Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:27:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234035.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_SRR6234035 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234035.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:27:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,102,861
Mapped reads	824,320 / 74.74%
Unmapped reads	278,541 / 25.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,130 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	29,460 / 2.67%
Duplication rate	3.04%
Clipped reads	389,318 / 35.3%

2.2. ACGT Content

Number/percentage of A's	15,007,398 / 27.82%
Number/percentage of C's	9,373,086 / 17.37%
Number/percentage of T's	17,804,356 / 33%
Number/percentage of G's	11,756,241 / 21.79%
Number/percentage of N's	11,217 / 0.02%
GC Percentage	39.16%

2.3. Coverage

Mean	0.0174

Standard Deviation	0.1826

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

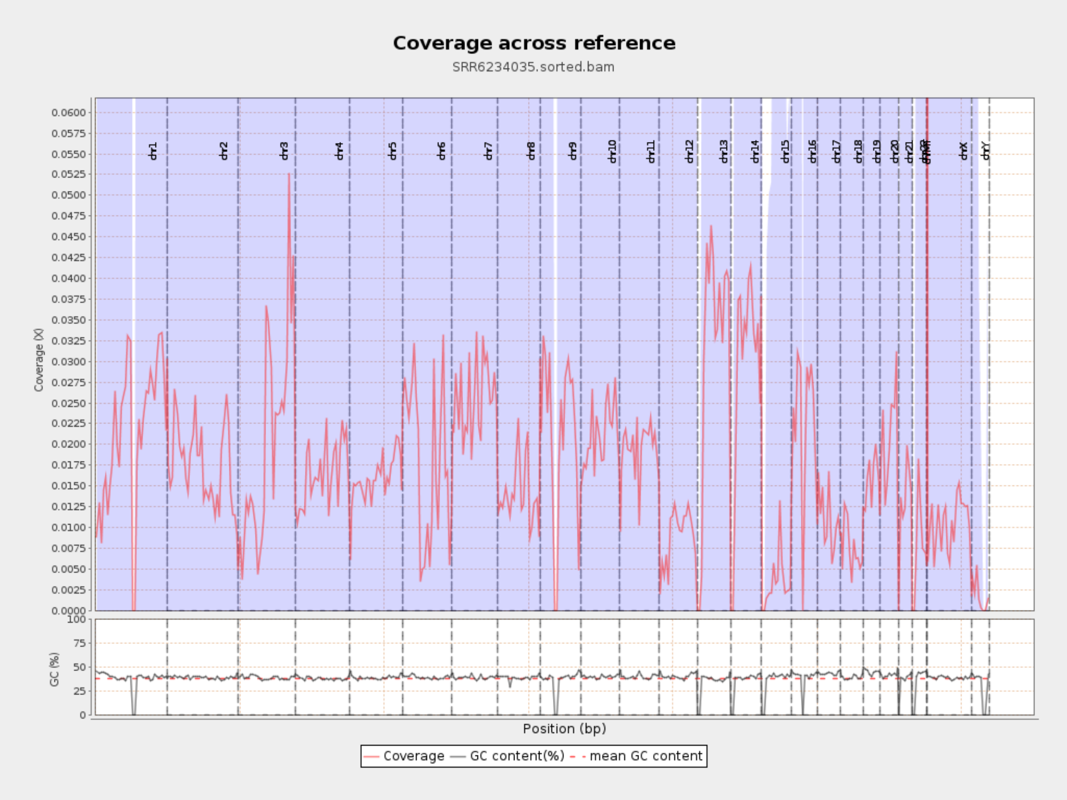
General error rate	0.83%
Mismatches	439,190
Insertions	4,379
Mapped reads with at least one insertion	0.53%
Deletions	16,953
Mapped reads with at least one deletion	2.03%
Homopolymer indels	45.17%

2.6. Chromosome stats

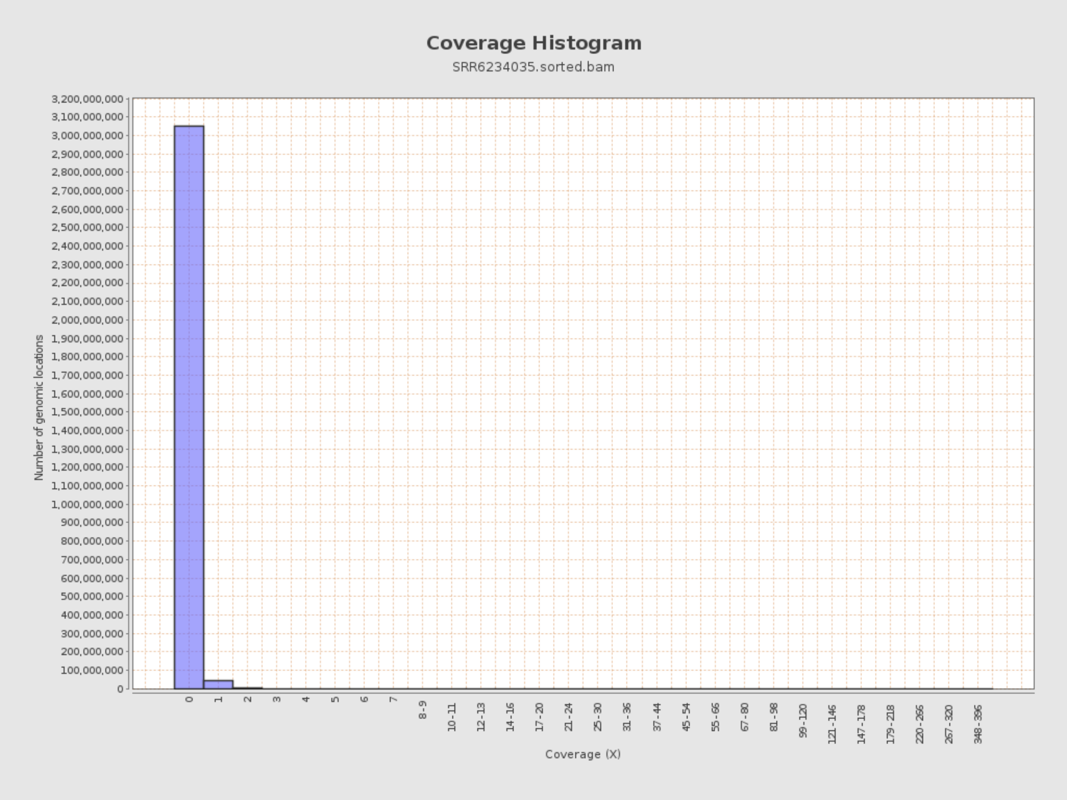
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5277947	0.0212	0.2485
chr2	243199373	4253378	0.0175	0.2009
chr3	198022430	4009960	0.0203	0.161
chr4	191154276	3155114	0.0165	0.1464
chr5	180915260	2910006	0.0161	0.1421
chr6	171115067	3053498	0.0178	0.1598
chr7	159138663	4075174	0.0256	0.2448

chr8	146364022	2054760	0.014	0.2691
chr9	141213431	2955040	0.0209	0.1794
chr10	135534747	2850813	0.021	0.1842
chr11	135006516	2638737	0.0195	0.1751
chr12	133851895	1161583	0.0087	0.1052
chr13	115169878	3654760	0.0317	0.201
chr14	107349540	3084439	0.0287	0.1941
chr15	102531392	348548	0.0034	0.0675
chr16	90354753	1994874	0.0221	0.1725
chr17	81195210	892067	0.011	0.12
chr18	78077248	572666	0.0073	0.2563
chr19	59128983	928159	0.0157	0.193
chr20	63025520	1317869	0.0209	0.163
chr21	48129895	634345	0.0132	0.1308
chr22	51304566	419177	0.0082	0.0993
chrMT	16571	25504	1.5391	1.8873
chrX	155270560	1609897	0.0104	0.1172
chrY	59373566	103544	0.0017	0.0512

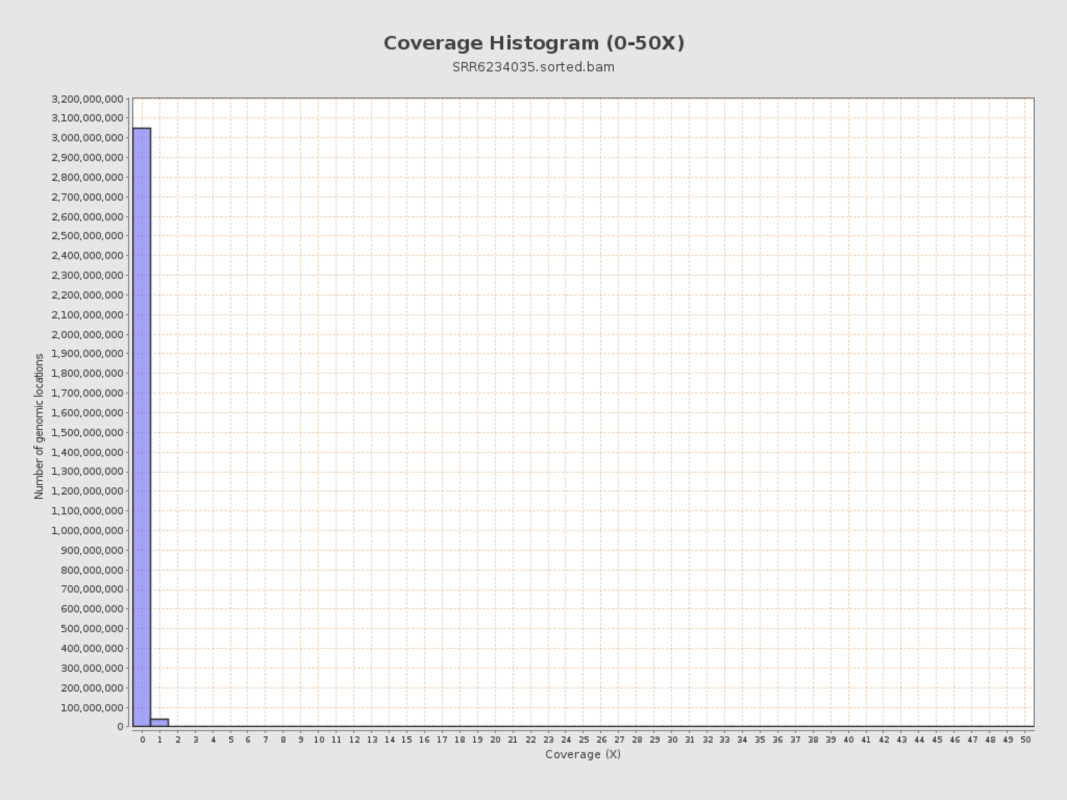
3. Results : Coverage across reference



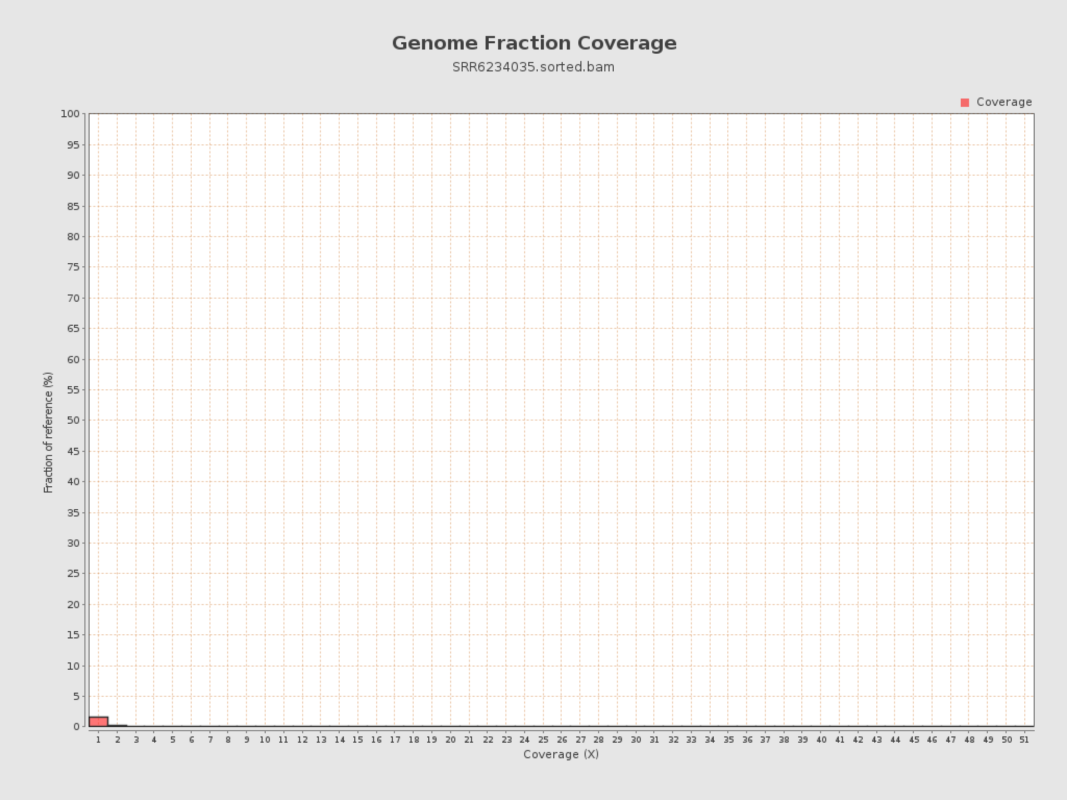
4. Results : Coverage Histogram



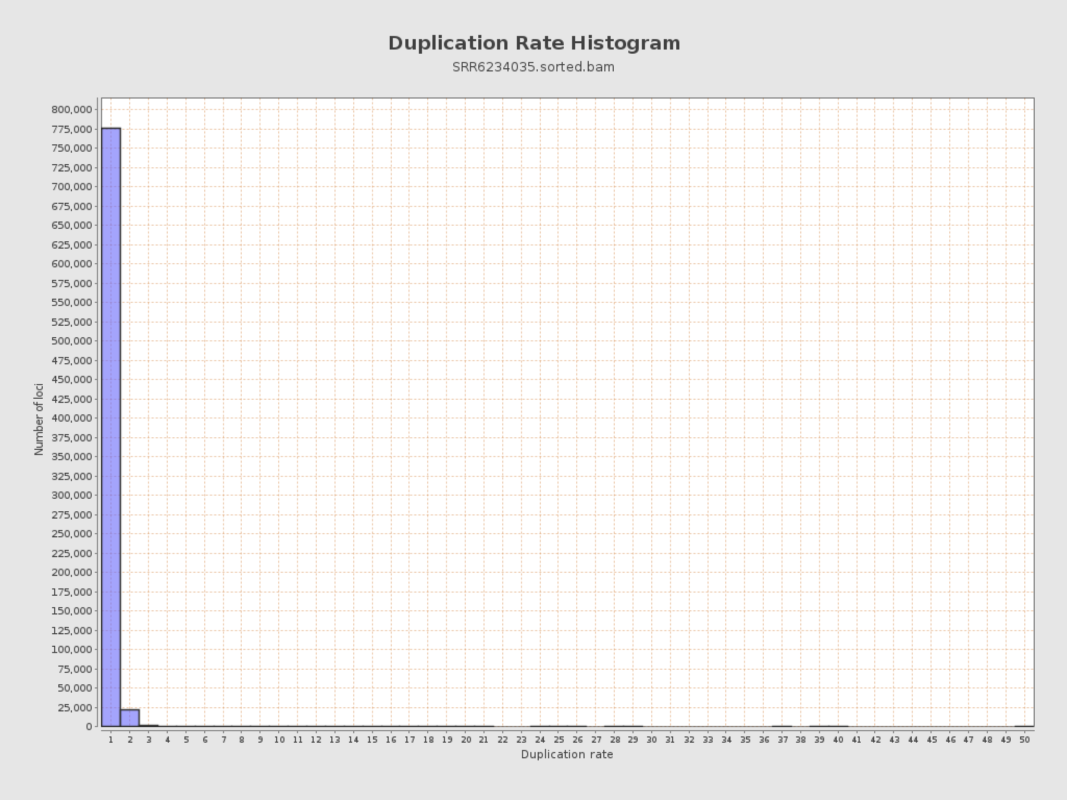
5. Results : Coverage Histogram (0-50X)



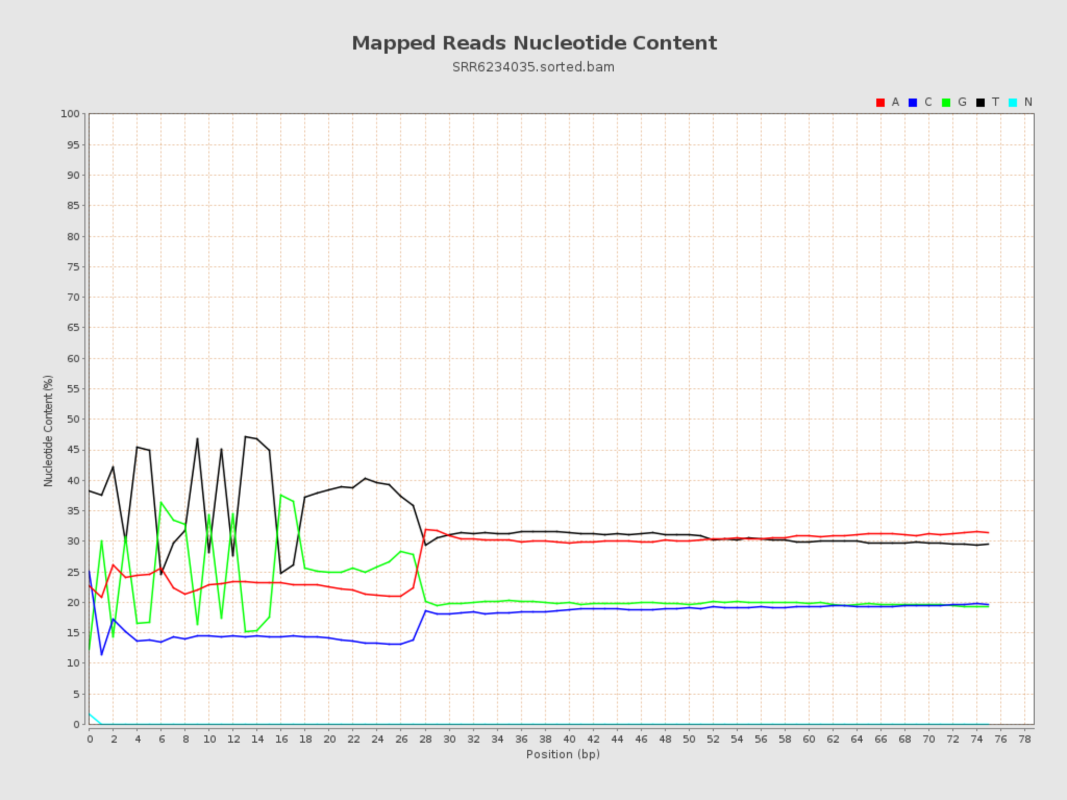
6. Results : Genome Fraction Coverage



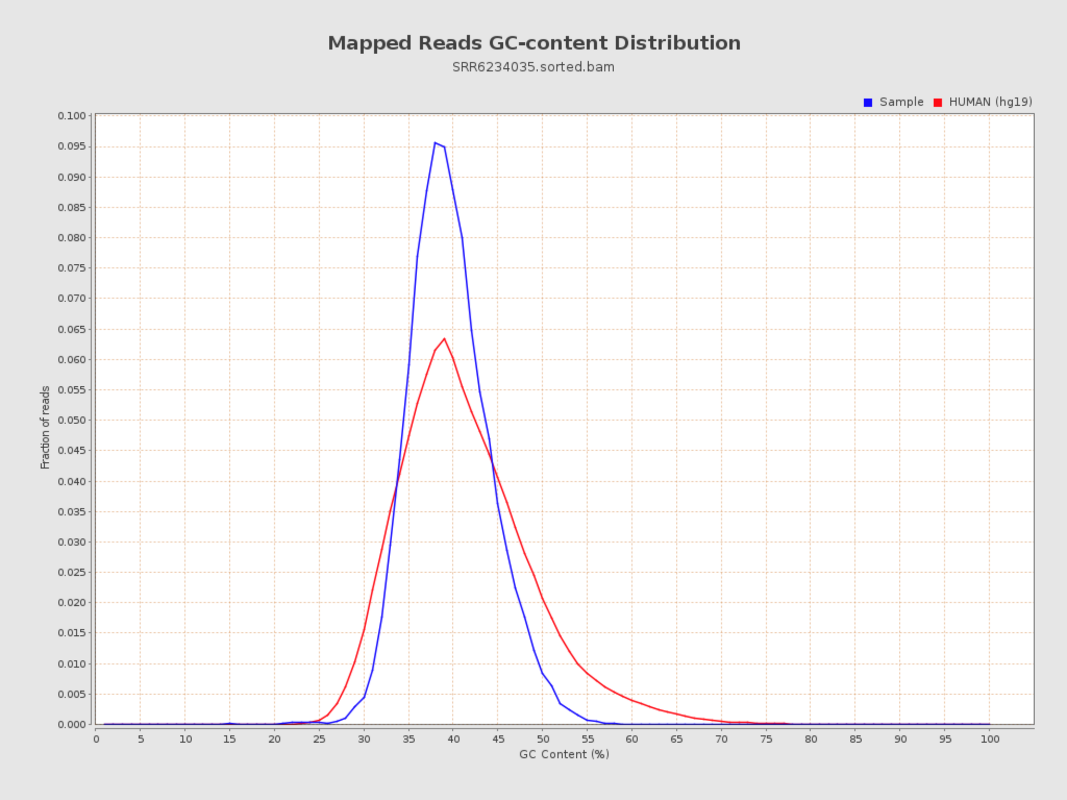
7. Results : Duplication Rate Histogram



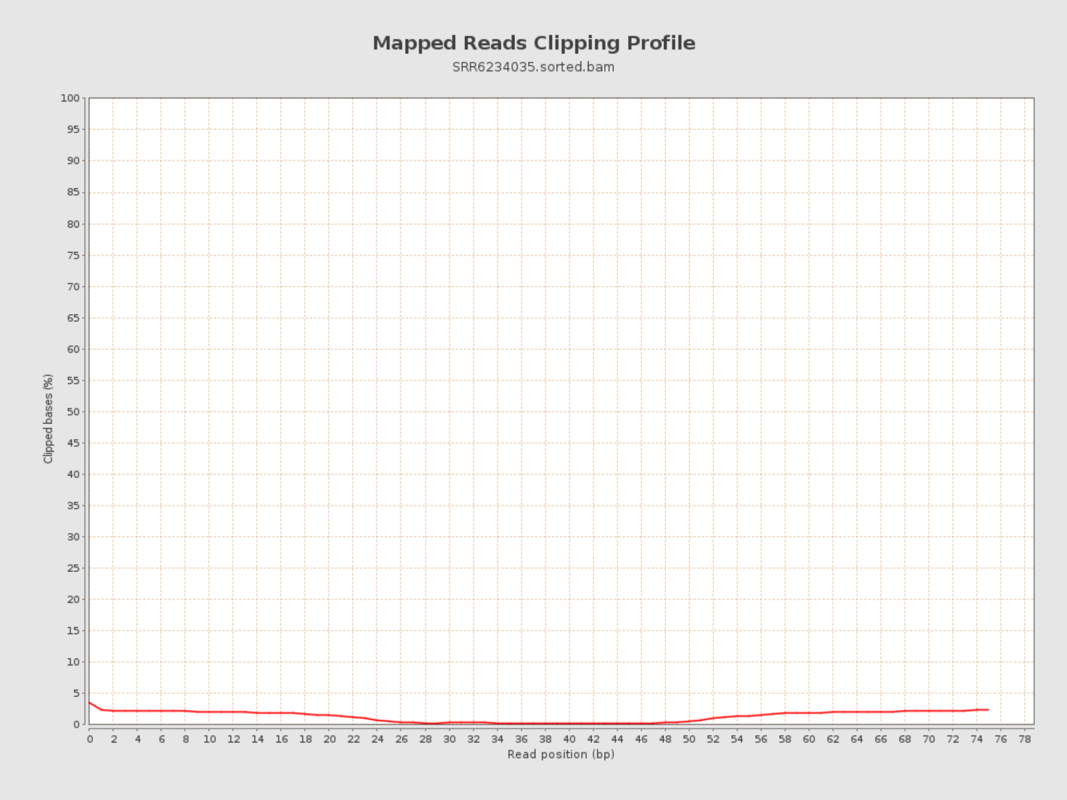
8. Results : Mapped Reads Nucleotide Content



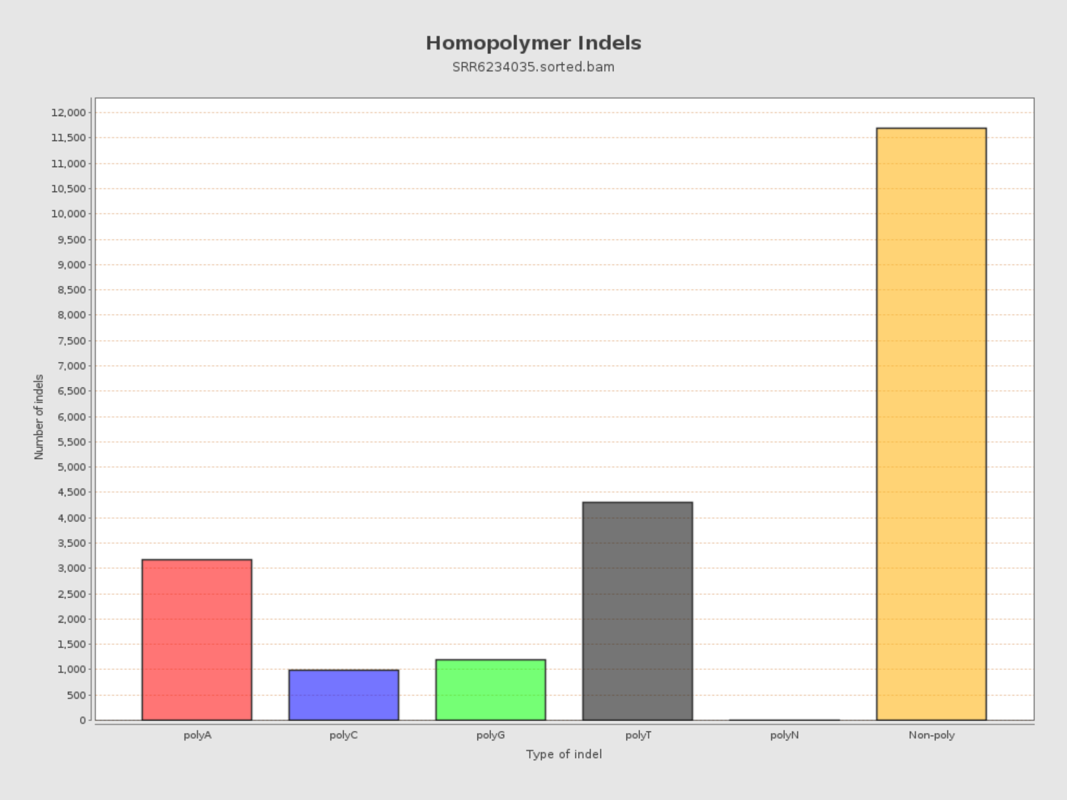
9. Results : Mapped Reads GC-content Distribution



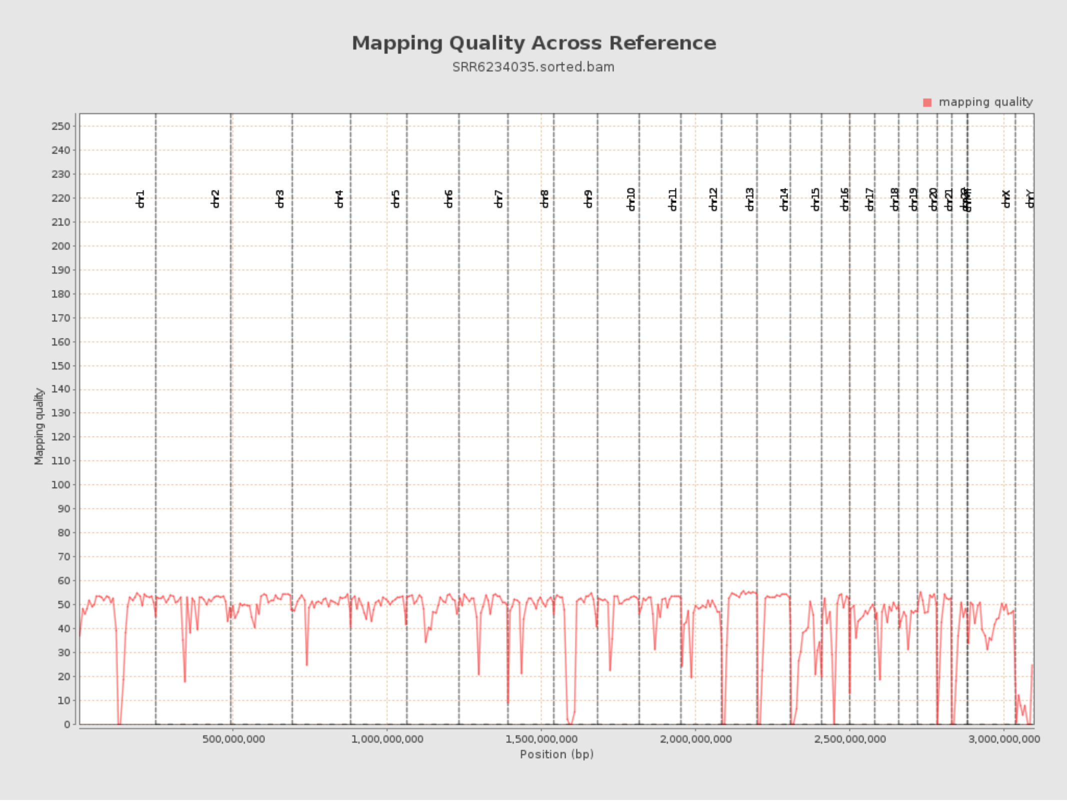
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram