Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:35:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080647.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_SRR3080647 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080647.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:35:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080647.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,419,294
Mapped reads	1,277,790 / 90.03%
Unmapped reads	141,504 / 9.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,511 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	51,782 / 3.65%
Duplication rate	3.56%
Clipped reads	611,777 / 43.1%

2.2. ACGT Content

Number/percentage of A's	22,665,953 / 26.94%
Number/percentage of C's	15,574,245 / 18.51%
Number/percentage of T's	26,603,619 / 31.62%
Number/percentage of G's	19,284,815 / 22.92%
Number/percentage of N's	3,557 / 0%
GC Percentage	41.43%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.2202

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

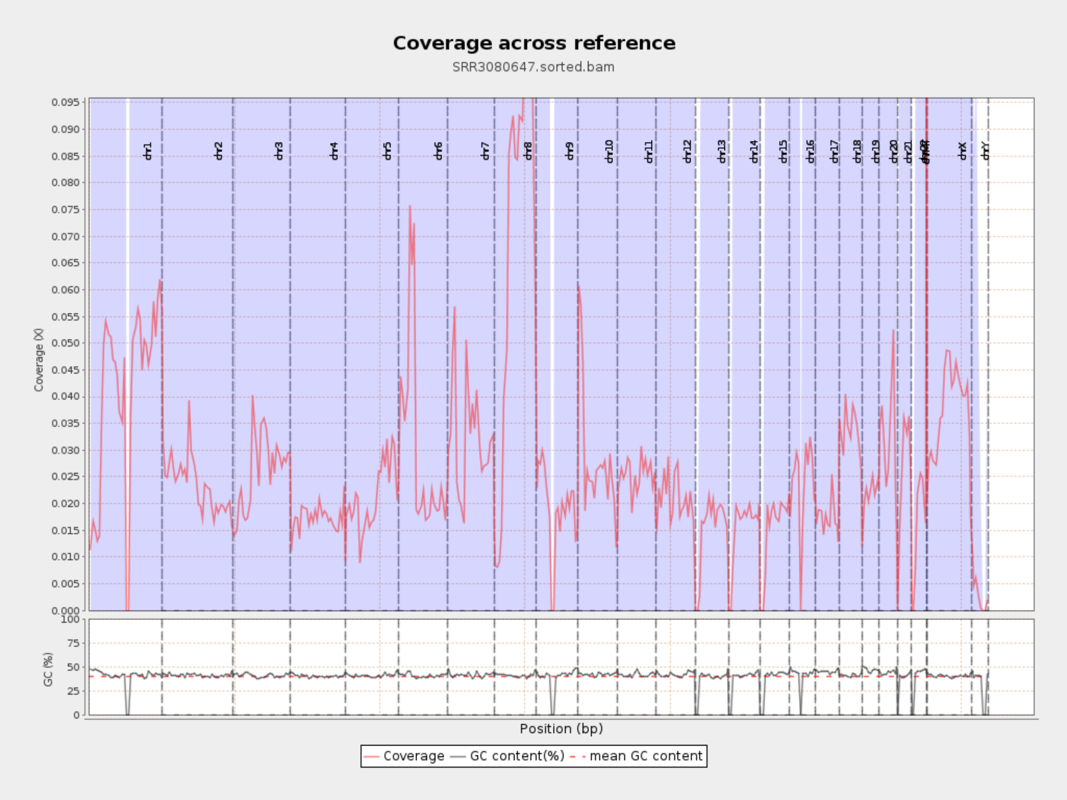
General error rate	0.7%
Mismatches	576,020
Insertions	6,382
Mapped reads with at least one insertion	0.5%
Deletions	19,413
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.93%

2.6. Chromosome stats

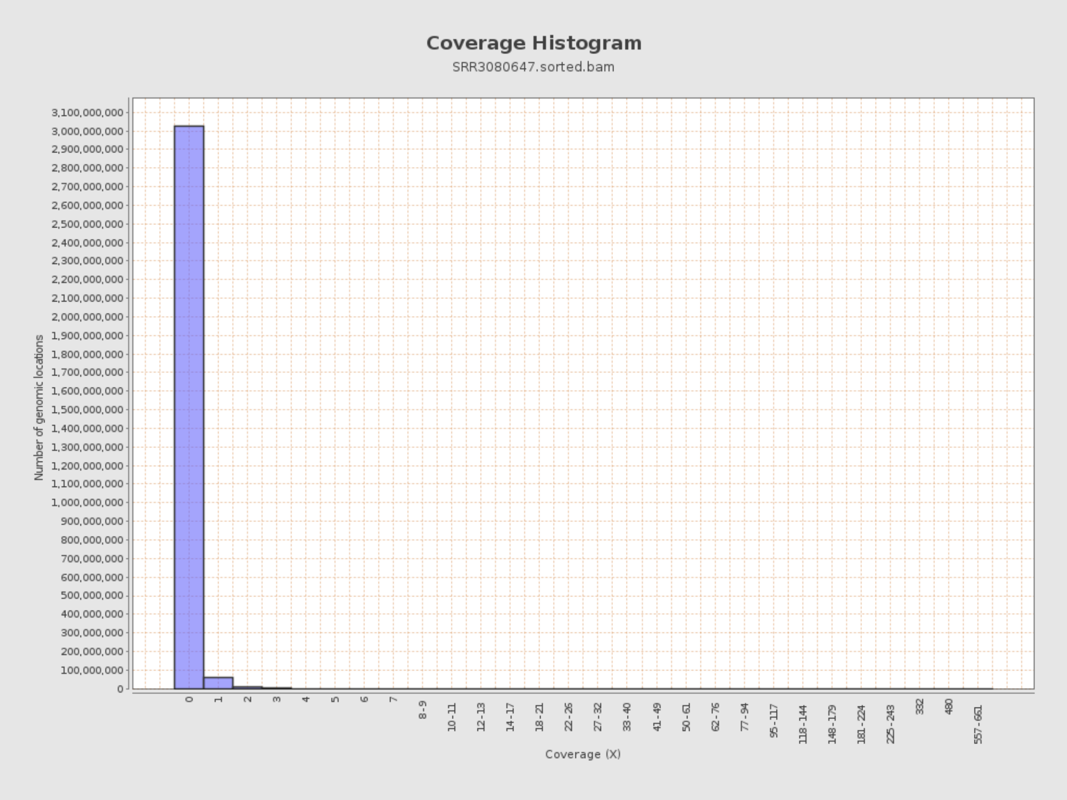
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10079511	0.0404	0.2577
chr2	243199373	5733921	0.0236	0.326
chr3	198022430	5197070	0.0262	0.1838
chr4	191154276	3310874	0.0173	0.1519
chr5	180915260	3863551	0.0214	0.166
chr6	171115067	5204512	0.0304	0.2263
chr7	159138663	5244210	0.033	0.3334

chr8	146364022	10227465	0.0699	0.3254
chr9	141213431	2687911	0.019	0.1691
chr10	135534747	3936253	0.029	0.2006
chr11	135006516	3394018	0.0251	0.1919
chr12	133851895	2779889	0.0208	0.1641
chr13	115169878	1735942	0.0151	0.1396
chr14	107349540	1623053	0.0151	0.1404
chr15	102531392	1550676	0.0151	0.1481
chr16	90354753	2157834	0.0239	0.1784
chr17	81195210	1402512	0.0173	0.1506
chr18	78077248	2653498	0.034	0.2353
chr19	59128983	1300116	0.022	0.1862
chr20	63025520	2030943	0.0322	0.2069
chr21	48129895	1240344	0.0258	0.1848
chr22	51304566	799056	0.0156	0.1401
chrMT	16571	3694	0.2229	0.5058
chrX	155270560	5832286	0.0376	0.2249
chrY	59373566	174317	0.0029	0.0624

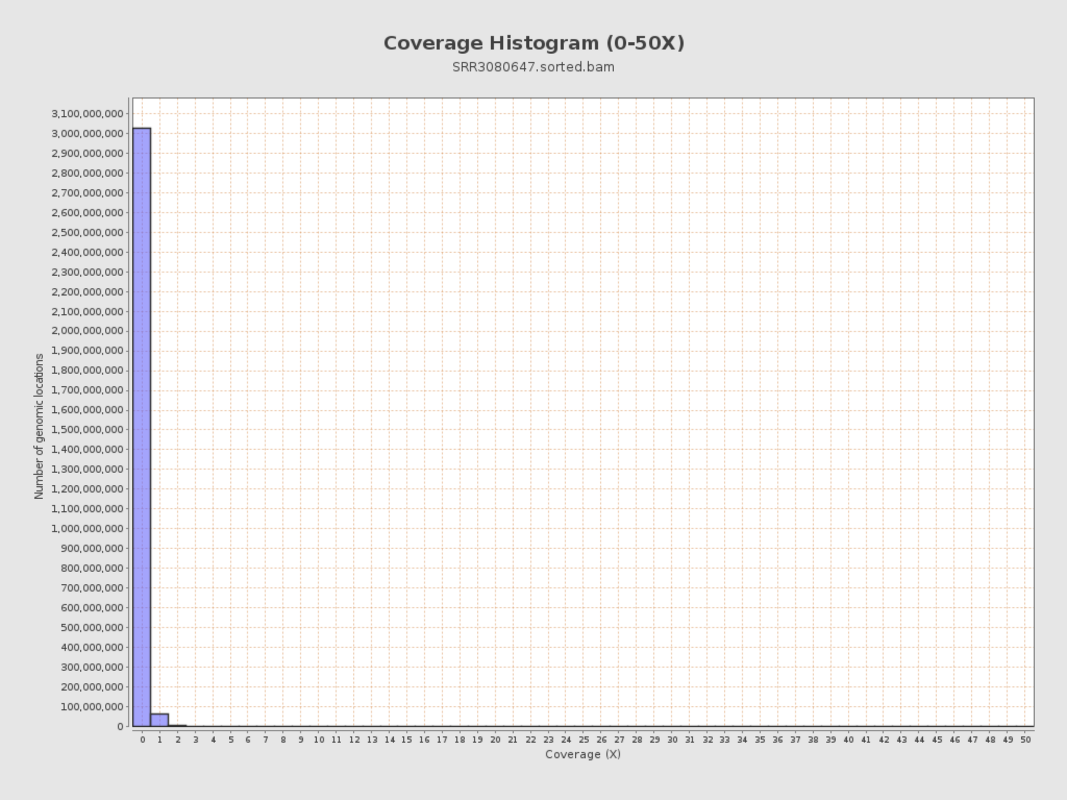
3. Results : Coverage across reference



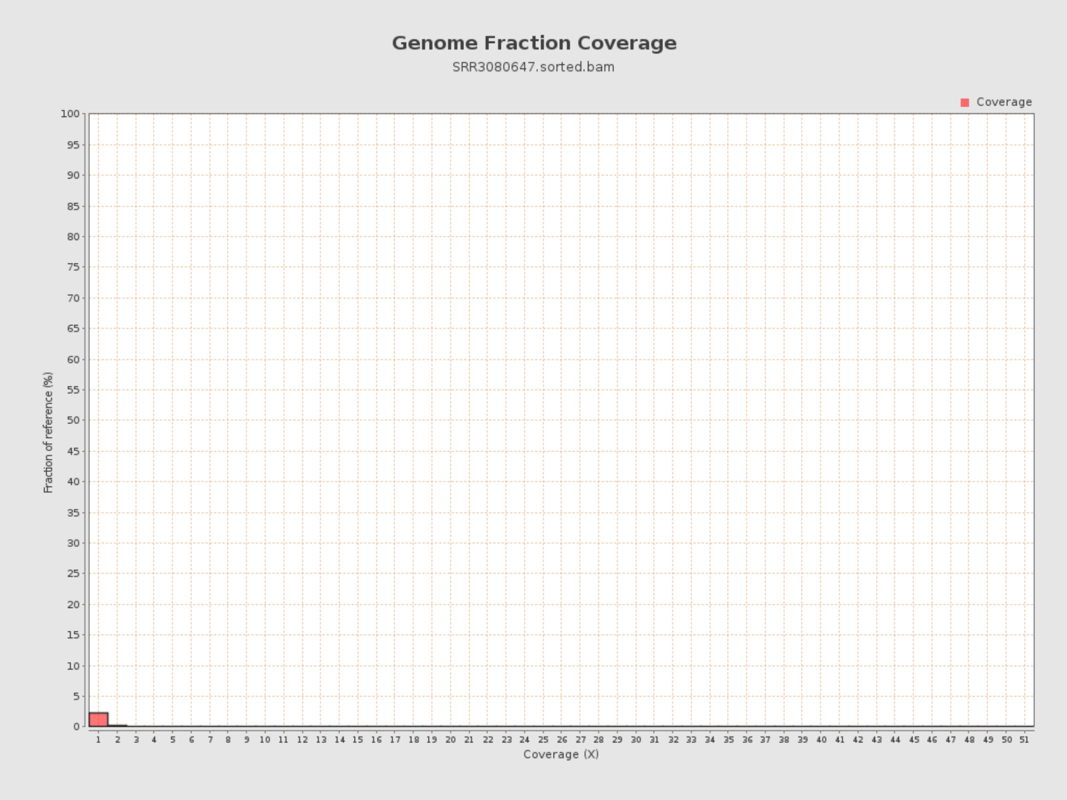
4. Results : Coverage Histogram



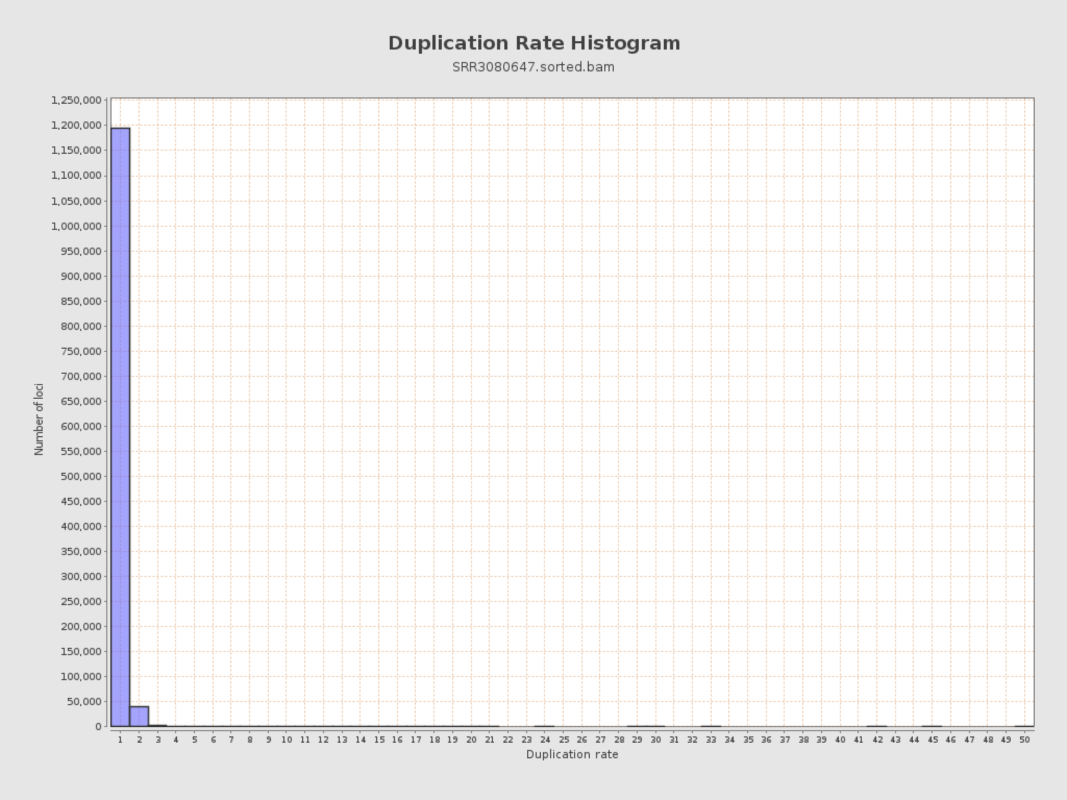
5. Results : Coverage Histogram (0-50X)



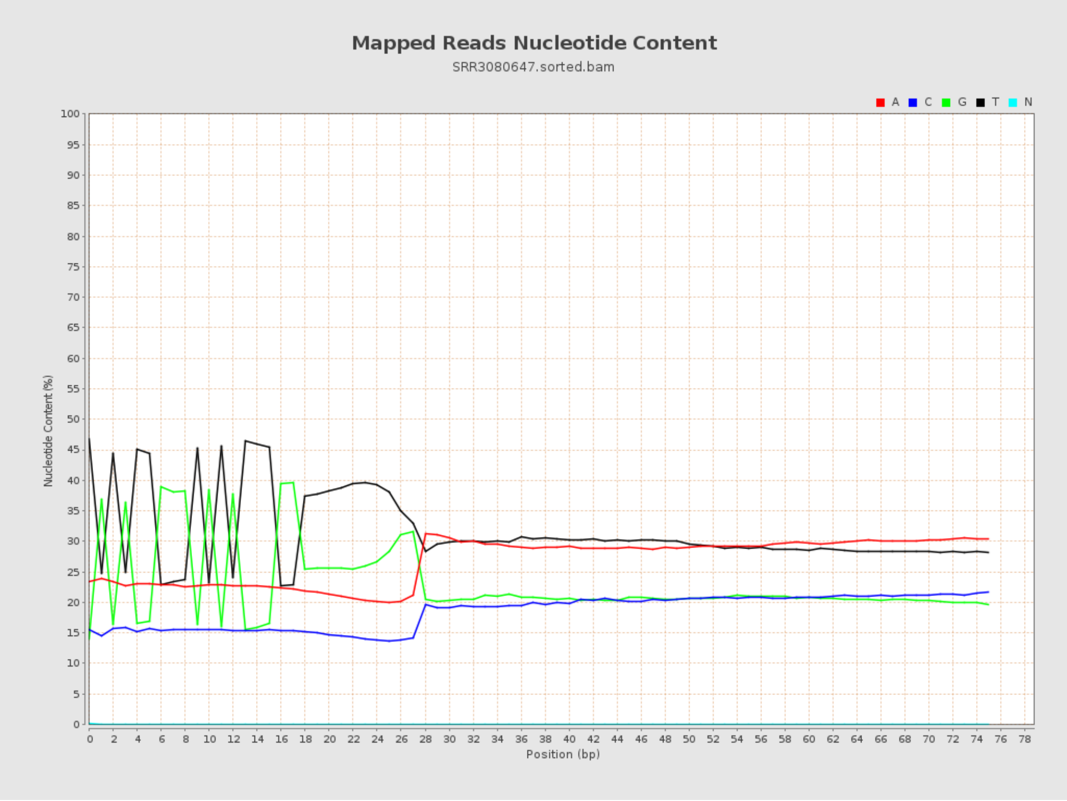
6. Results : Genome Fraction Coverage



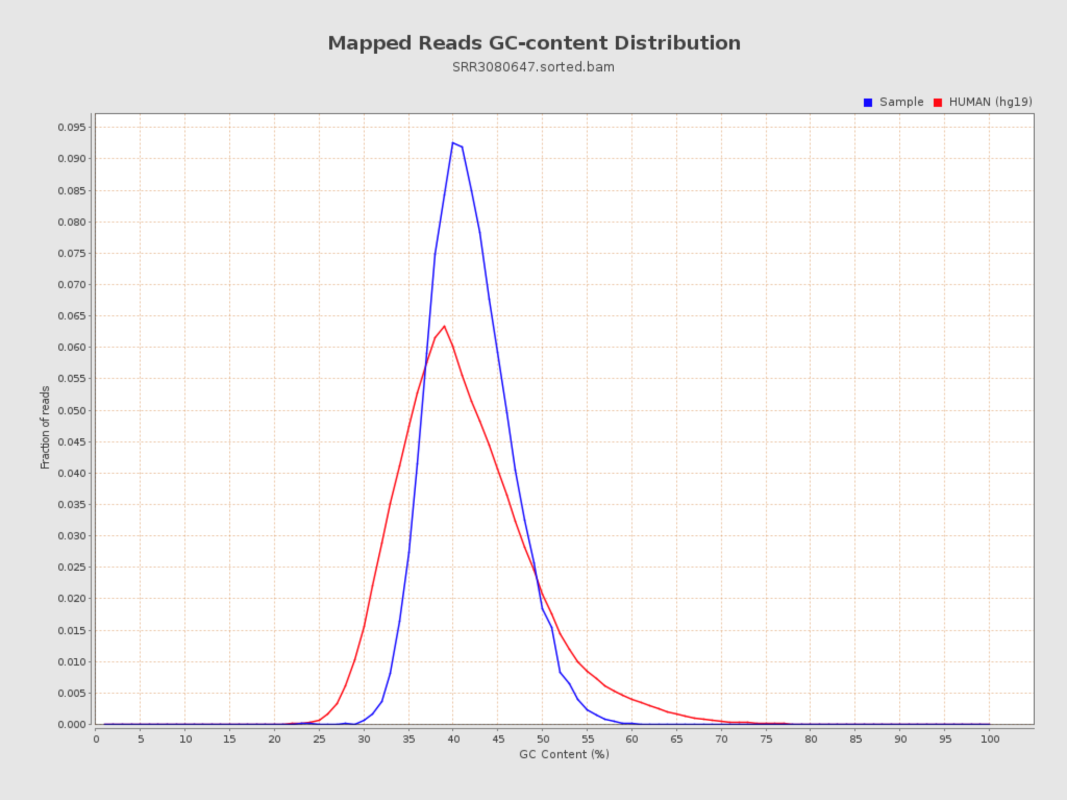
7. Results : Duplication Rate Histogram



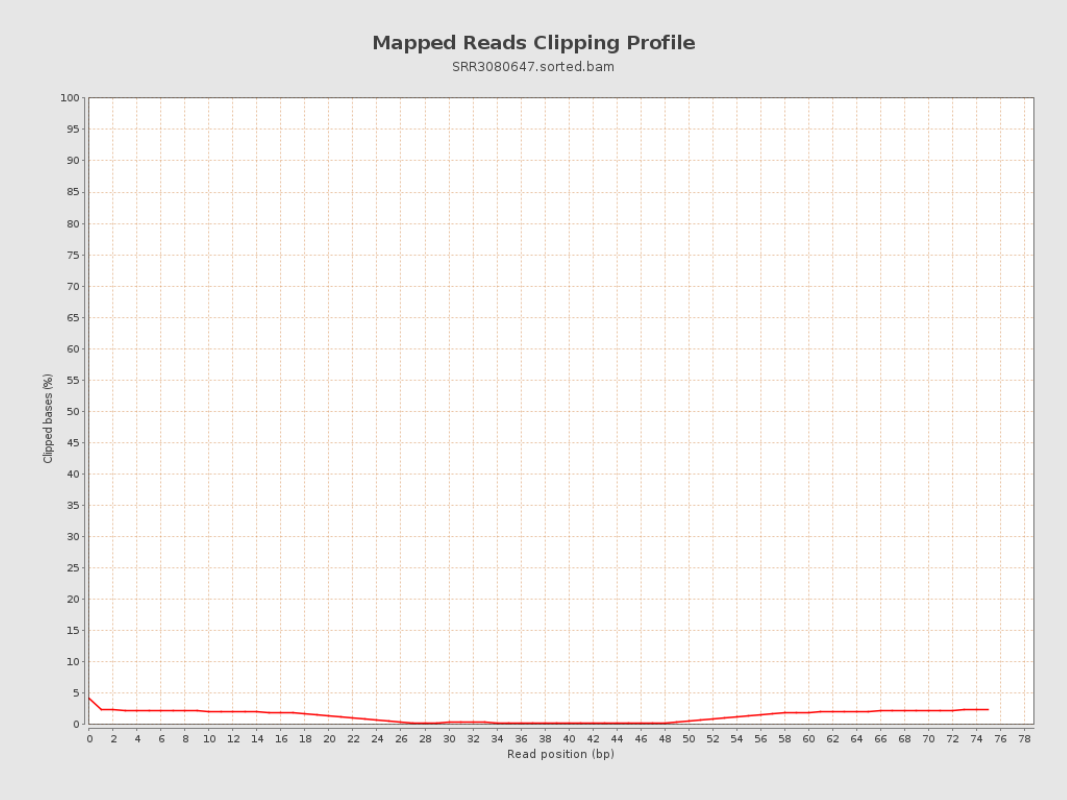
8. Results : Mapped Reads Nucleotide Content



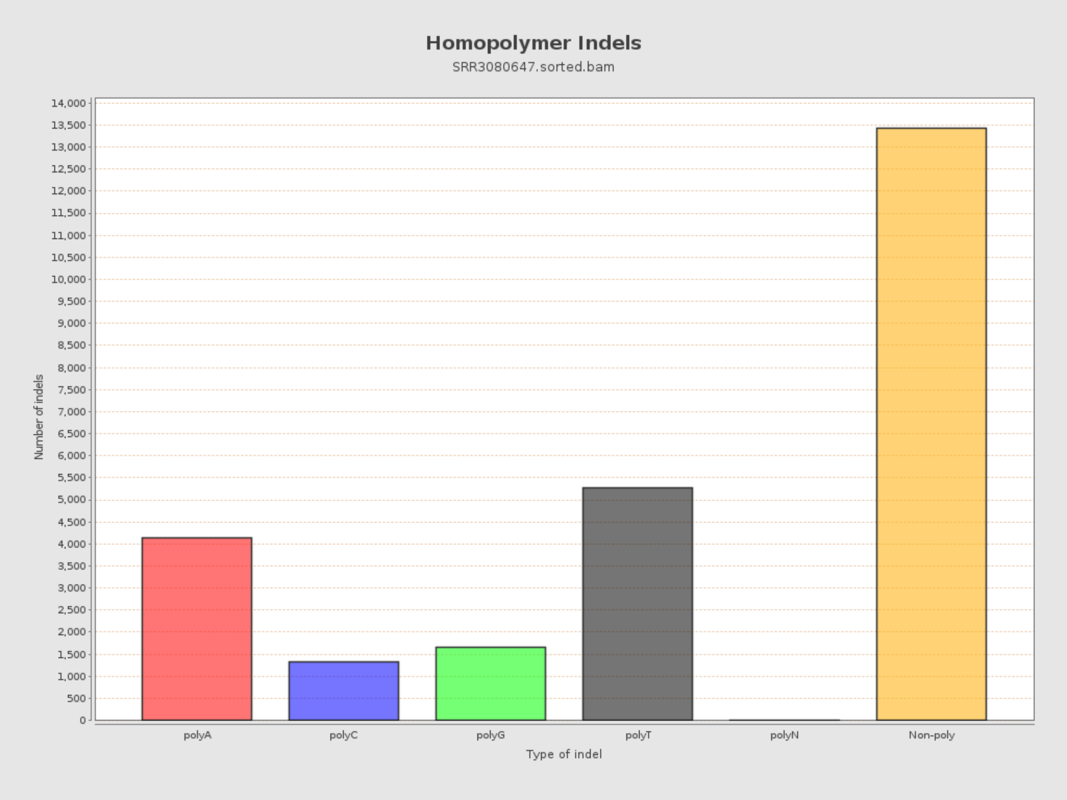
9. Results : Mapped Reads GC-content Distribution



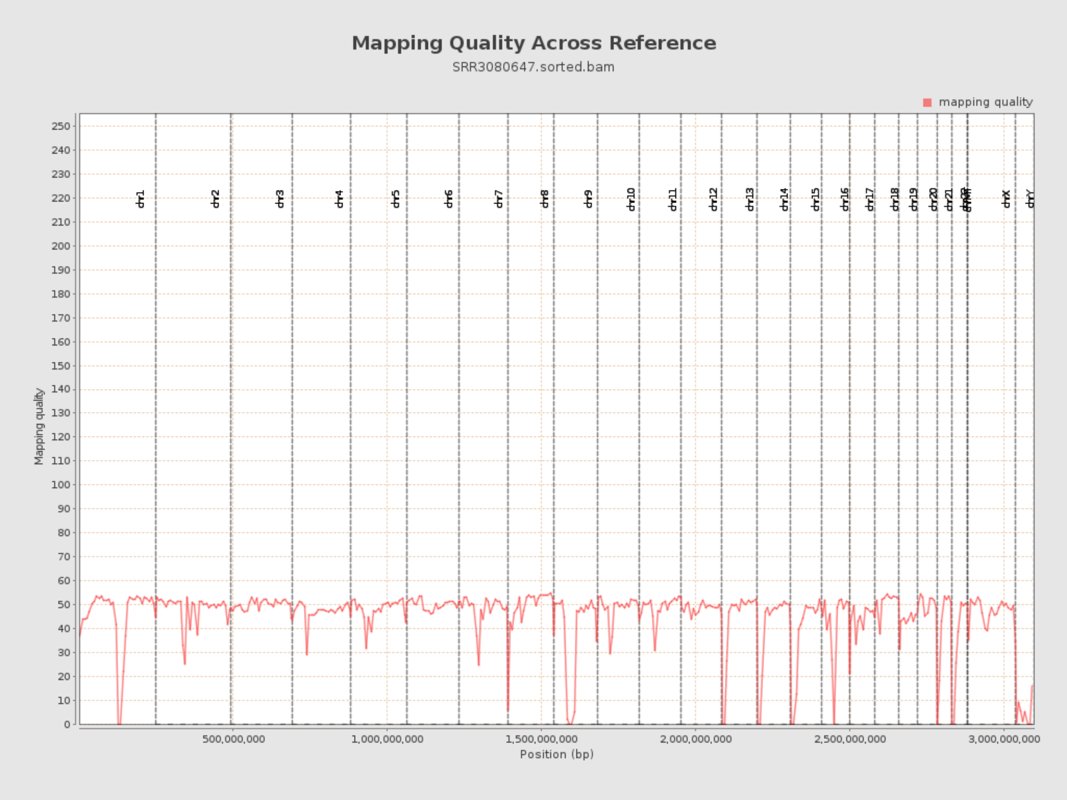
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram