Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:21:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004097.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_SRR6004097 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004097.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:21:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004097.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,989,520
Mapped reads	3,227,576 / 80.9%
Unmapped reads	761,944 / 19.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,998 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	254,902 / 6.39%
Duplication rate	6.47%
Clipped reads	1,584,462 / 39.72%

2.2. ACGT Content

Number/percentage of A's	59,077,262 / 27.7%
Number/percentage of C's	38,991,983 / 18.28%
Number/percentage of T's	68,981,295 / 32.35%
Number/percentage of G's	46,187,426 / 21.66%
Number/percentage of N's	28,244 / 0.01%
GC Percentage	39.94%

2.3. Coverage

Mean	0.0689

Standard Deviation	0.5393

2.4. Mapping Quality

Mean Mapping Quality	46.93

2.5. Mismatches and indels

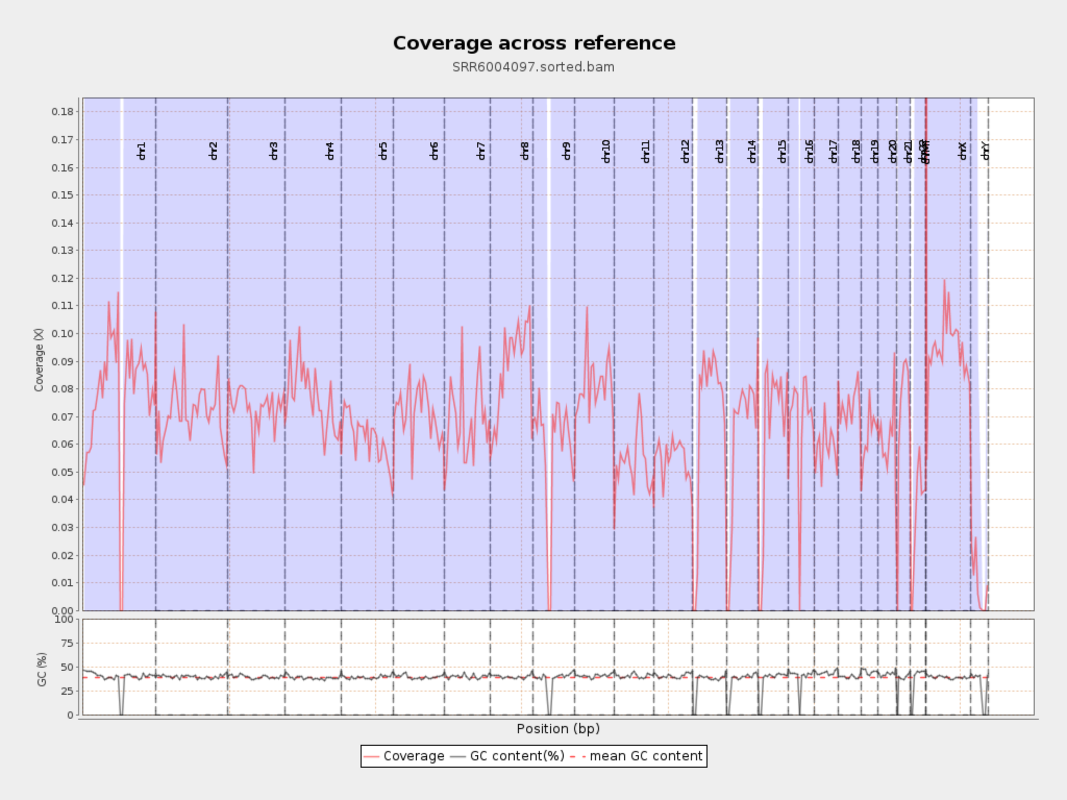
General error rate	0.96%
Mismatches	2,015,116
Insertions	17,297
Mapped reads with at least one insertion	0.53%
Deletions	60,927
Mapped reads with at least one deletion	1.86%
Homopolymer indels	47.35%

2.6. Chromosome stats

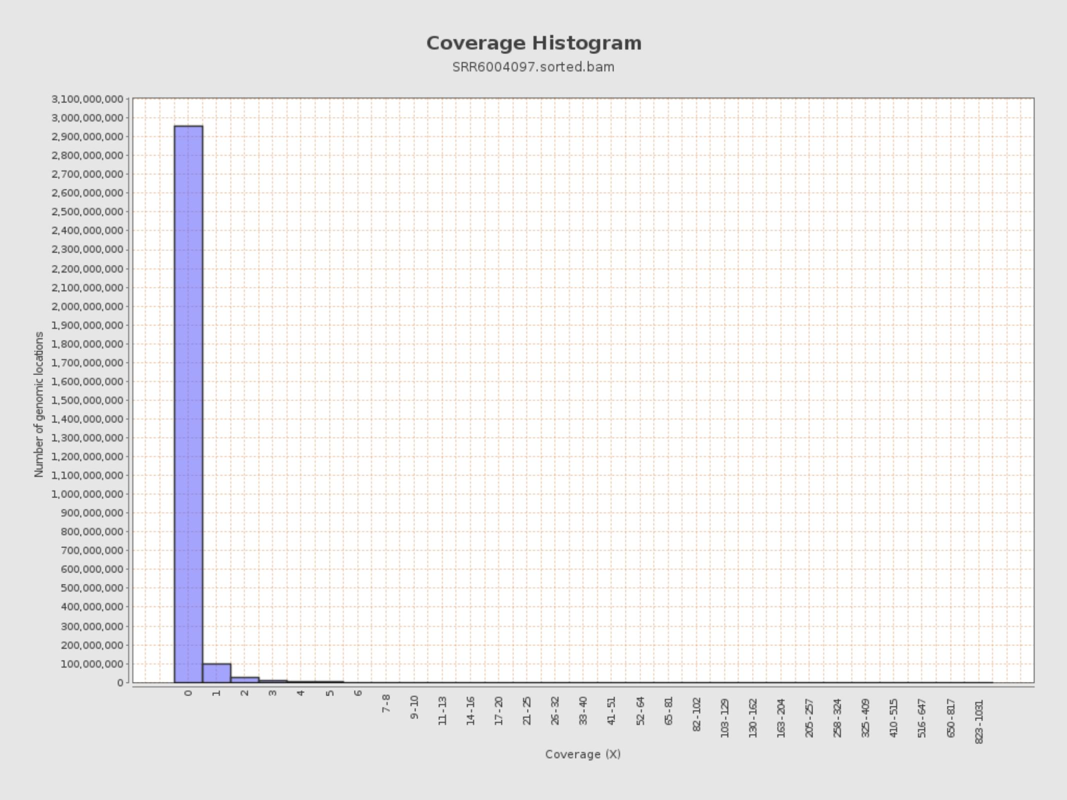
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19402799	0.0778	0.9793
chr2	243199373	17372493	0.0714	0.6048
chr3	198022430	14550063	0.0735	0.389
chr4	191154276	14772345	0.0773	0.4156
chr5	180915260	11194372	0.0619	0.3552
chr6	171115067	12307380	0.0719	0.4495
chr7	159138663	10954925	0.0688	0.6861

chr8	146364022	12869945	0.0879	0.6572
chr9	141213431	8284949	0.0587	0.4622
chr10	135534747	11082346	0.0818	0.5513
chr11	135006516	7245767	0.0537	0.4059
chr12	133851895	7384085	0.0552	0.3356
chr13	115169878	8032601	0.0697	0.3798
chr14	107349540	6675898	0.0622	0.3706
chr15	102531392	6475997	0.0632	0.365
chr16	90354753	6015542	0.0666	0.3863
chr17	81195210	4778344	0.0589	0.3862
chr18	78077248	5809079	0.0744	0.8058
chr19	59128983	3762155	0.0636	0.6606
chr20	63025520	4002182	0.0635	0.3689
chr21	48129895	3411741	0.0709	0.4017
chr22	51304566	1752811	0.0342	0.2546
chrMT	16571	99183	5.9853	4.8873
chrX	155270560	14580568	0.0939	0.4751
chrY	59373566	548964	0.0092	0.1732

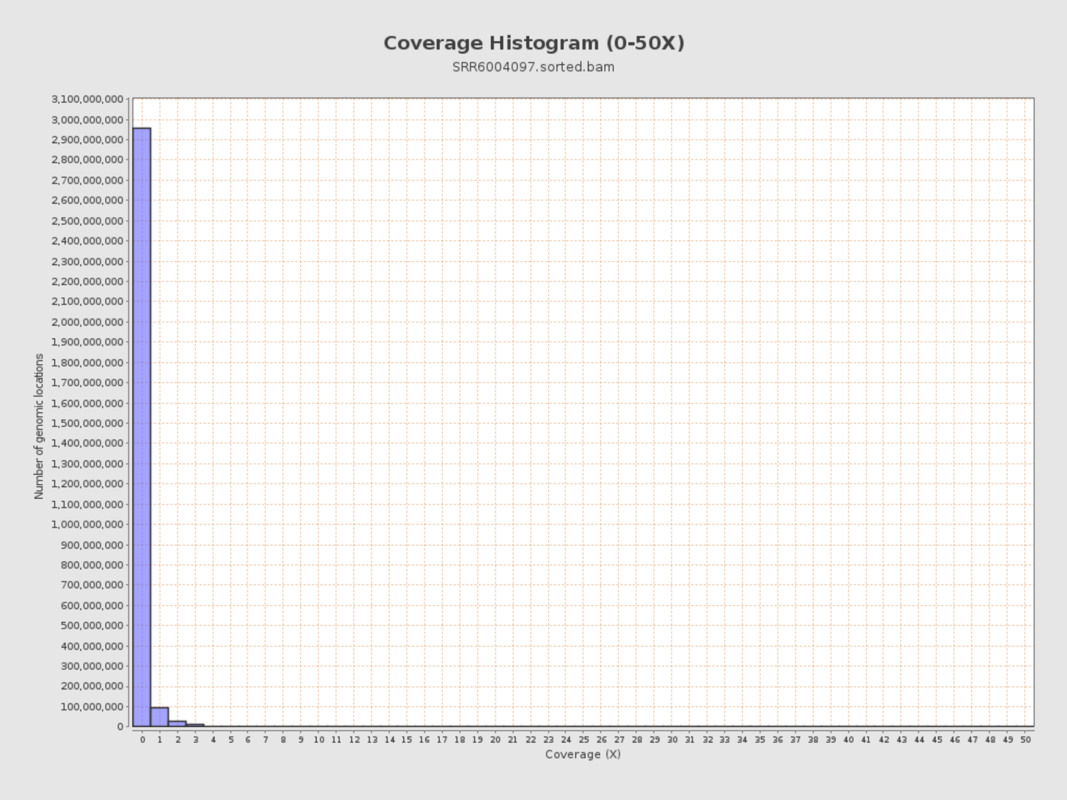
3. Results : Coverage across reference



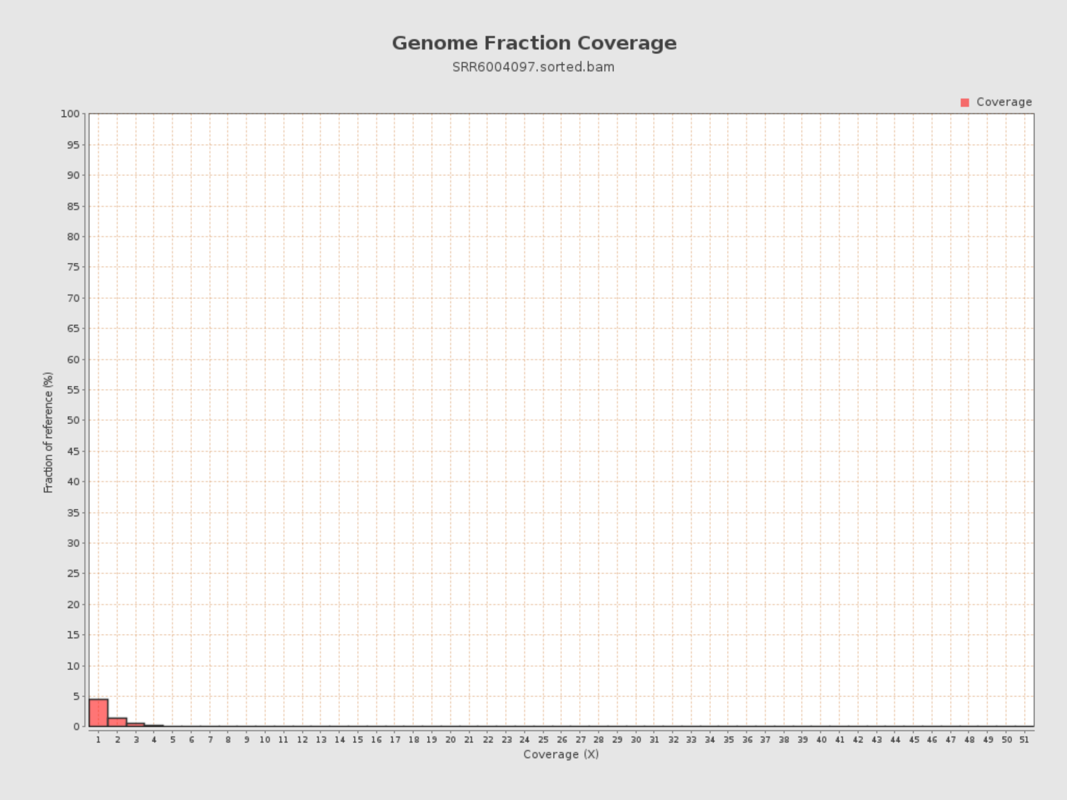
4. Results : Coverage Histogram



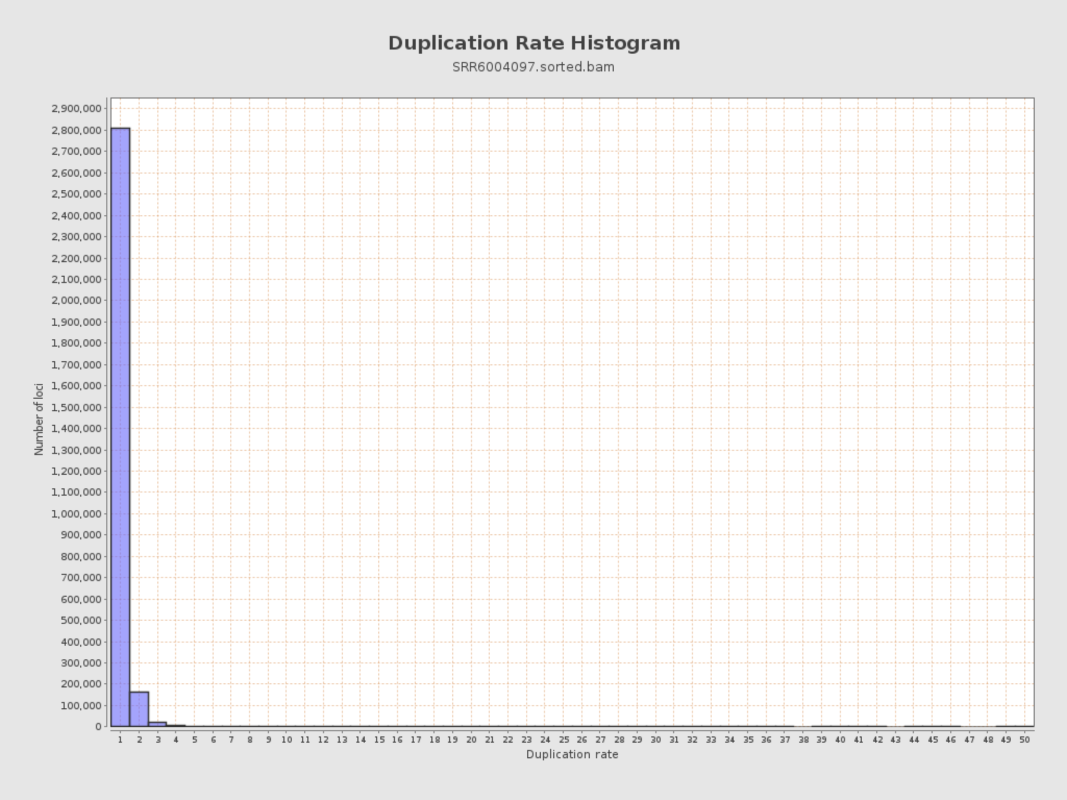
5. Results : Coverage Histogram (0-50X)



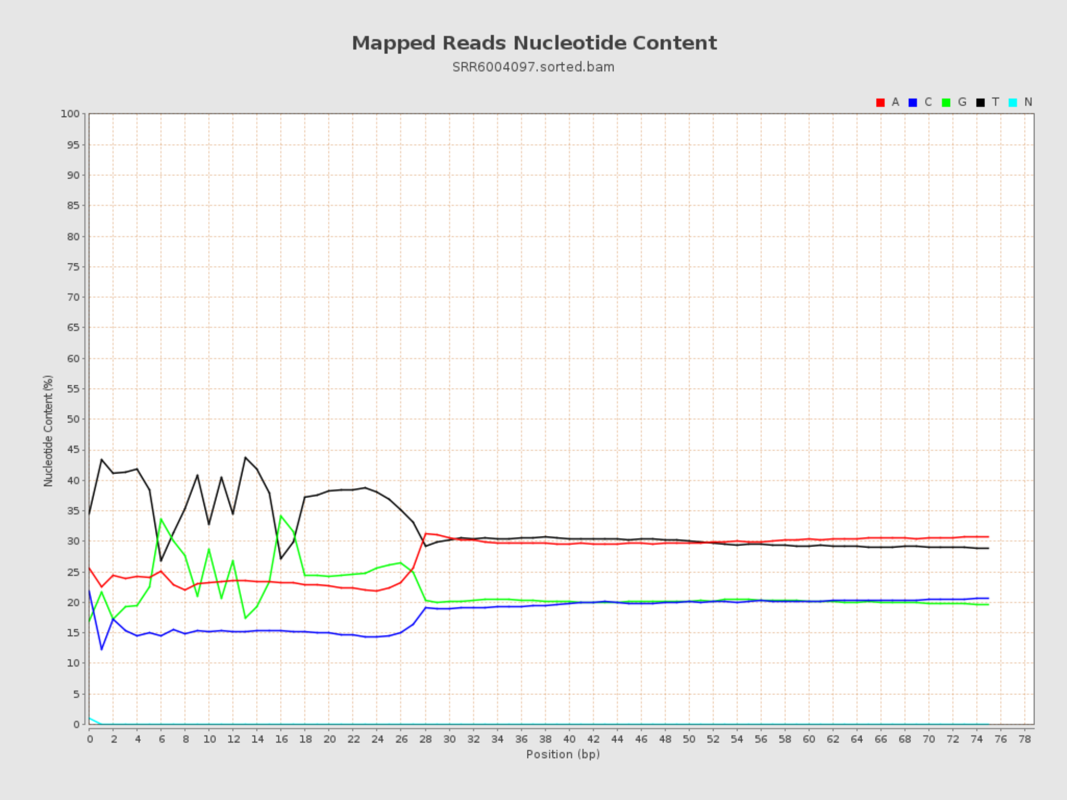
6. Results : Genome Fraction Coverage



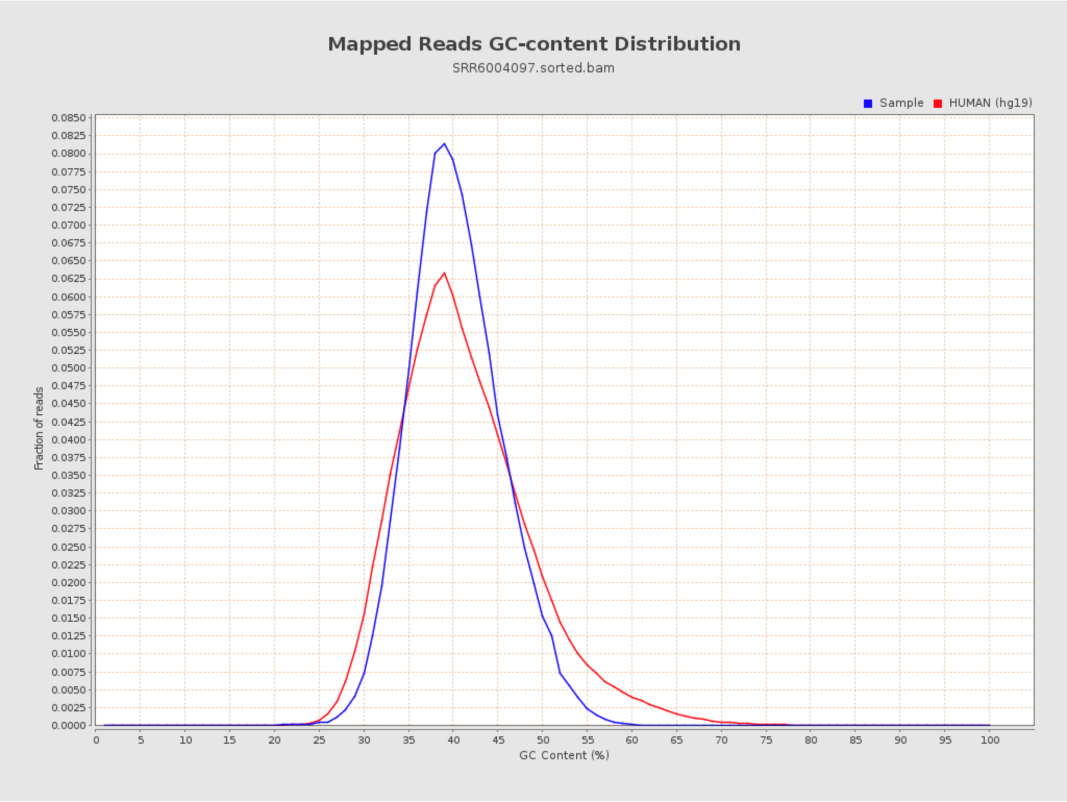
7. Results : Duplication Rate Histogram



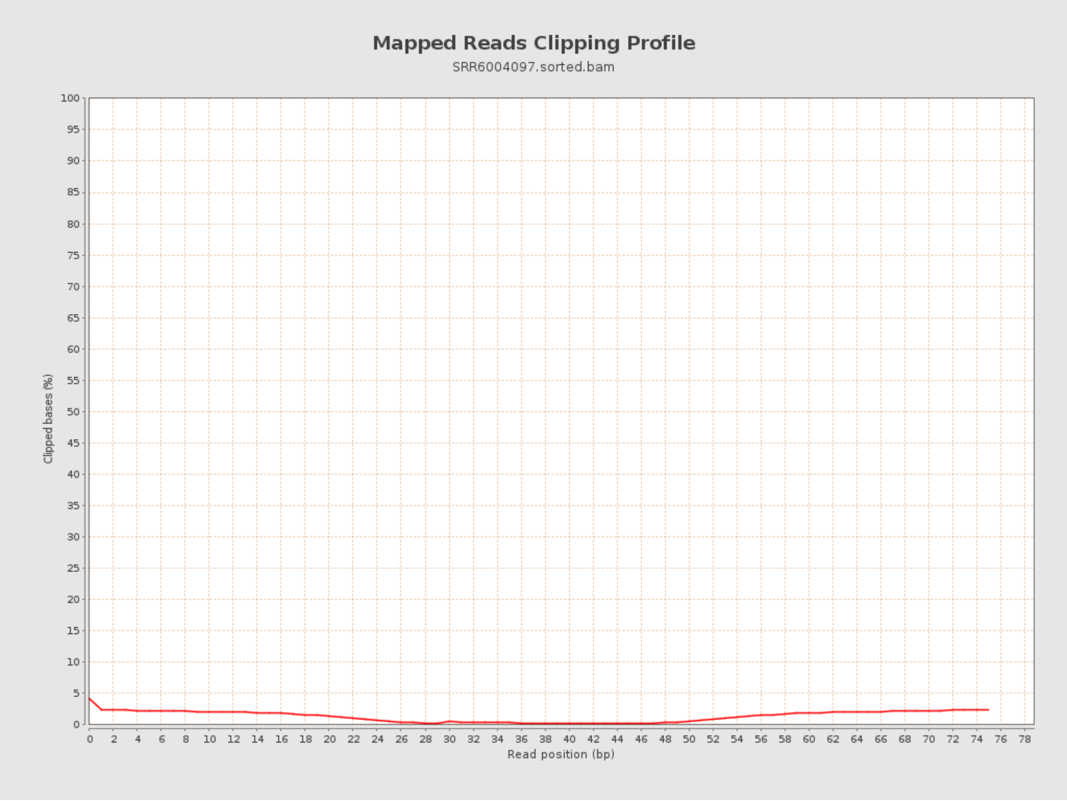
8. Results : Mapped Reads Nucleotide Content



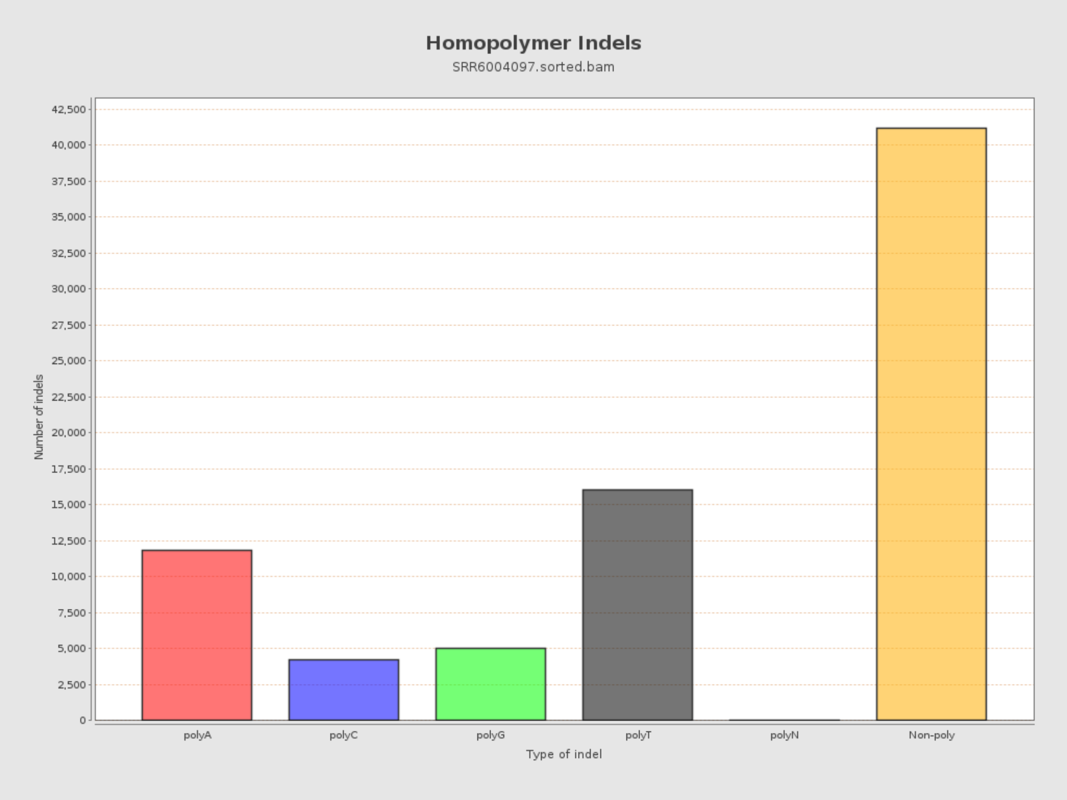
9. Results : Mapped Reads GC-content Distribution



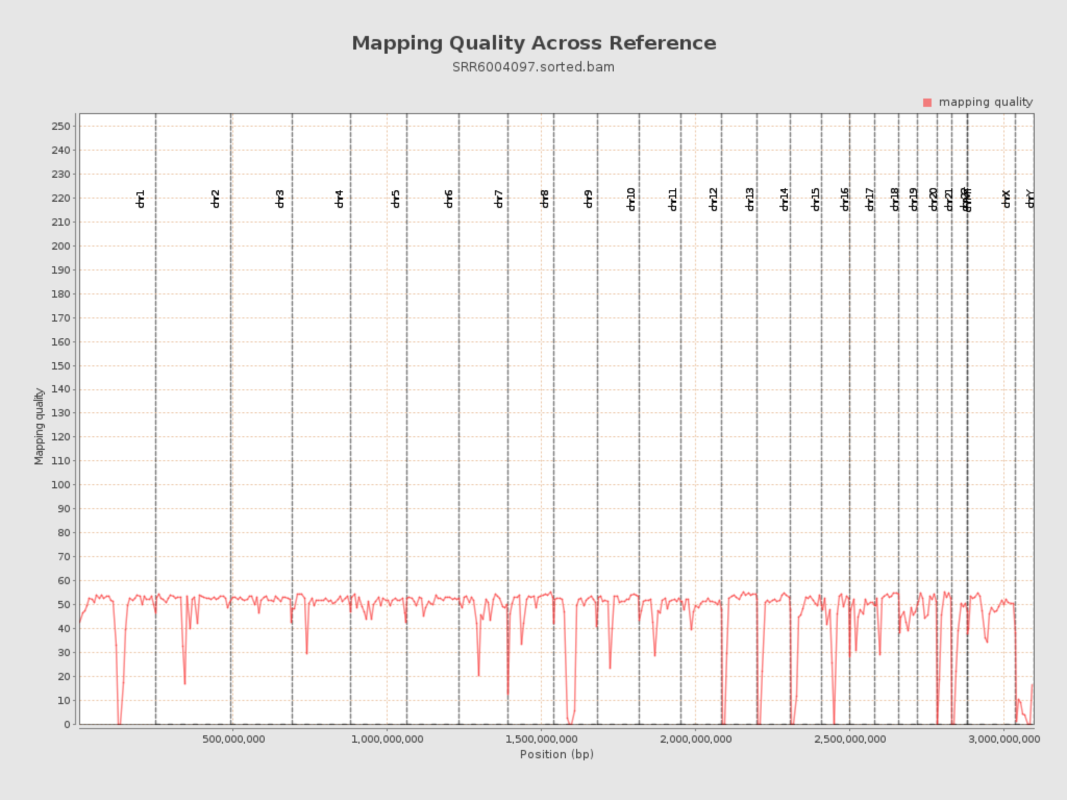
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram