Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:53:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234023.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_SRR6234023 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234023.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:53:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234023.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,092,471
Mapped reads	876,979 / 80.27%
Unmapped reads	215,492 / 19.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,295 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	21,462 / 1.96%
Duplication rate	1.93%
Clipped reads	411,732 / 37.69%

2.2. ACGT Content

Number/percentage of A's	16,183,920 / 28.17%
Number/percentage of C's	9,917,661 / 17.26%
Number/percentage of T's	18,548,974 / 32.28%
Number/percentage of G's	12,799,956 / 22.28%
Number/percentage of N's	10,445 / 0.02%
GC Percentage	39.54%

2.3. Coverage

Mean	0.0186

Standard Deviation	0.1881

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

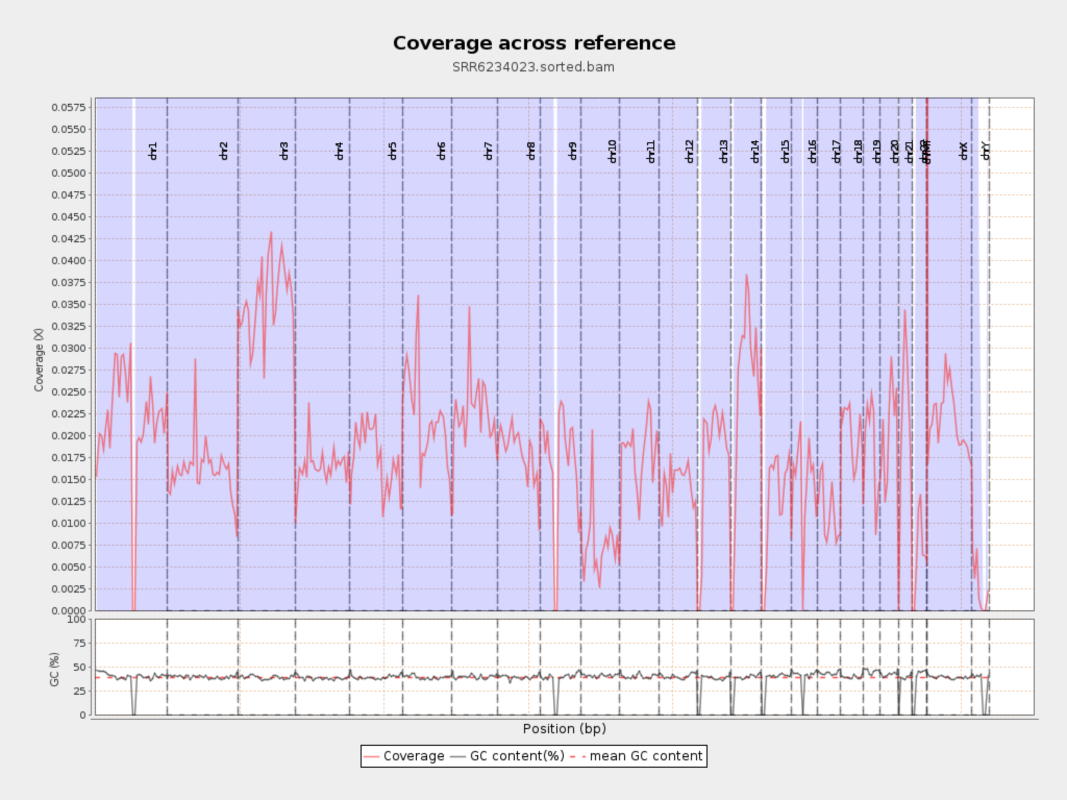
General error rate	0.82%
Mismatches	460,160
Insertions	4,436
Mapped reads with at least one insertion	0.5%
Deletions	16,048
Mapped reads with at least one deletion	1.81%
Homopolymer indels	45.93%

2.6. Chromosome stats

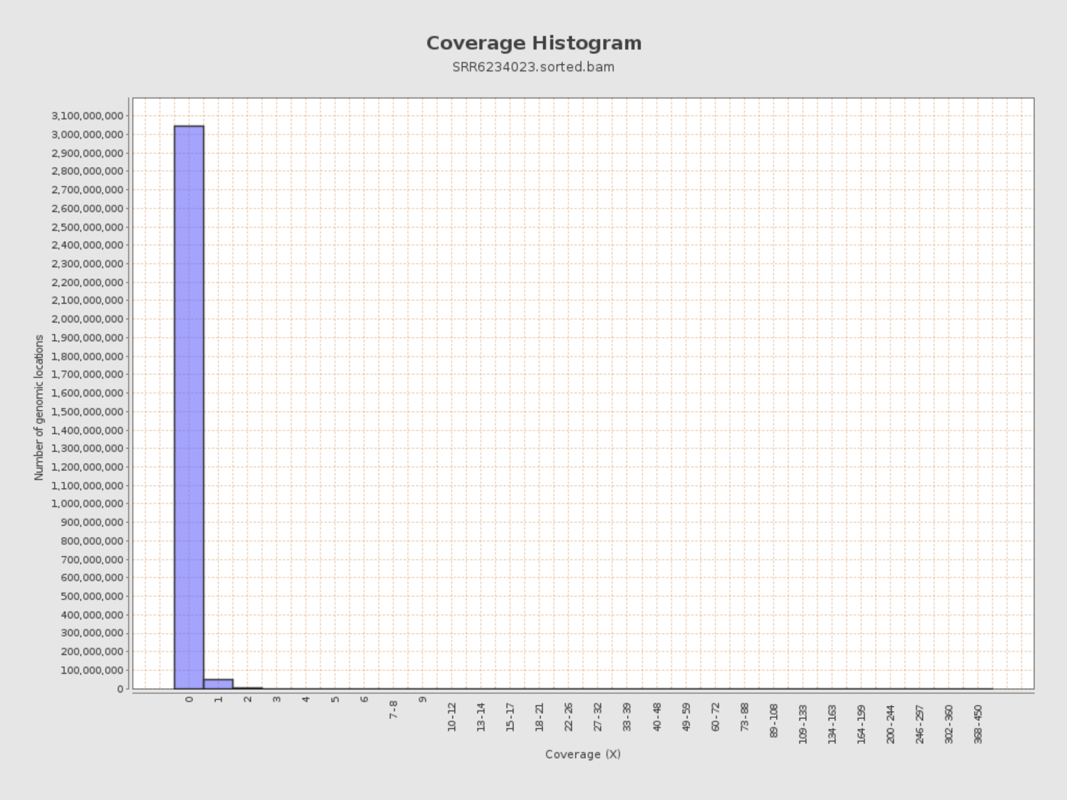
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5348020	0.0215	0.266
chr2	243199373	3883981	0.016	0.1954
chr3	198022430	7047408	0.0356	0.2005
chr4	191154276	3148255	0.0165	0.1392
chr5	180915260	3173346	0.0175	0.1404
chr6	171115067	3795357	0.0222	0.1777
chr7	159138663	3615747	0.0227	0.2563

chr8	146364022	2648244	0.0181	0.3103
chr9	141213431	2382111	0.0169	0.1694
chr10	135534747	1031430	0.0076	0.1402
chr11	135006516	2431365	0.018	0.1605
chr12	133851895	1902105	0.0142	0.1295
chr13	115169878	1980504	0.0172	0.1392
chr14	107349540	2681659	0.025	0.1726
chr15	102531392	1291555	0.0126	0.1194
chr16	90354753	1286288	0.0142	0.1357
chr17	81195210	910762	0.0112	0.116
chr18	78077248	1587217	0.0203	0.269
chr19	59128983	1119718	0.0189	0.1913
chr20	63025520	1280896	0.0203	0.1527
chr21	48129895	1048017	0.0218	0.1598
chr22	51304566	339336	0.0066	0.0849
chrMT	16571	11874	0.7166	0.959
chrX	155270560	3393280	0.0219	0.162
chrY	59373566	150602	0.0025	0.0631

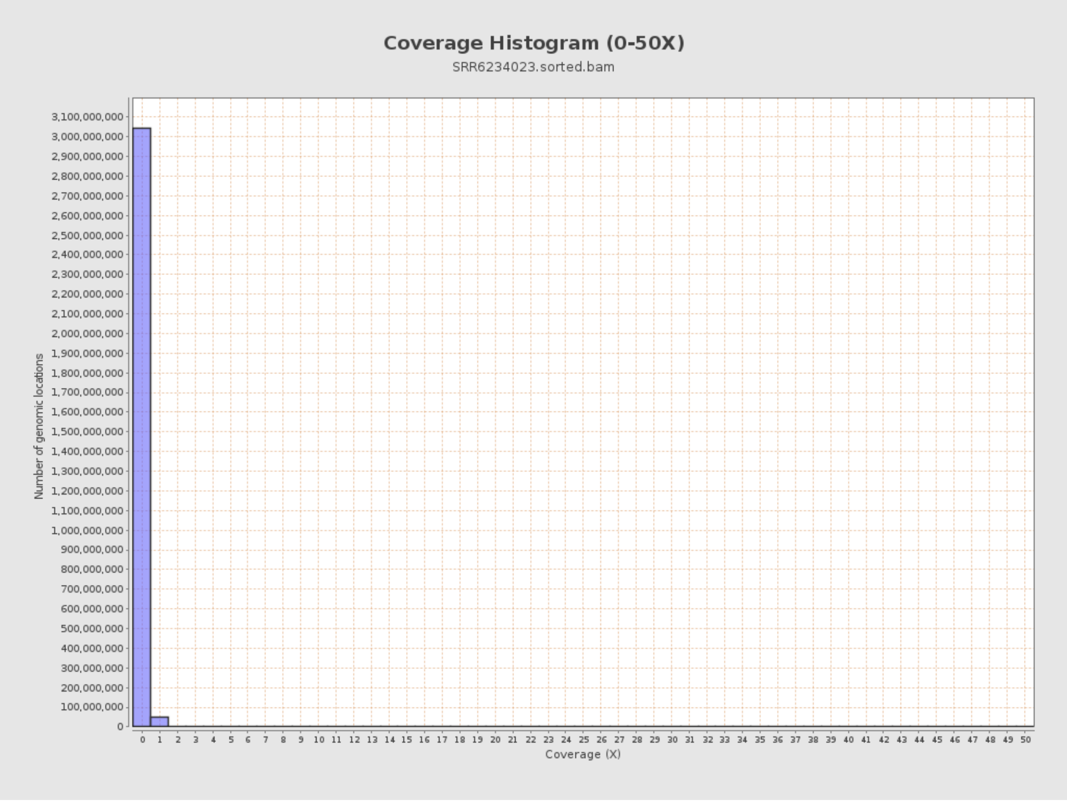
3. Results : Coverage across reference



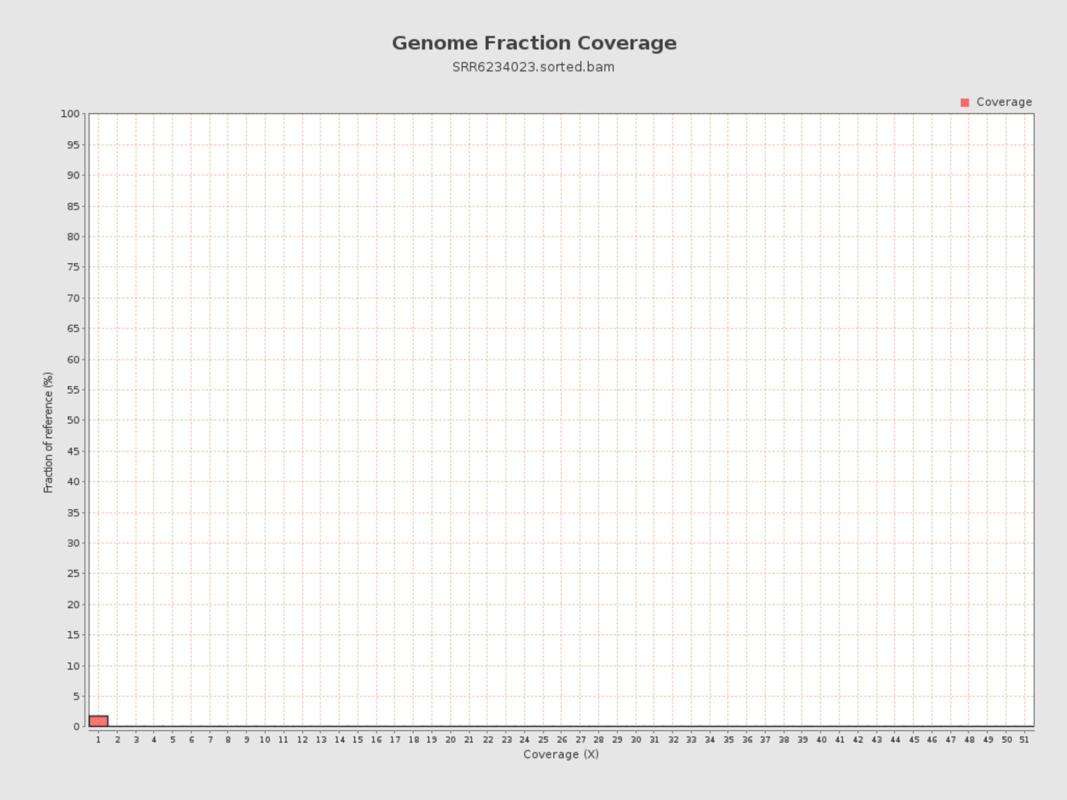
4. Results : Coverage Histogram



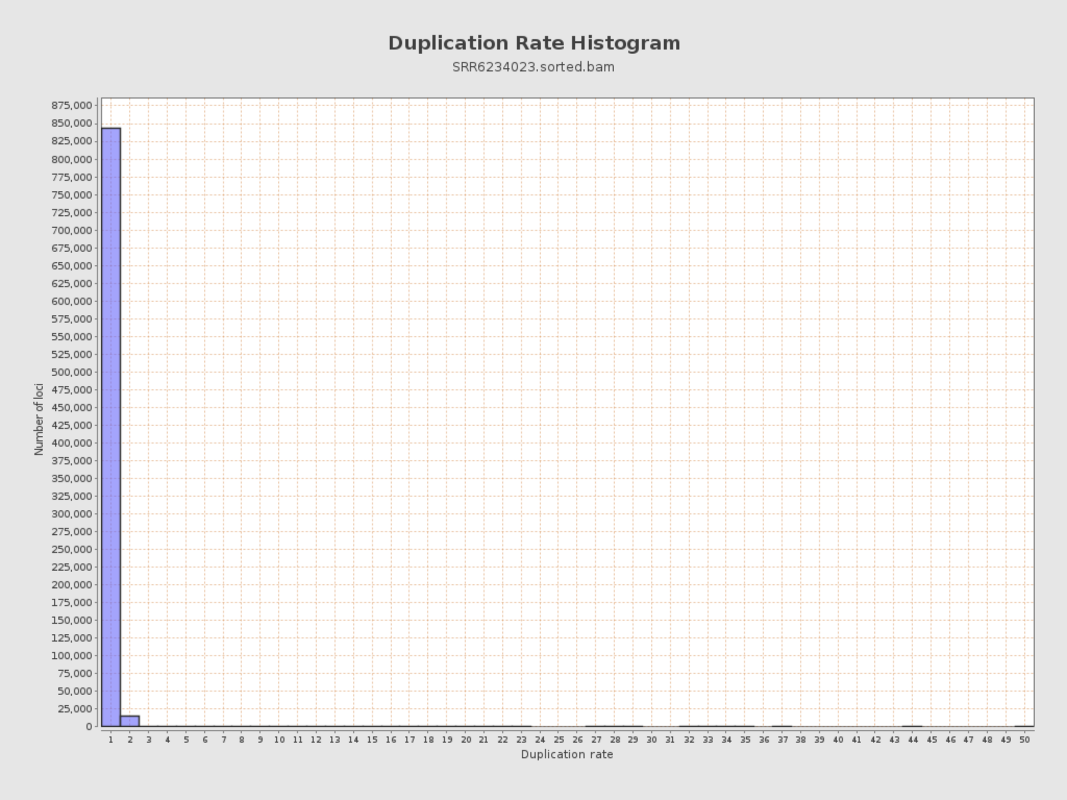
5. Results : Coverage Histogram (0-50X)



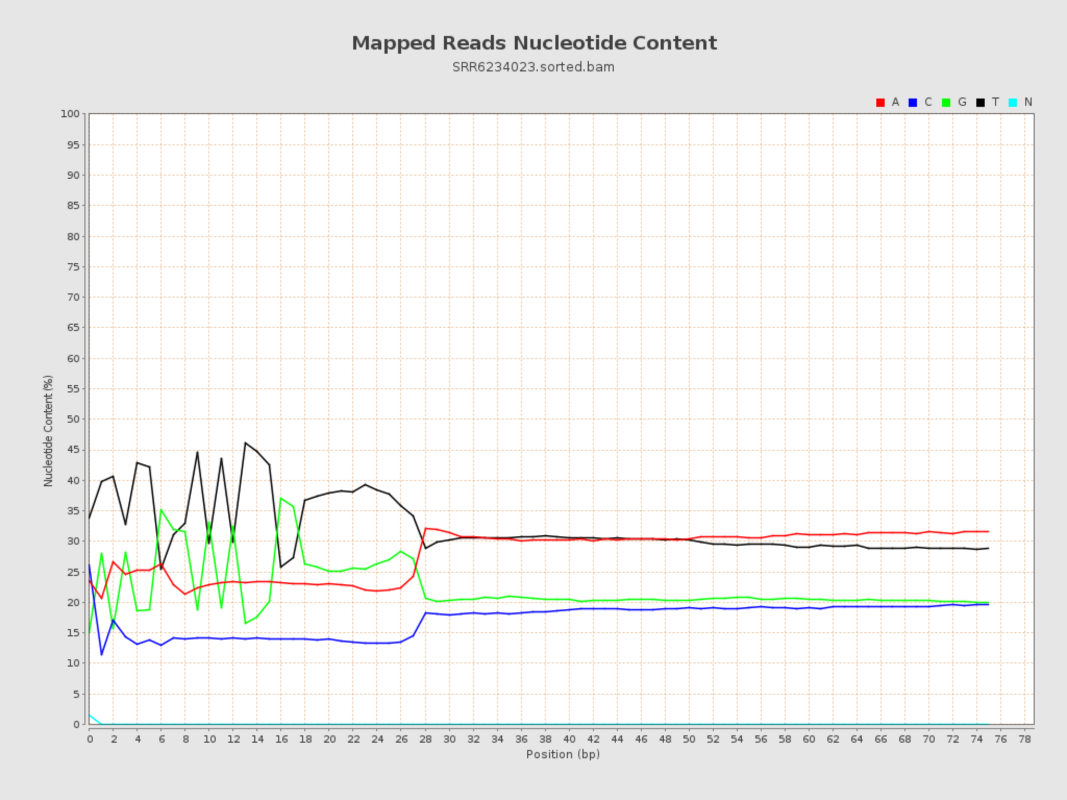
6. Results : Genome Fraction Coverage



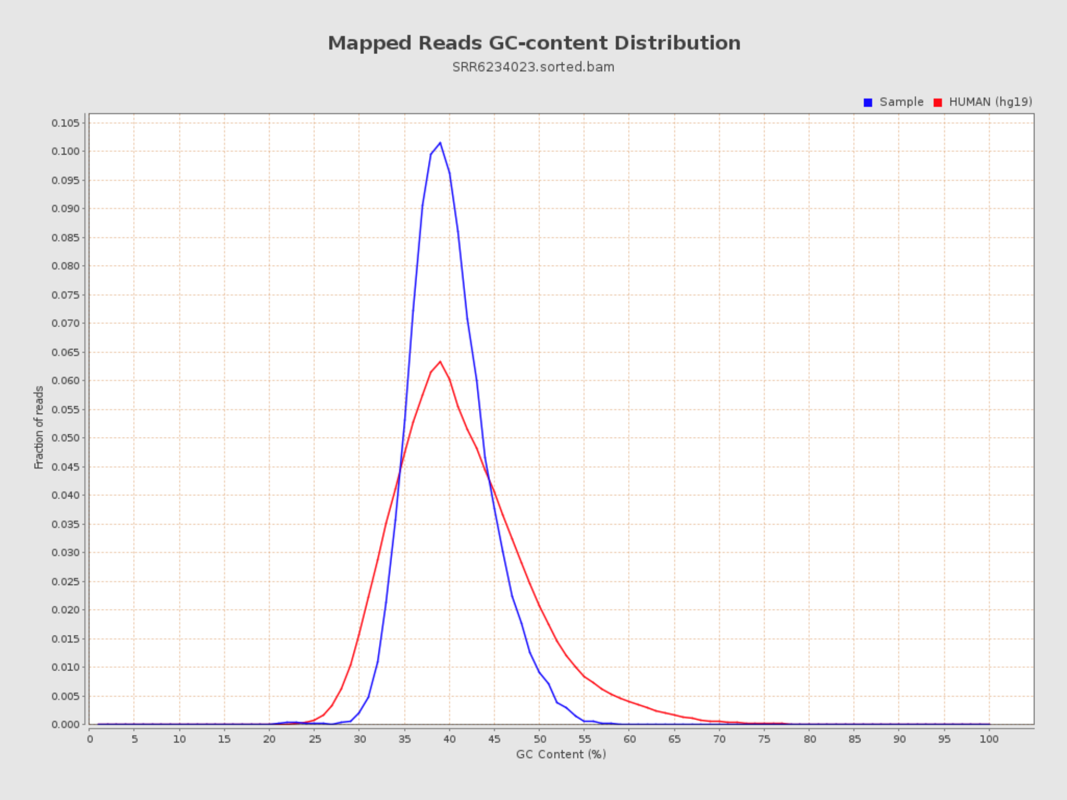
7. Results : Duplication Rate Histogram



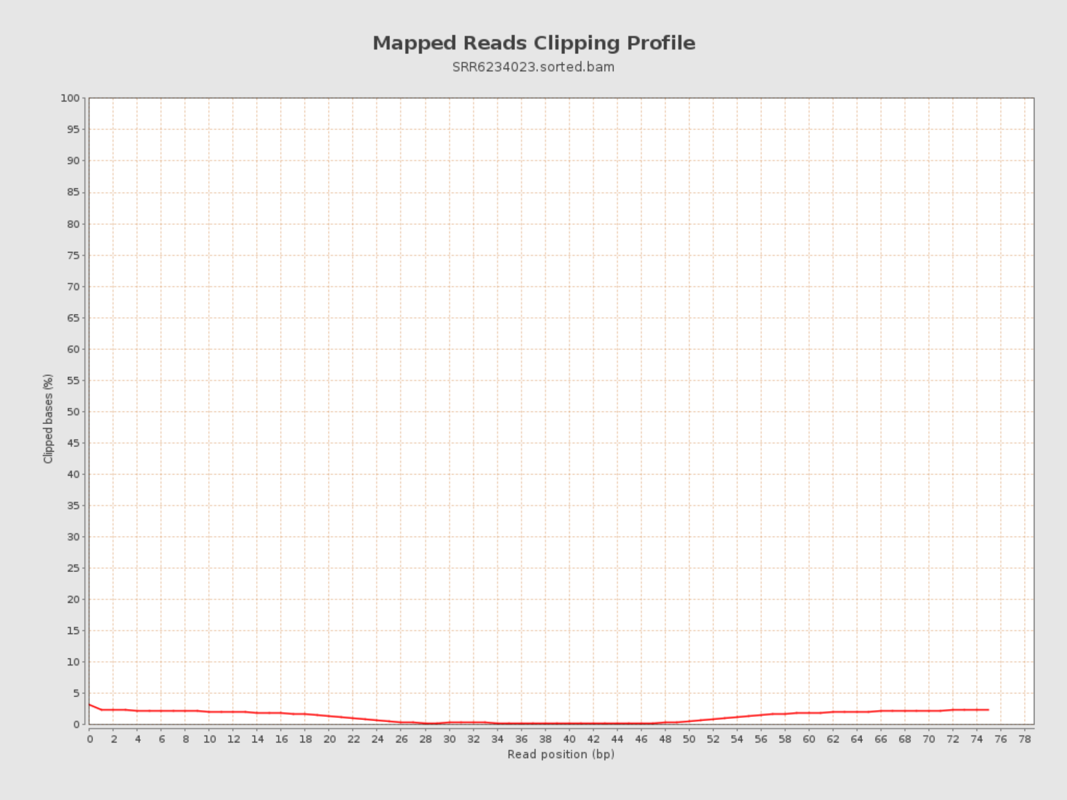
8. Results : Mapped Reads Nucleotide Content



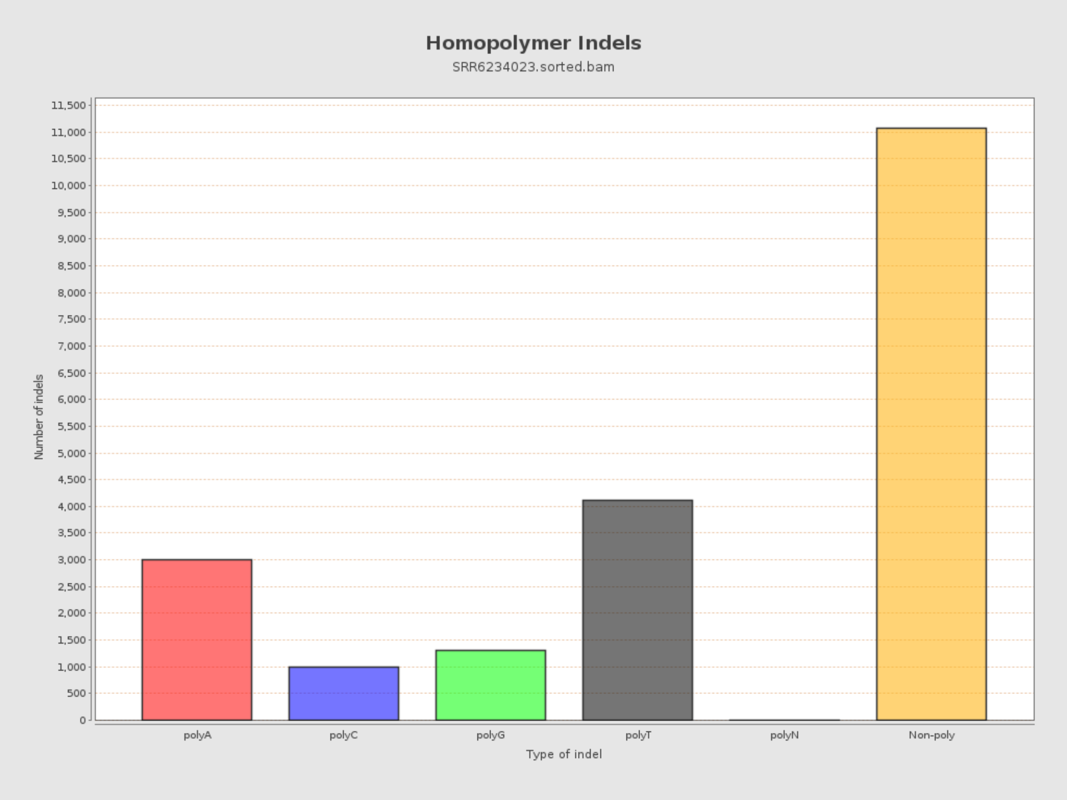
9. Results : Mapped Reads GC-content Distribution



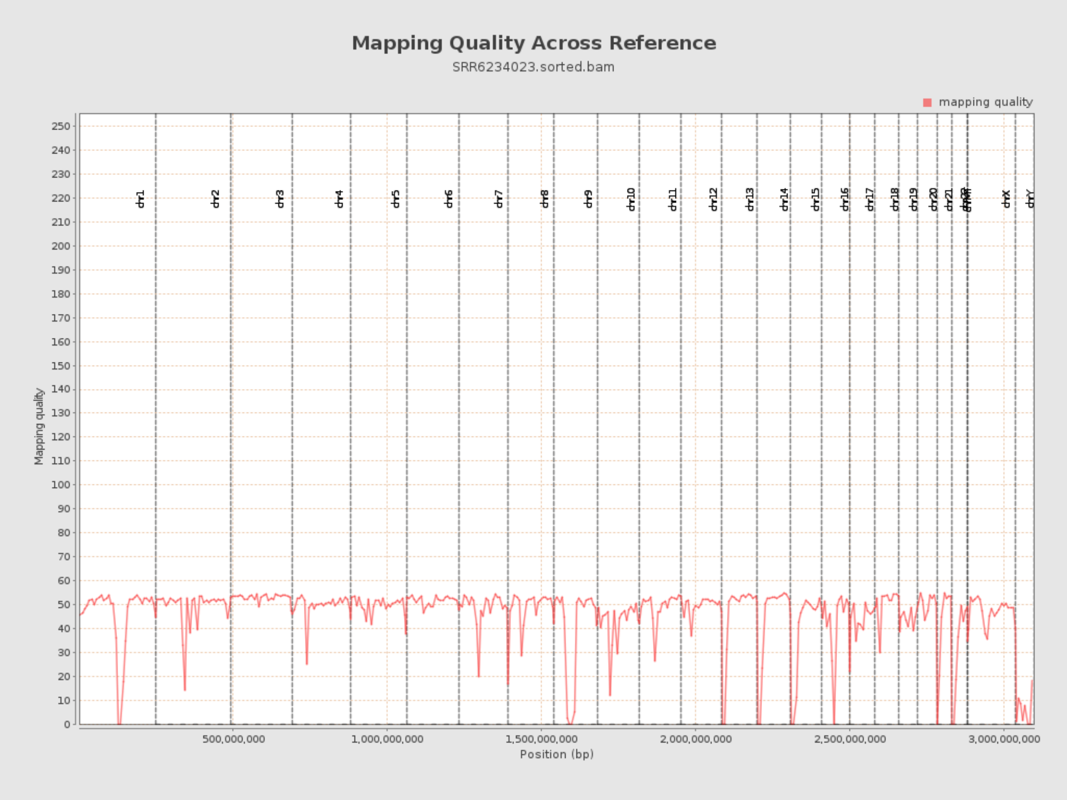
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram