Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:56:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234024.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_SRR6234024 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234024.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:56:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,545,310
Mapped reads	2,230,149 / 87.62%
Unmapped reads	315,161 / 12.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,586 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	78,061 / 3.07%
Duplication rate	2.53%
Clipped reads	909,723 / 35.74%

2.2. ACGT Content

Number/percentage of A's	41,384,894 / 27.57%
Number/percentage of C's	28,282,792 / 18.84%
Number/percentage of T's	46,927,666 / 31.26%
Number/percentage of G's	33,464,956 / 22.3%
Number/percentage of N's	38,286 / 0.03%
GC Percentage	41.14%

2.3. Coverage

Mean	0.0485

Standard Deviation	0.4966

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

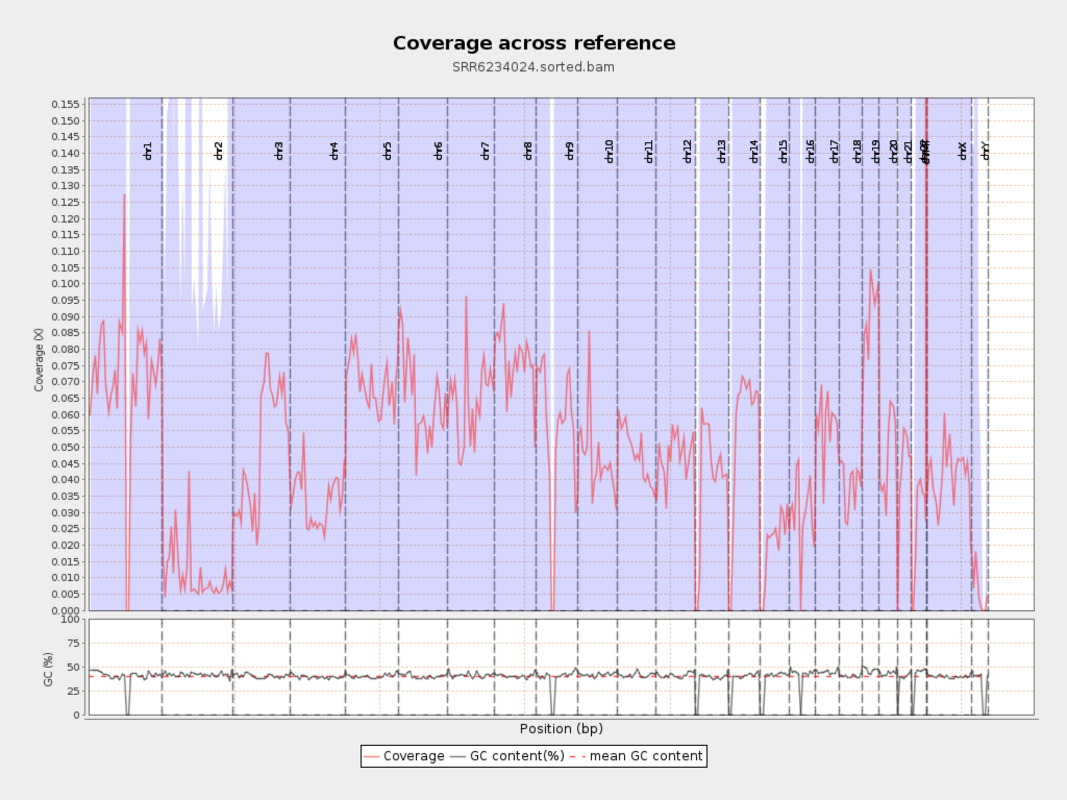
General error rate	0.77%
Mismatches	1,127,287
Insertions	11,306
Mapped reads with at least one insertion	0.5%
Deletions	43,315
Mapped reads with at least one deletion	1.92%
Homopolymer indels	46.07%

2.6. Chromosome stats

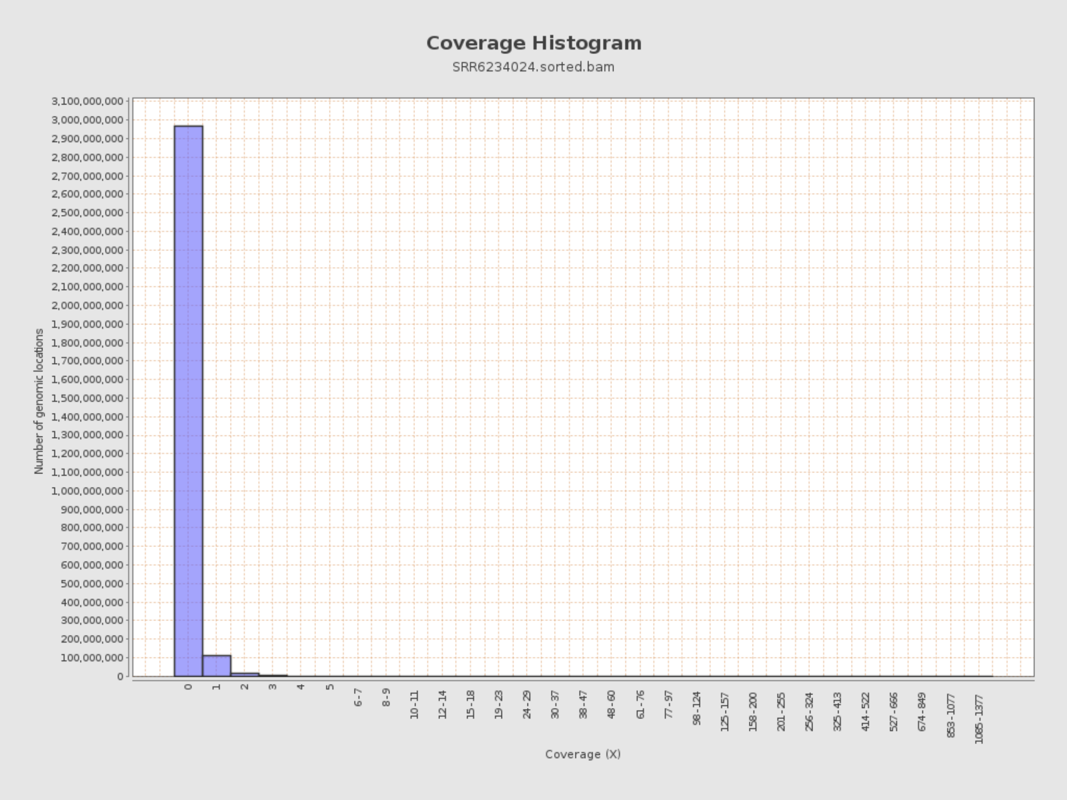
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17718274	0.0711	1.2392
chr2	243199373	2660191	0.0109	0.3927
chr3	198022430	9839886	0.0497	0.2562
chr4	191154276	6480010	0.0339	0.2291
chr5	180915260	12618930	0.0698	0.3018
chr6	171115067	11122470	0.065	0.3487
chr7	159138663	10221593	0.0642	0.6598

chr8	146364022	11244276	0.0768	0.4597
chr9	141213431	7693929	0.0545	0.3324
chr10	135534747	6306976	0.0465	0.4419
chr11	135006516	6447308	0.0478	0.3713
chr12	133851895	6302303	0.0471	0.248
chr13	115169878	4588098	0.0398	0.2265
chr14	107349540	5922729	0.0552	0.2827
chr15	102531392	2091628	0.0204	0.1642
chr16	90354753	2692237	0.0298	0.2279
chr17	81195210	4623837	0.0569	0.3126
chr18	78077248	3010442	0.0386	0.5886
chr19	59128983	5368049	0.0908	0.7687
chr20	63025520	2986834	0.0474	0.2584
chr21	48129895	2065285	0.0429	0.2538
chr22	51304566	1322123	0.0258	0.1803
chrMT	16571	47085	2.8414	2.3568
chrX	155270560	6462302	0.0416	0.2599
chrY	59373566	338971	0.0057	0.1291

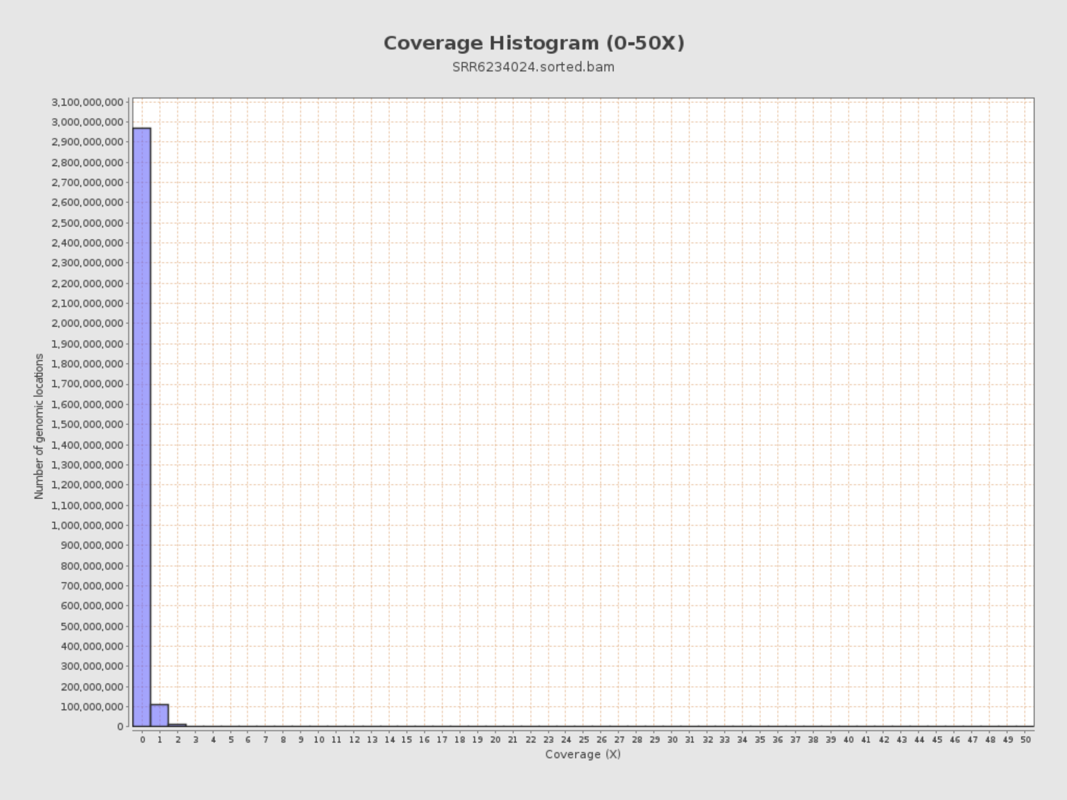
3. Results : Coverage across reference



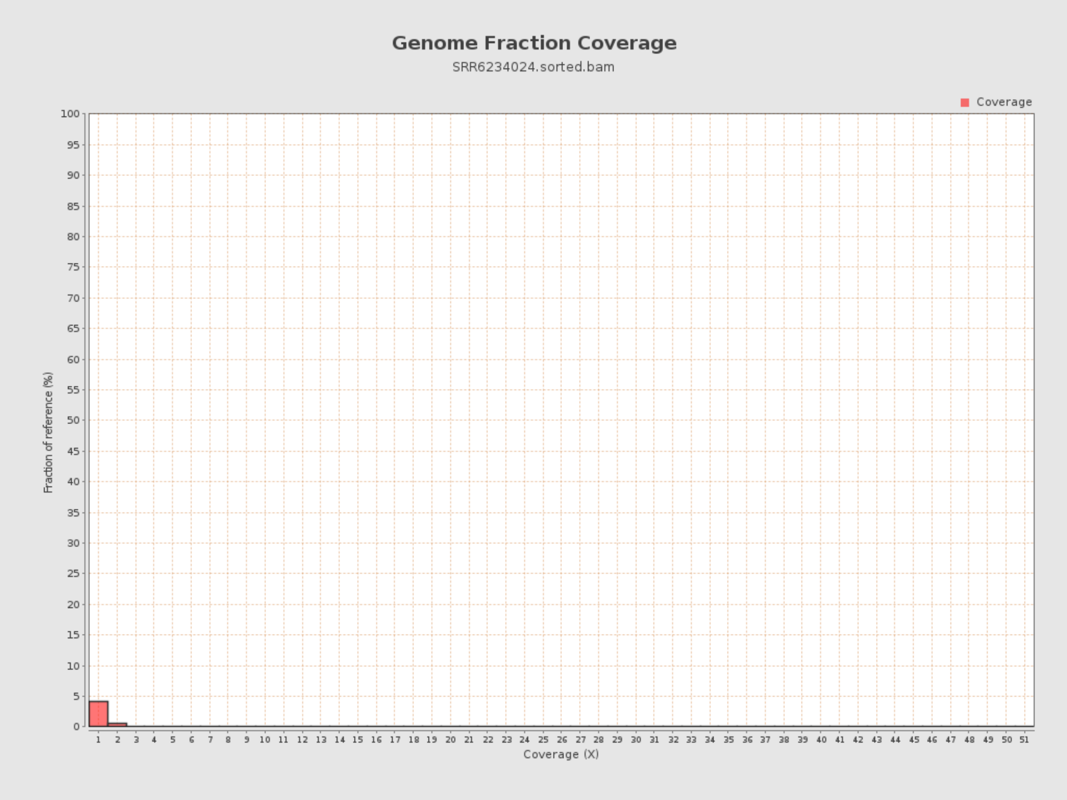
4. Results : Coverage Histogram



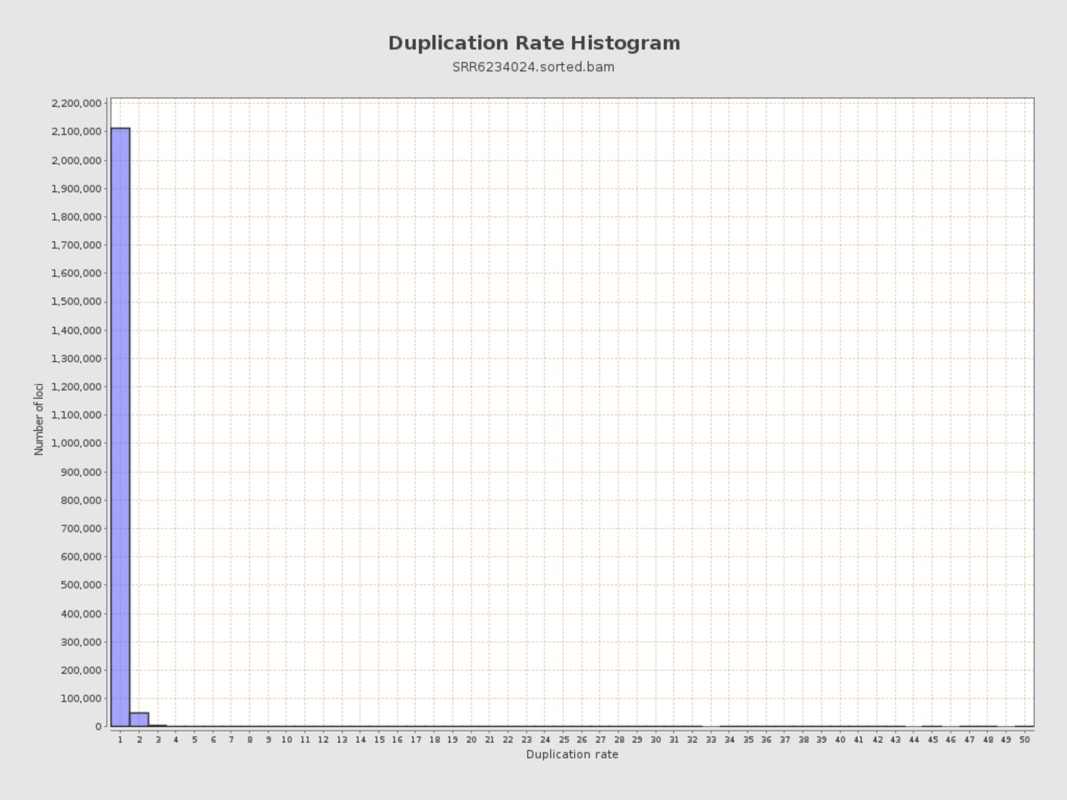
5. Results : Coverage Histogram (0-50X)



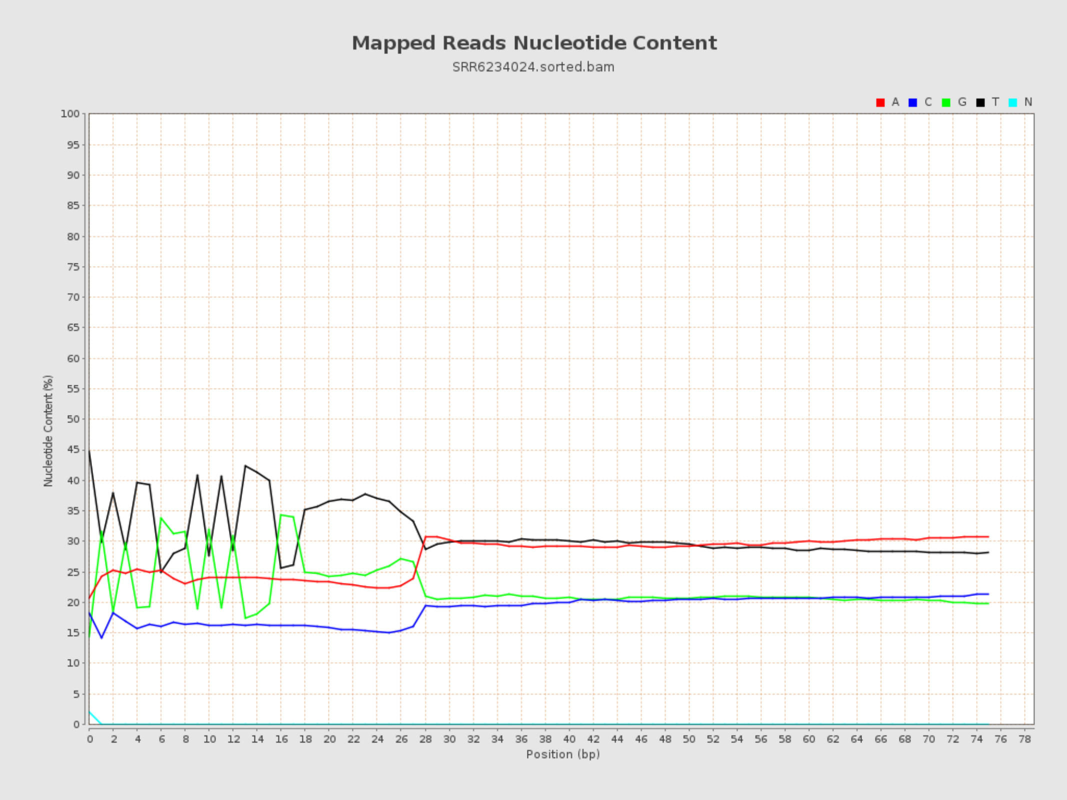
6. Results : Genome Fraction Coverage



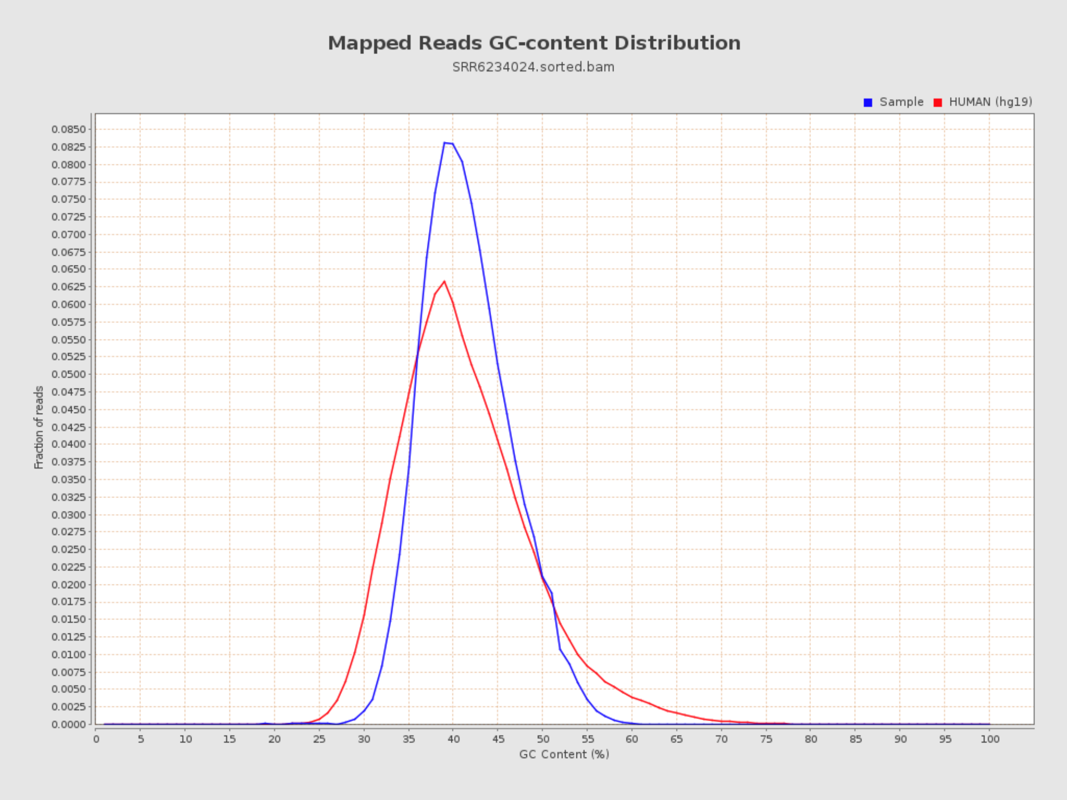
7. Results : Duplication Rate Histogram



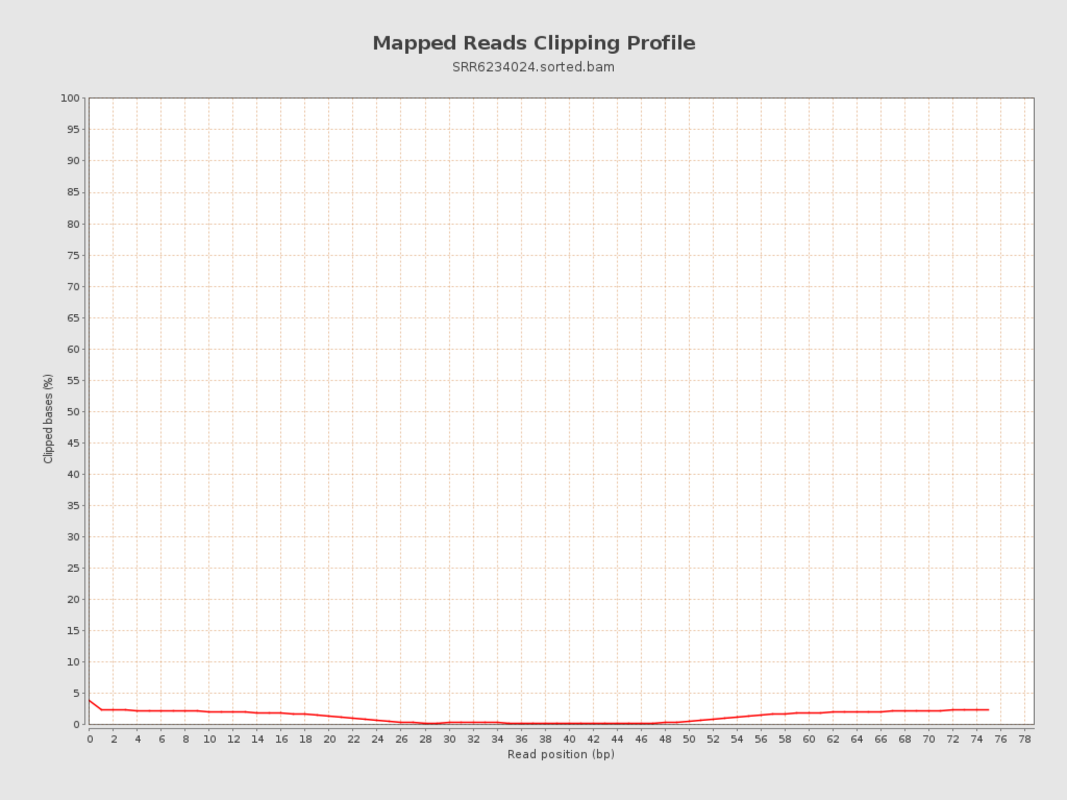
8. Results : Mapped Reads Nucleotide Content



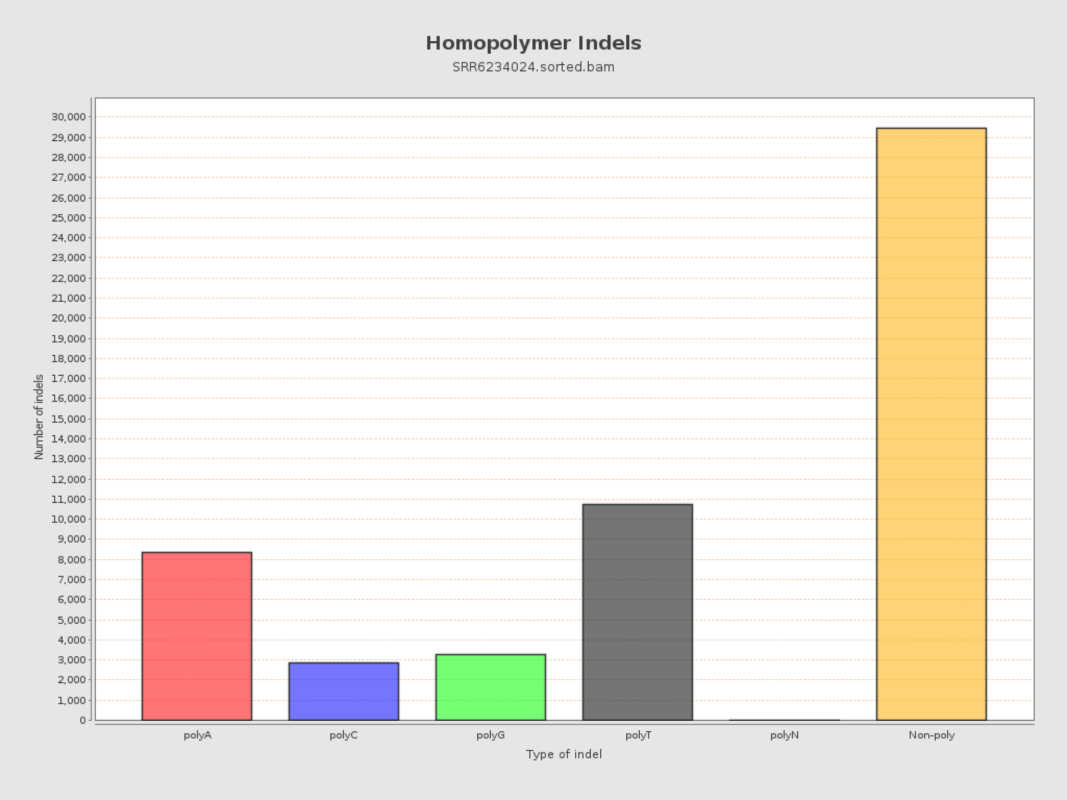
9. Results : Mapped Reads GC-content Distribution



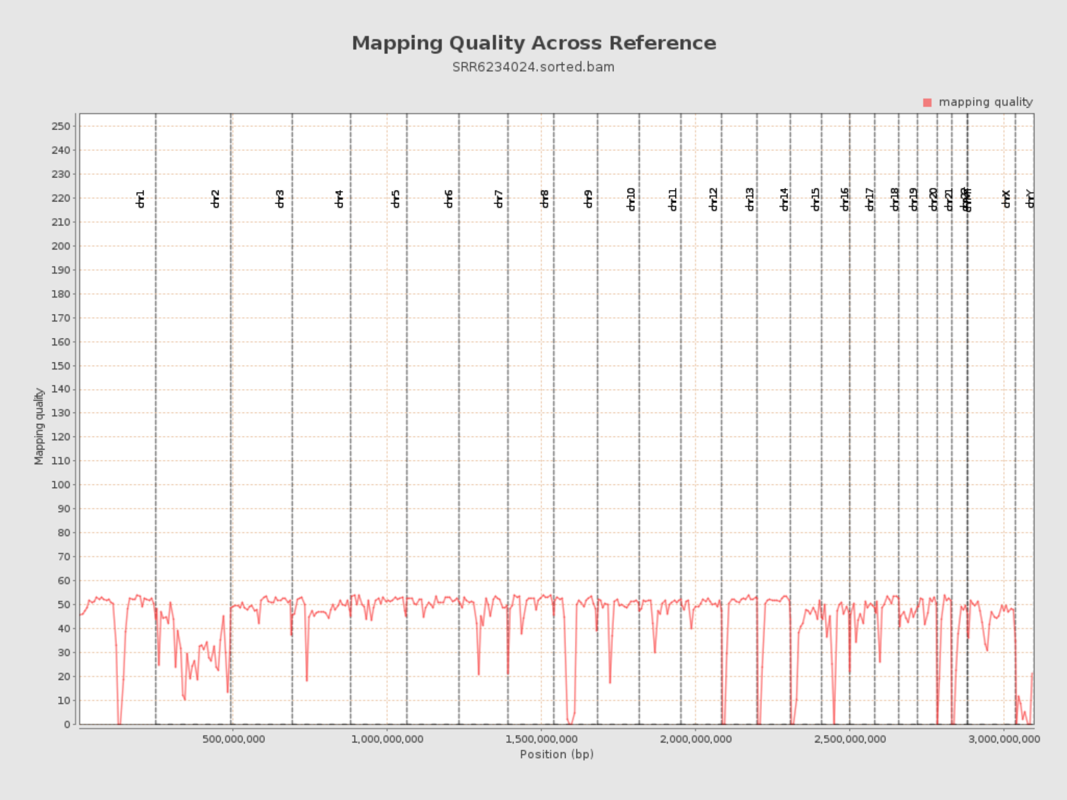
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram