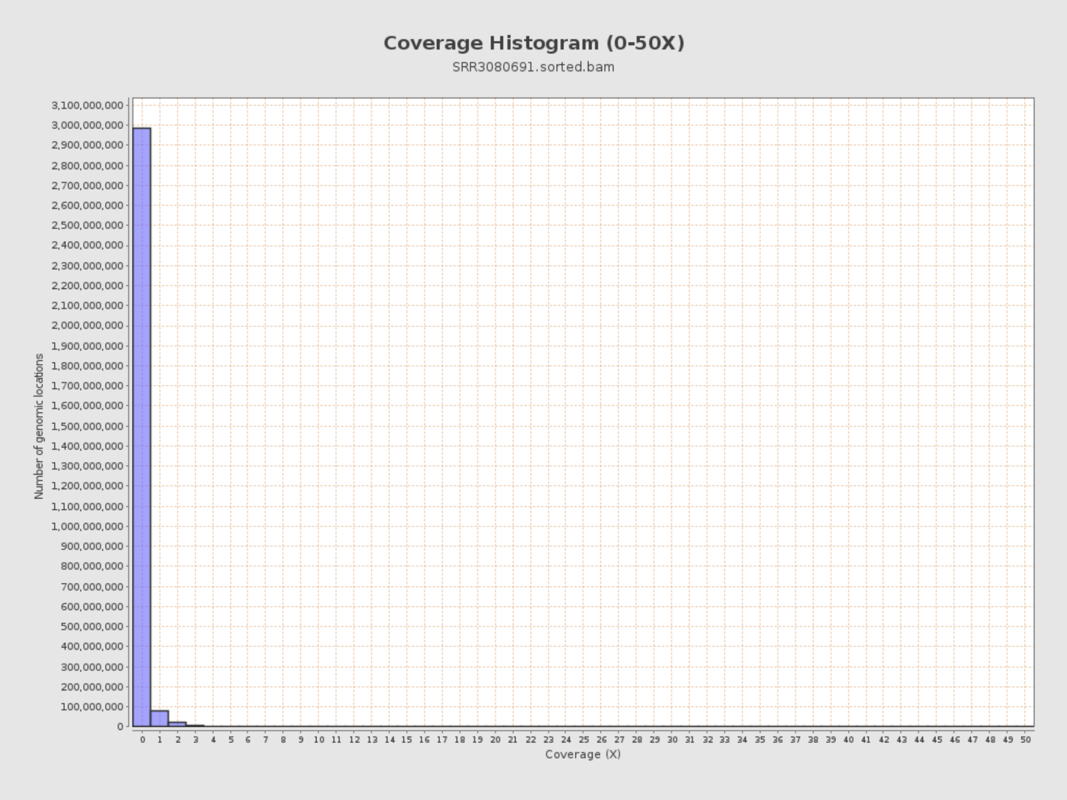
3. Results : Coverage across reference



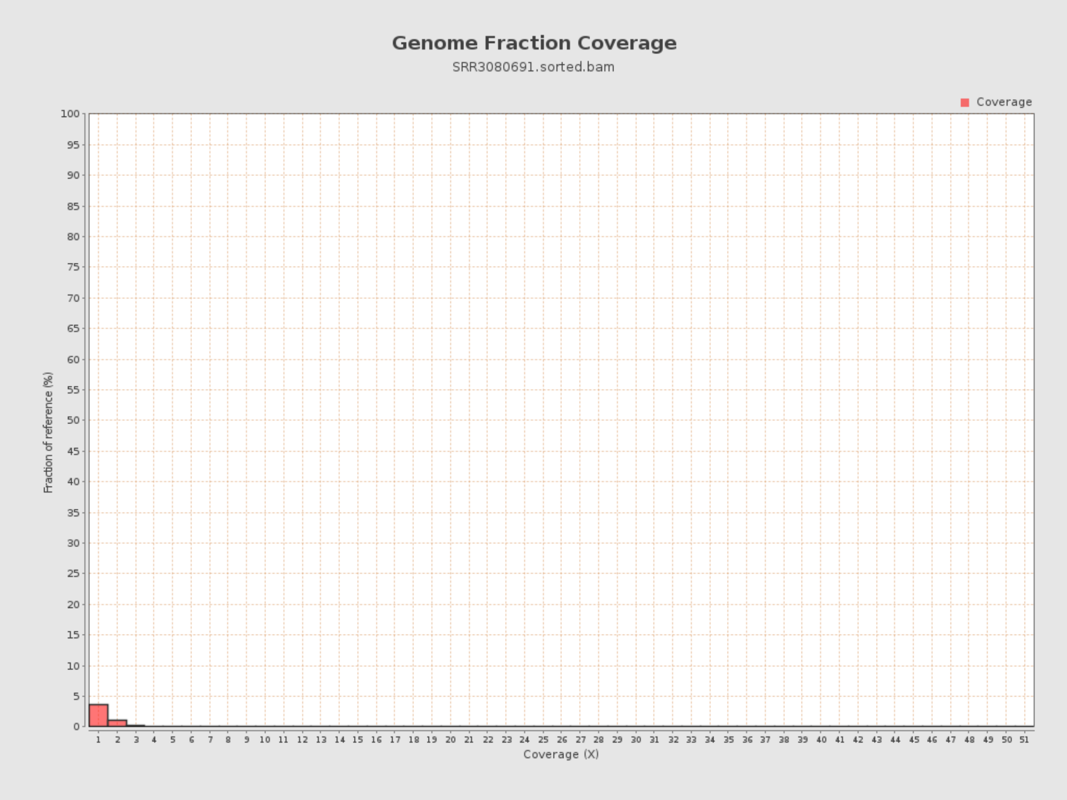
4. Results : Coverage Histogram



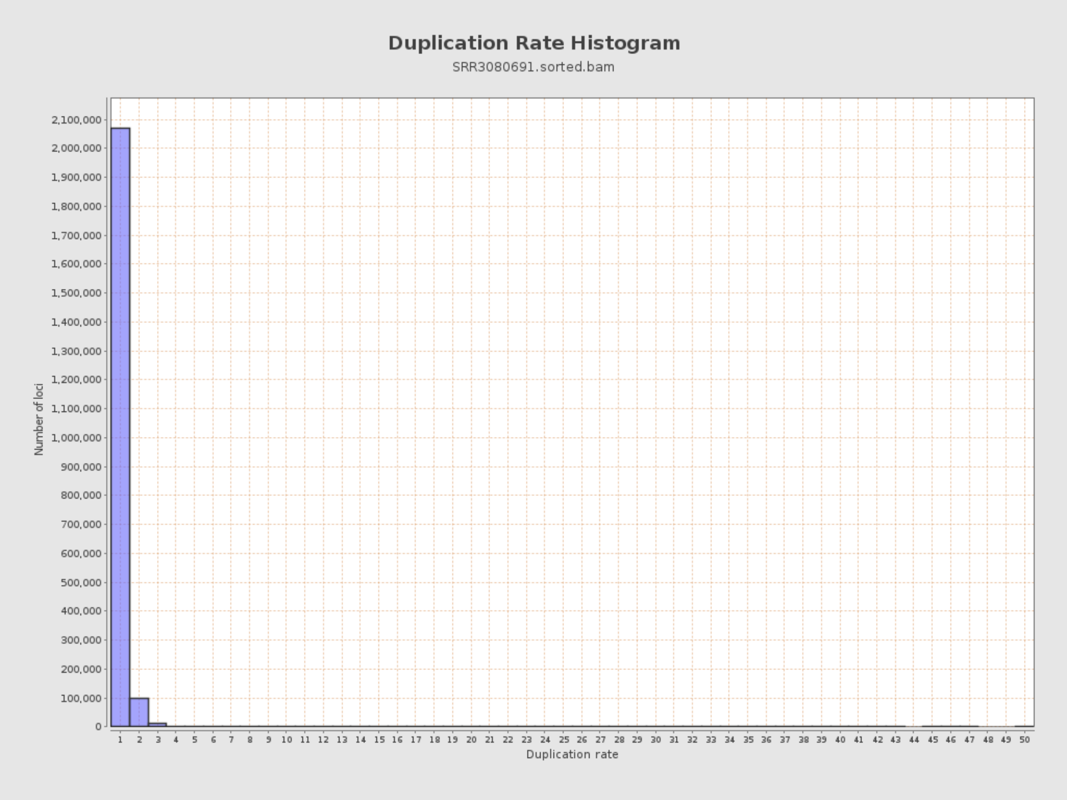
5. Results : Coverage Histogram (0-50X)



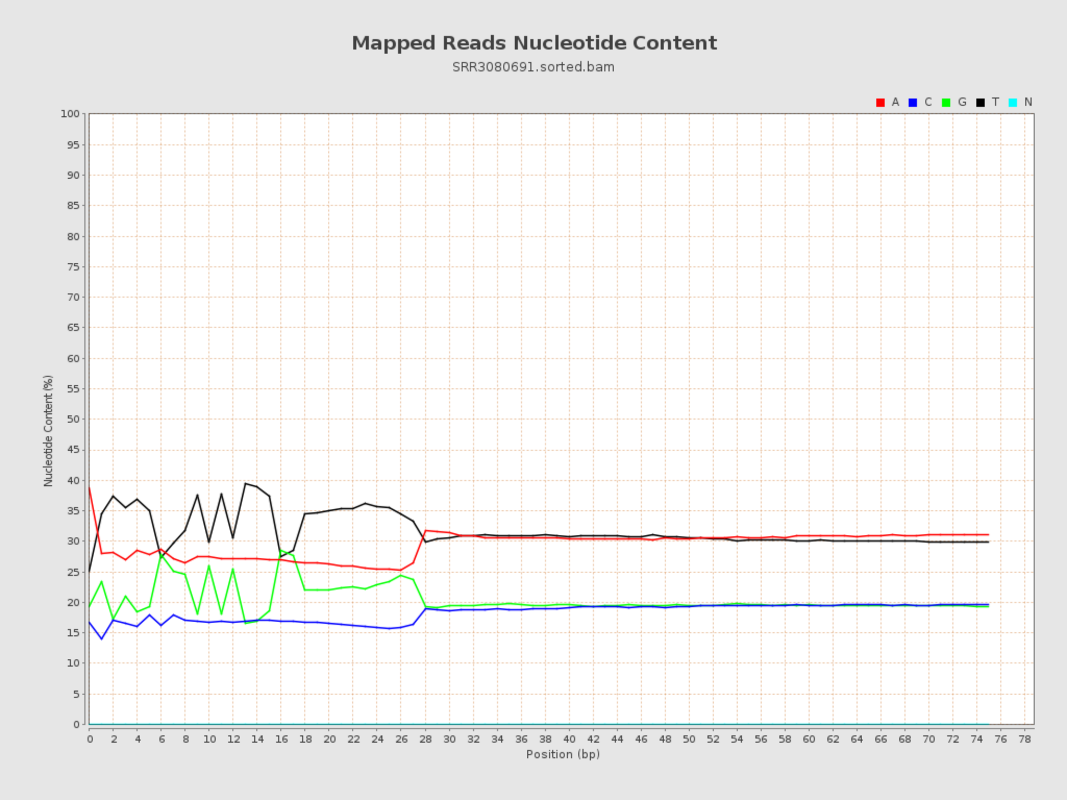
6. Results : Genome Fraction Coverage



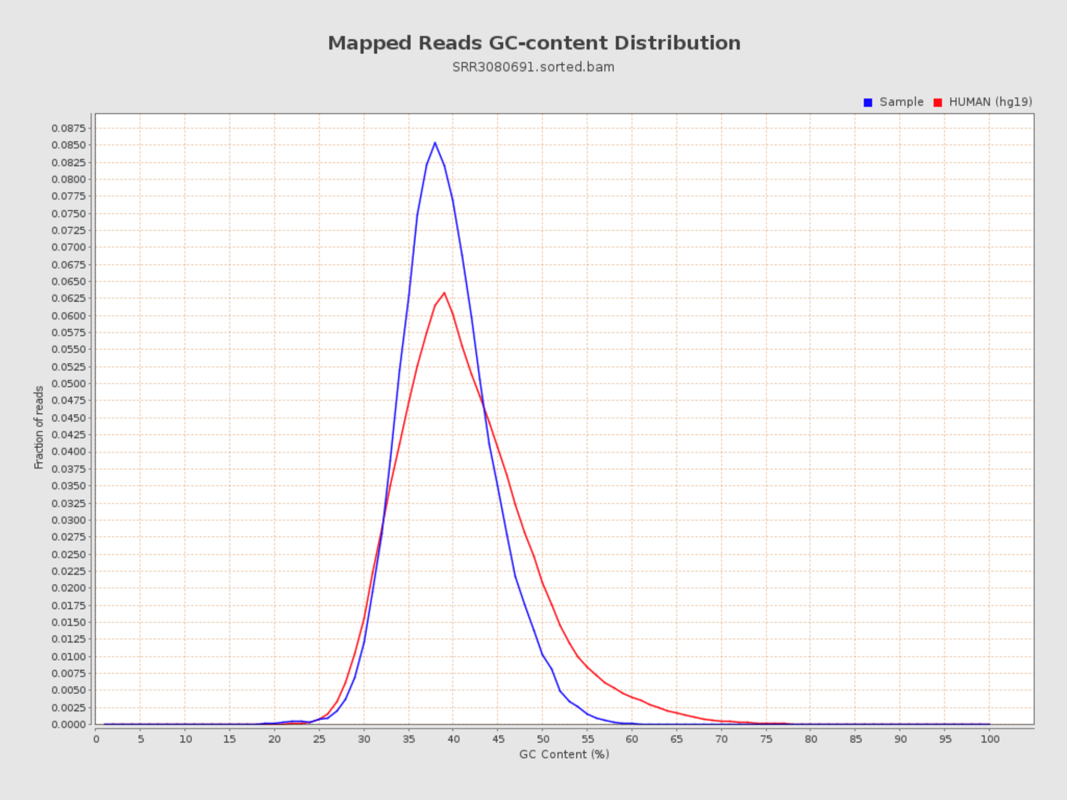
7. Results : Duplication Rate Histogram



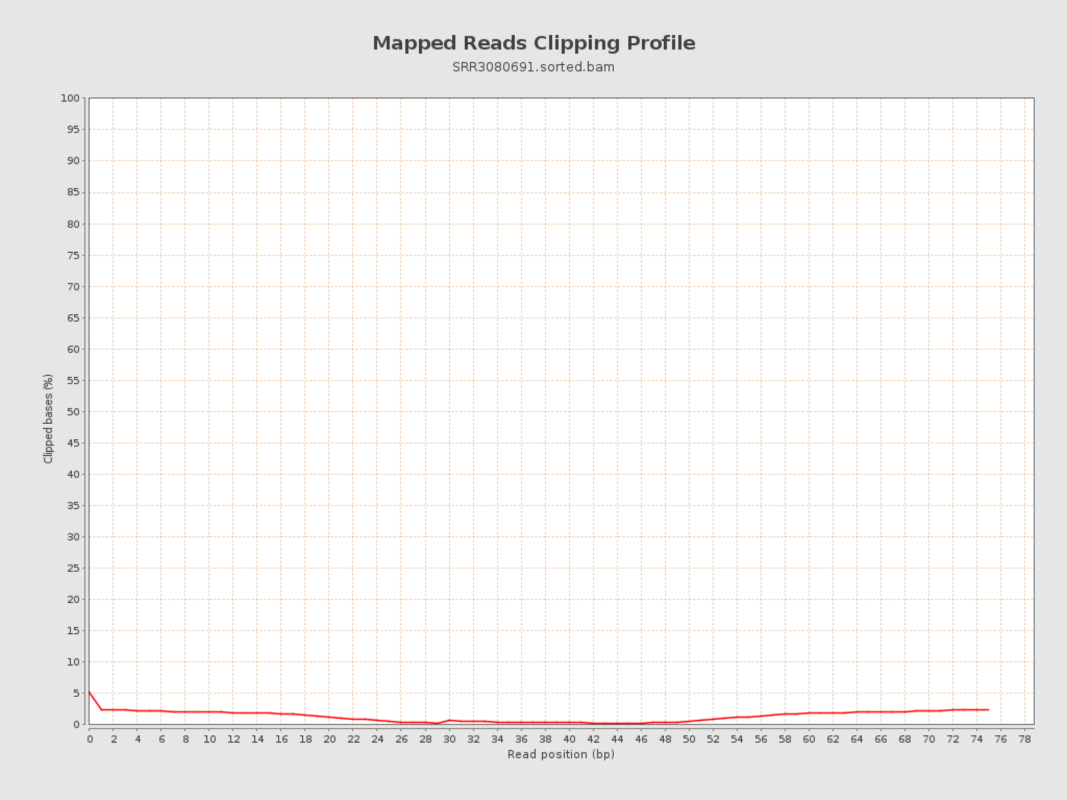
8. Results : Mapped Reads Nucleotide Content



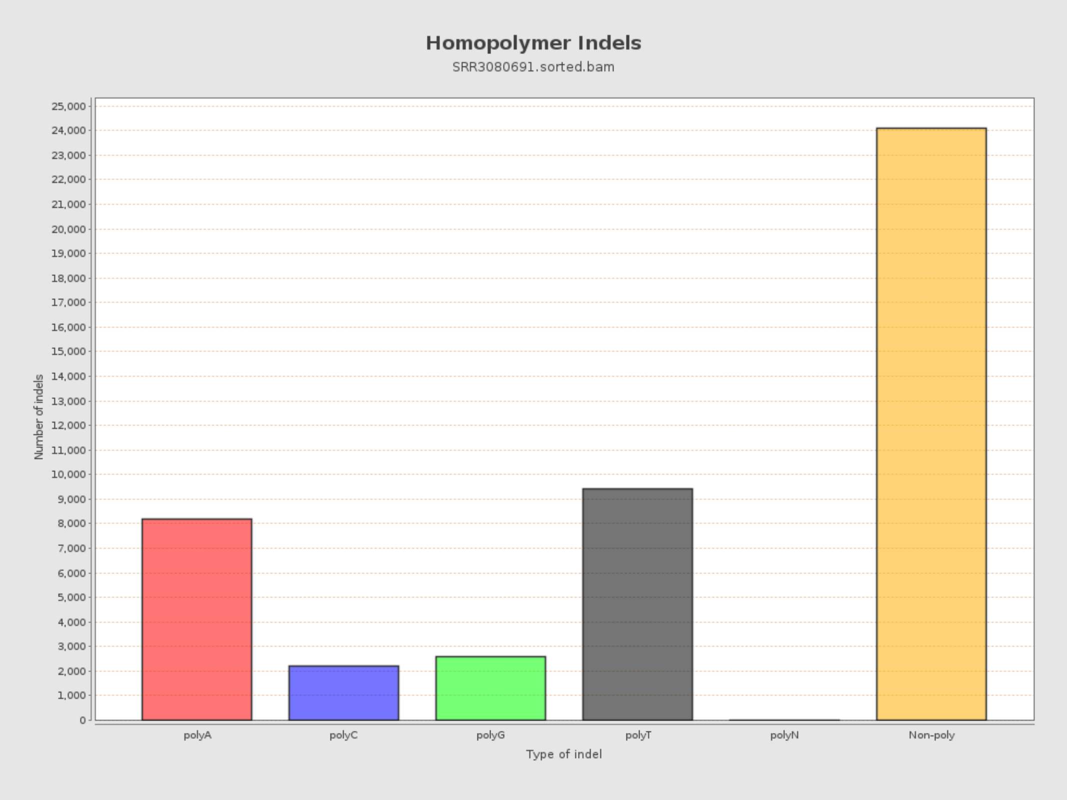
9. Results : Mapped Reads GC-content Distribution



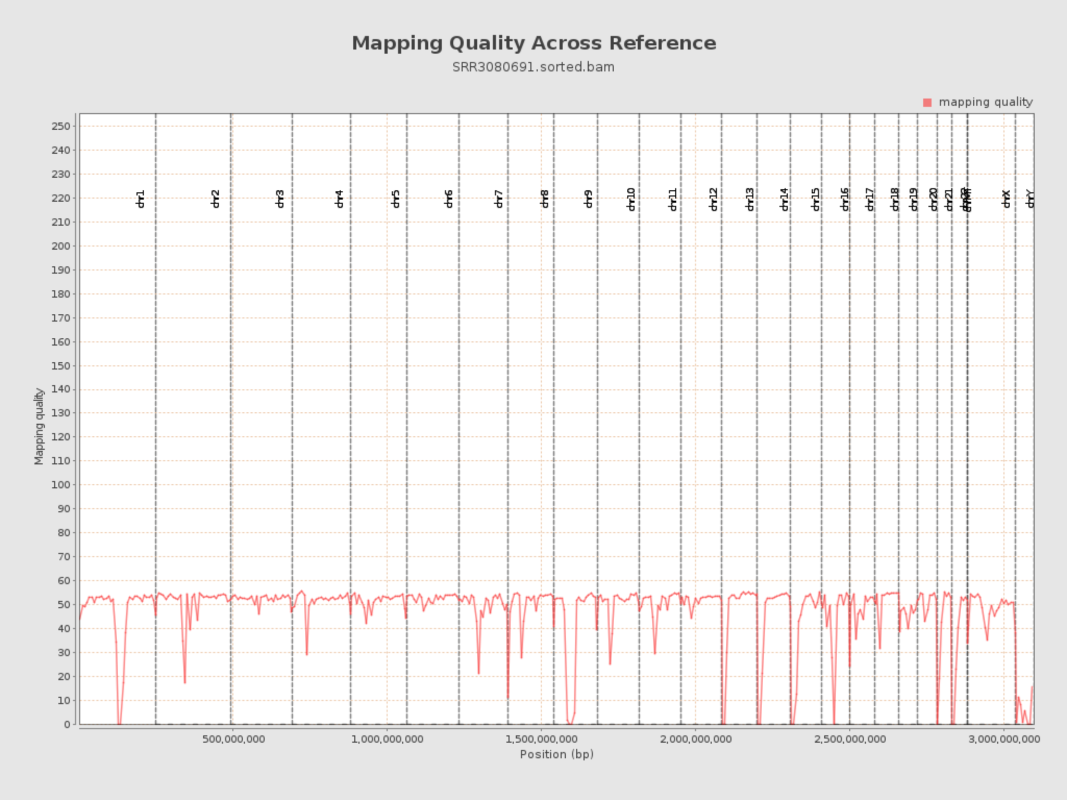
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram