Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 16:49:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234110.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_SRR6234110 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234110.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 16:49:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234110.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,435,760
Mapped reads	5,087,557 / 93.59%
Unmapped reads	348,203 / 6.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,695 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	399,929 / 7.36%
Duplication rate	3.04%
Clipped reads	1,947,384 / 35.83%

2.2. ACGT Content

Number/percentage of A's	92,312,583 / 26.58%
Number/percentage of C's	66,110,113 / 19.04%
Number/percentage of T's	99,427,370 / 28.63%
Number/percentage of G's	89,321,827 / 25.72%
Number/percentage of N's	78,079 / 0.02%
GC Percentage	44.76%

2.3. Coverage

Mean	0.1122

Standard Deviation	25.4432

2.4. Mapping Quality

Mean Mapping Quality	43.66

2.5. Mismatches and indels

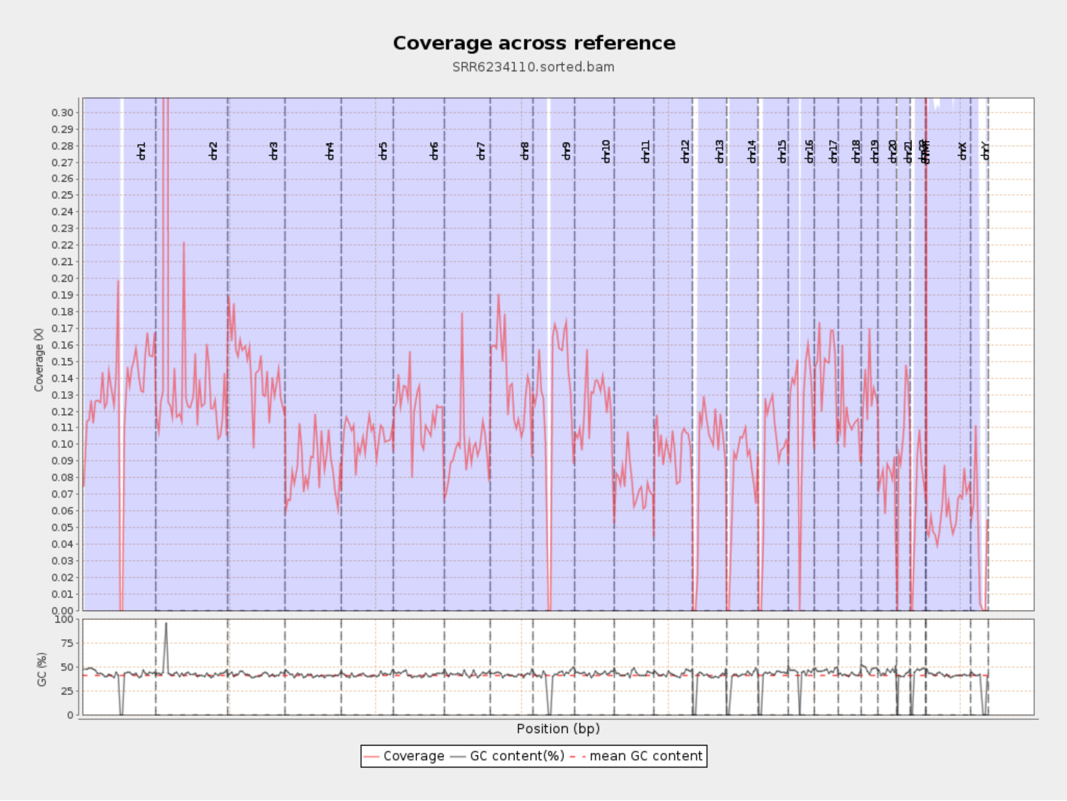
General error rate	0.69%
Mismatches	2,347,840
Insertions	25,797
Mapped reads with at least one insertion	0.5%
Deletions	79,100
Mapped reads with at least one deletion	1.54%
Homopolymer indels	46.35%

2.6. Chromosome stats

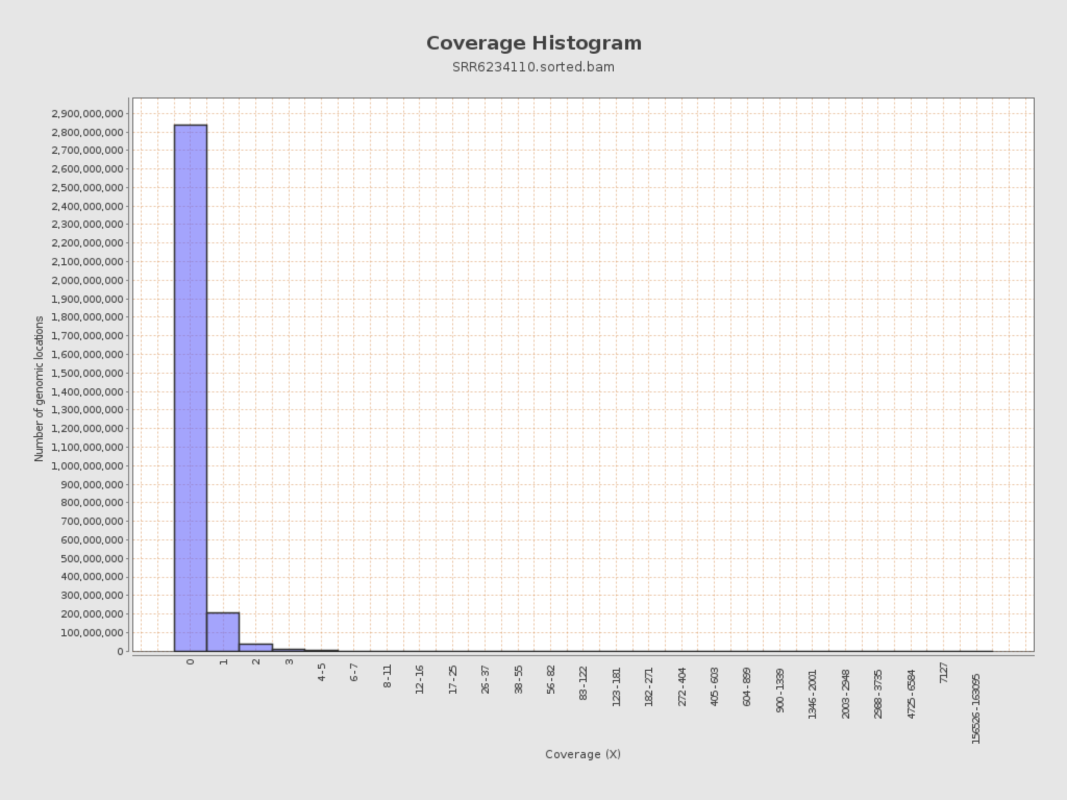
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31976448	0.1283	1.9117
chr2	243199373	44172361	0.1816	90.7155
chr3	198022430	28701961	0.1449	0.4784
chr4	191154276	16487897	0.0863	0.4378
chr5	180915260	18867415	0.1043	0.4224
chr6	171115067	20541365	0.12	0.5747
chr7	159138663	15537099	0.0976	1.3565

chr8	146364022	20113870	0.1374	1.0822
chr9	141213431	18045143	0.1278	1.111
chr10	135534747	16578933	0.1223	0.7412
chr11	135006516	10194426	0.0755	0.8444
chr12	133851895	13225940	0.0988	0.4403
chr13	115169878	10565335	0.0917	0.3738
chr14	107349540	8405165	0.0783	0.7084
chr15	102531392	9134642	0.0891	0.3781
chr16	90354753	10750649	0.119	0.605
chr17	81195210	12229478	0.1506	0.6075
chr18	78077248	9002892	0.1153	2.2789
chr19	59128983	7776954	0.1315	1.3667
chr20	63025520	4935352	0.0783	0.387
chr21	48129895	4992004	0.1037	0.5961
chr22	51304566	3277519	0.0639	0.3893
chrMT	16571	8464	0.5108	0.8533
chrX	155270560	9309937	0.06	0.4659
chrY	59373566	2548748	0.0429	0.3796

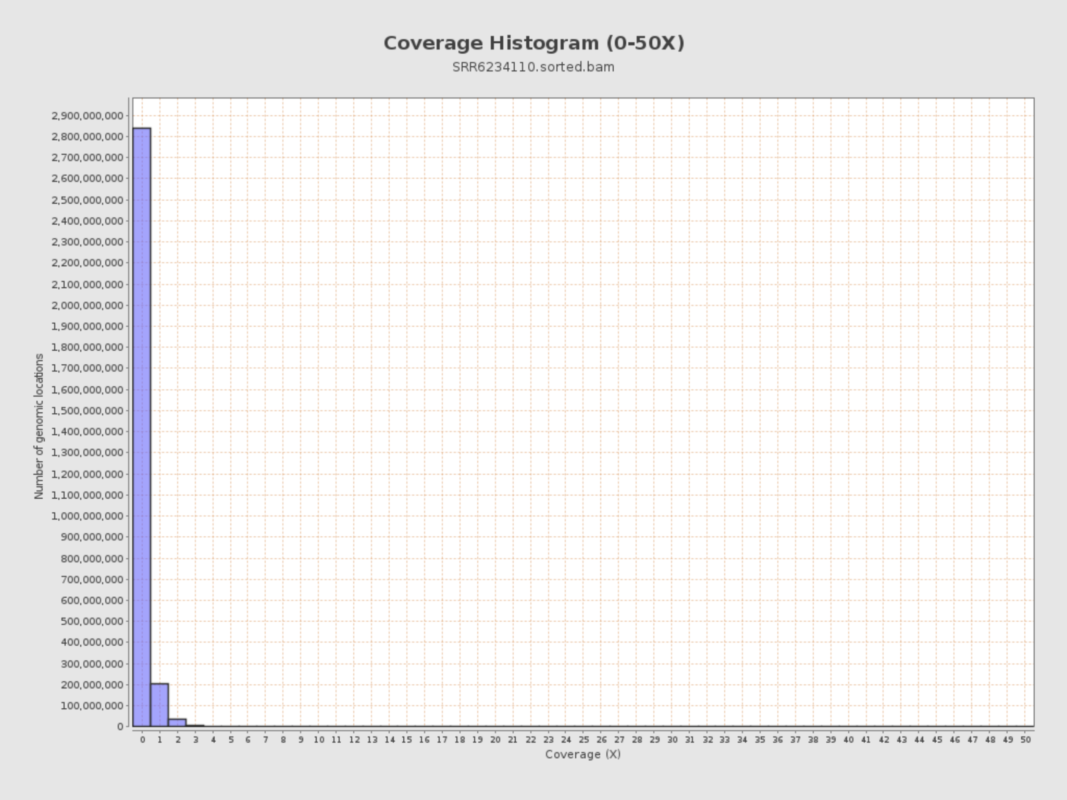
3. Results : Coverage across reference



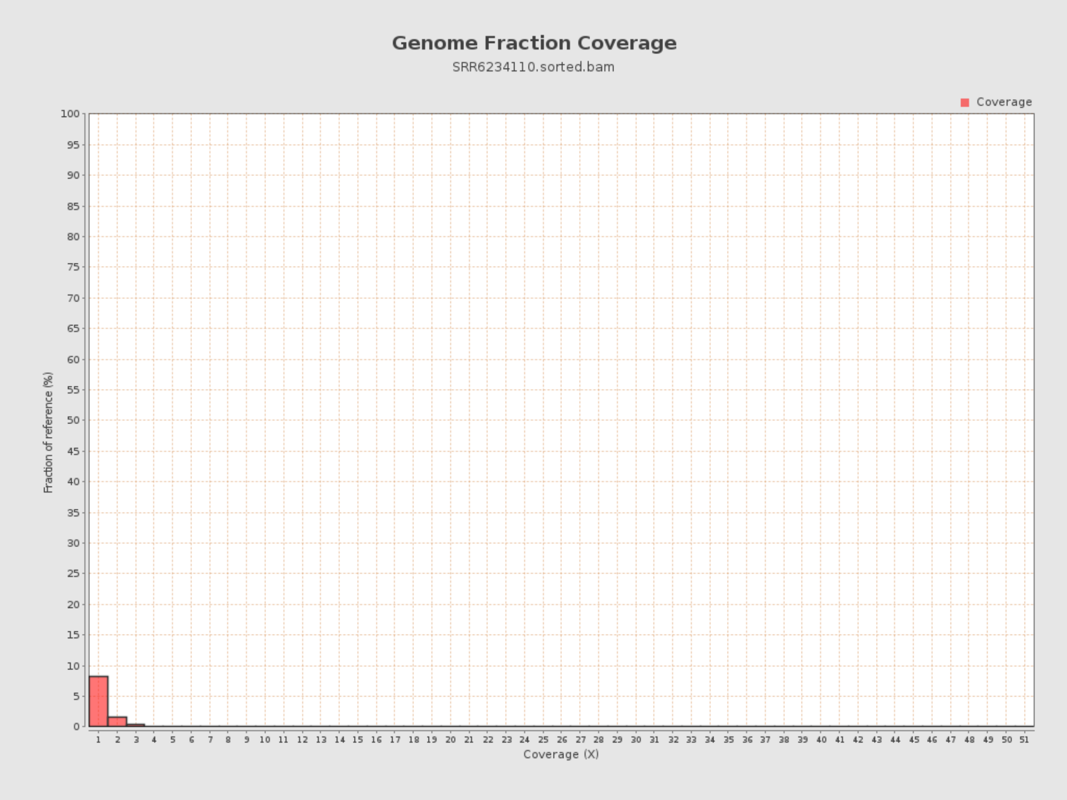
4. Results : Coverage Histogram



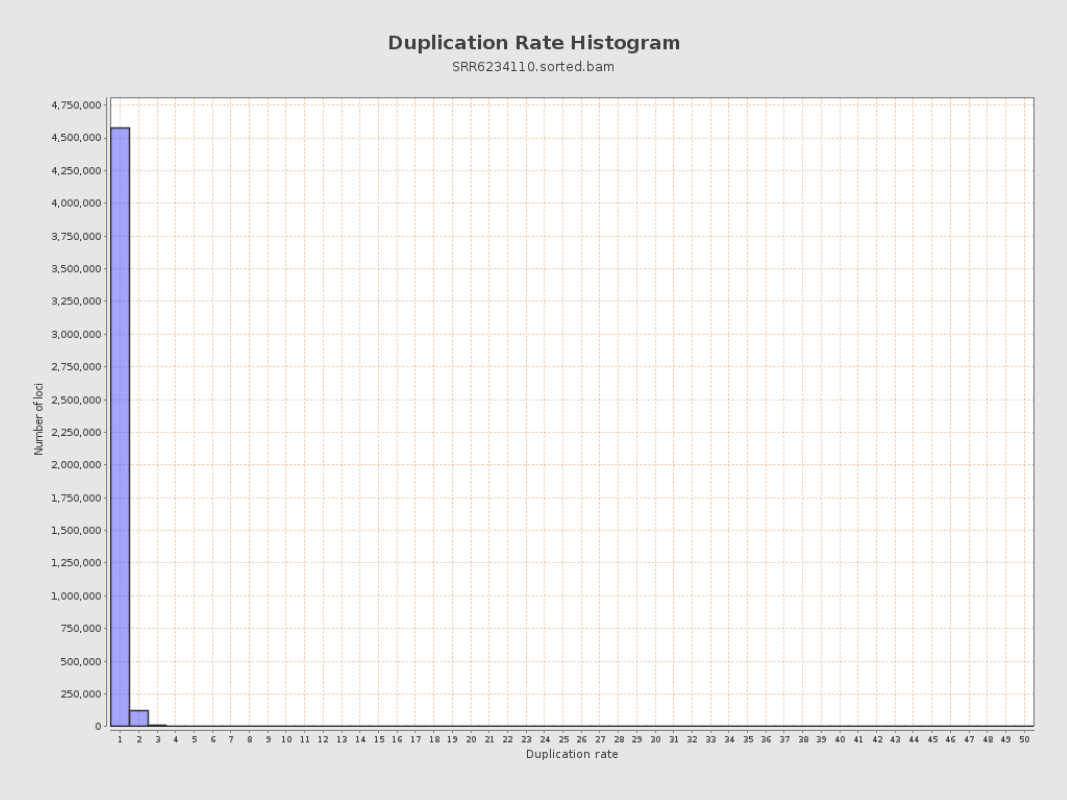
5. Results : Coverage Histogram (0-50X)



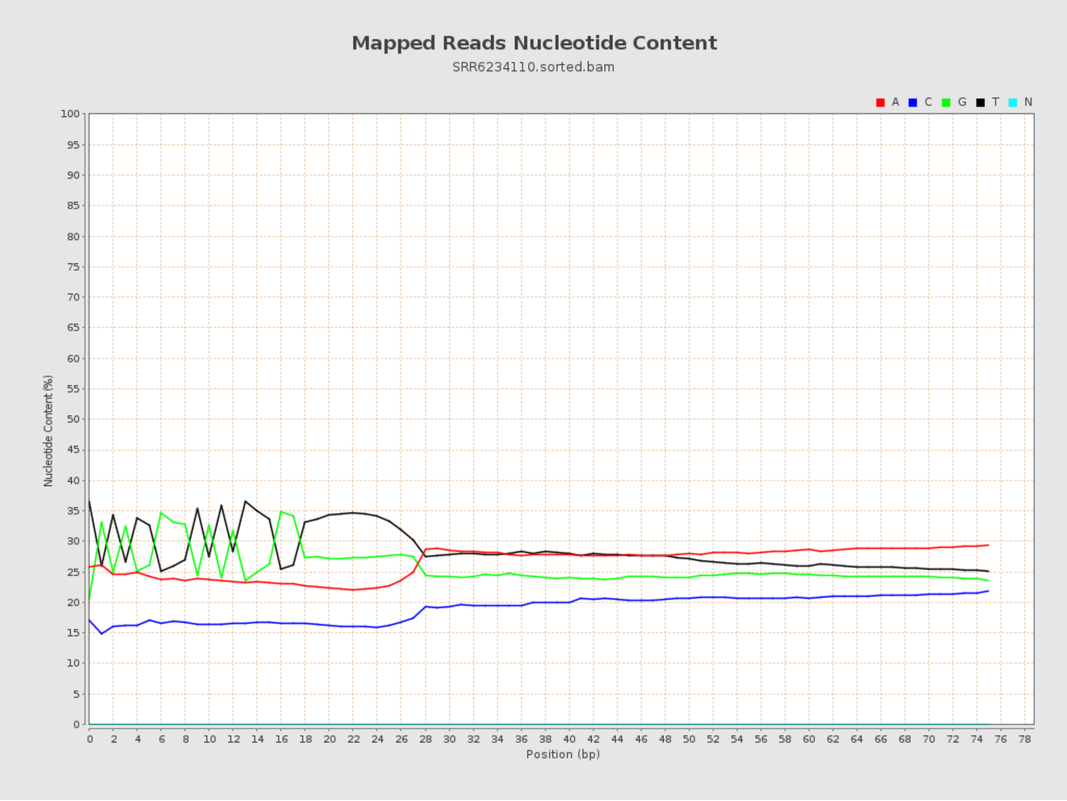
6. Results : Genome Fraction Coverage



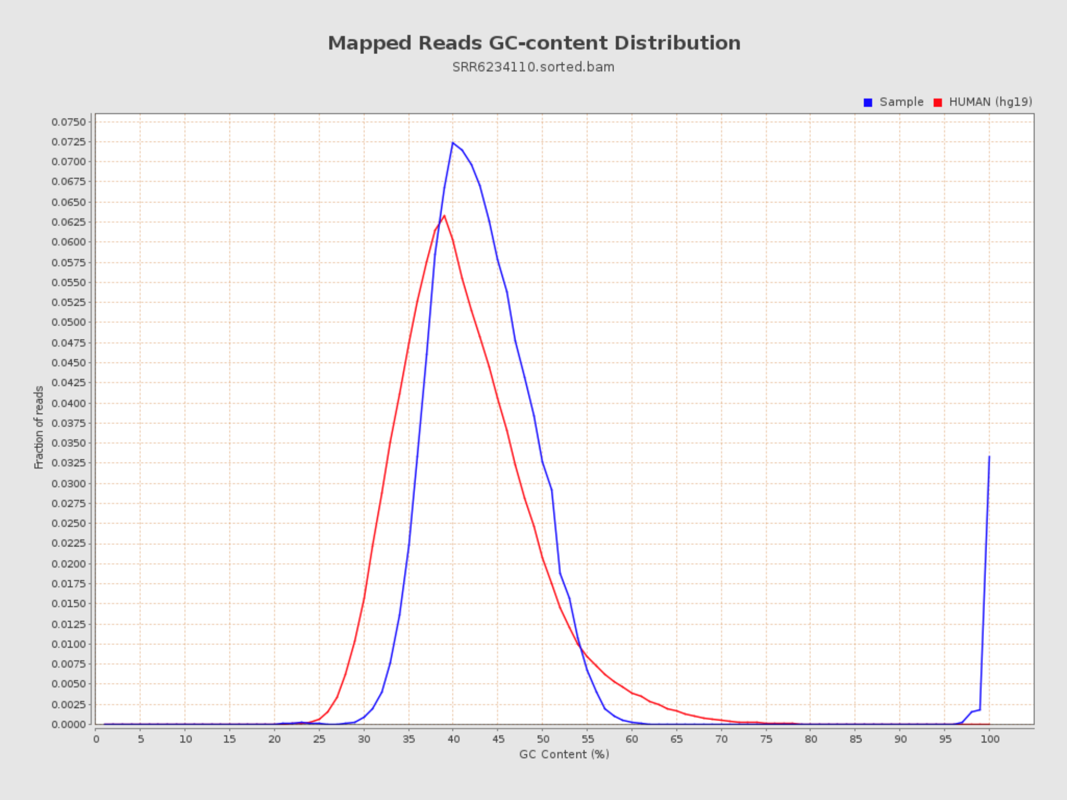
7. Results : Duplication Rate Histogram



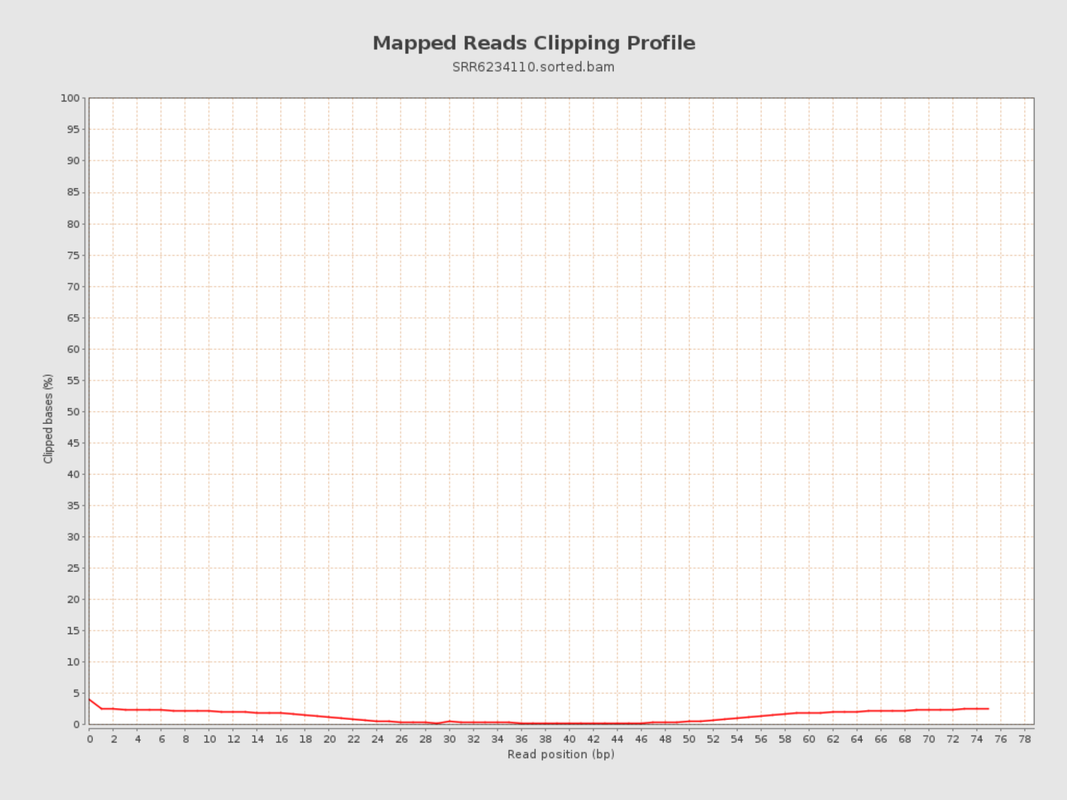
8. Results : Mapped Reads Nucleotide Content



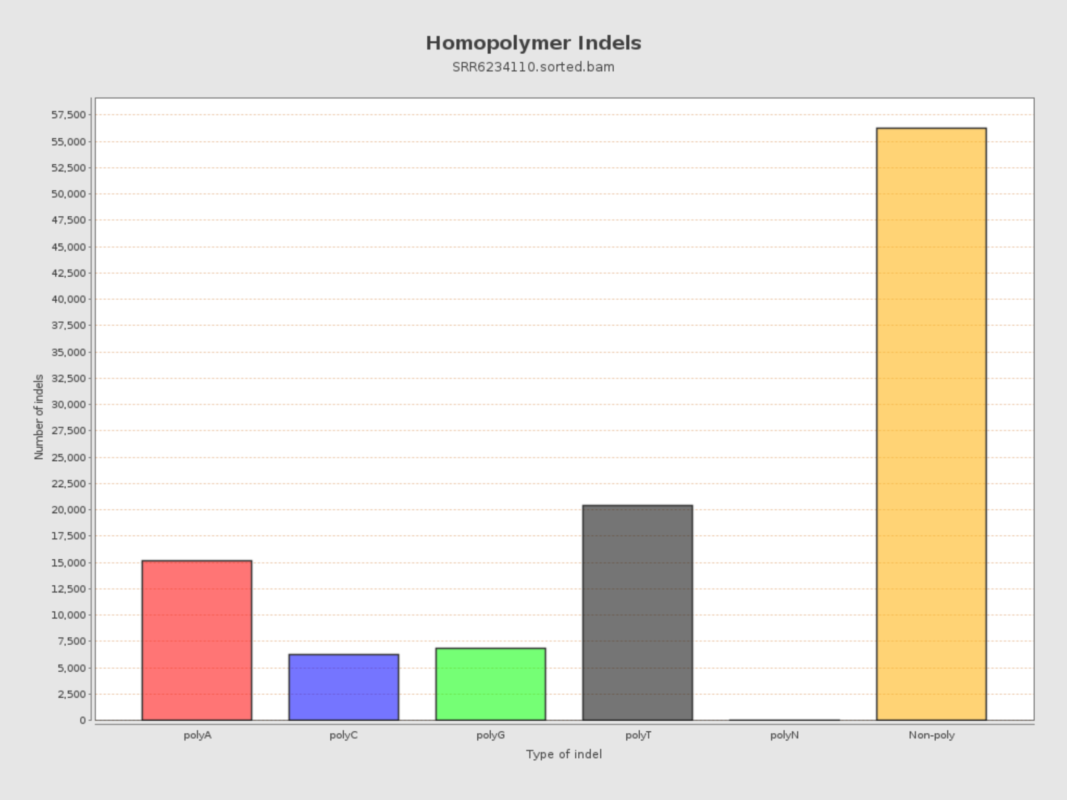
9. Results : Mapped Reads GC-content Distribution



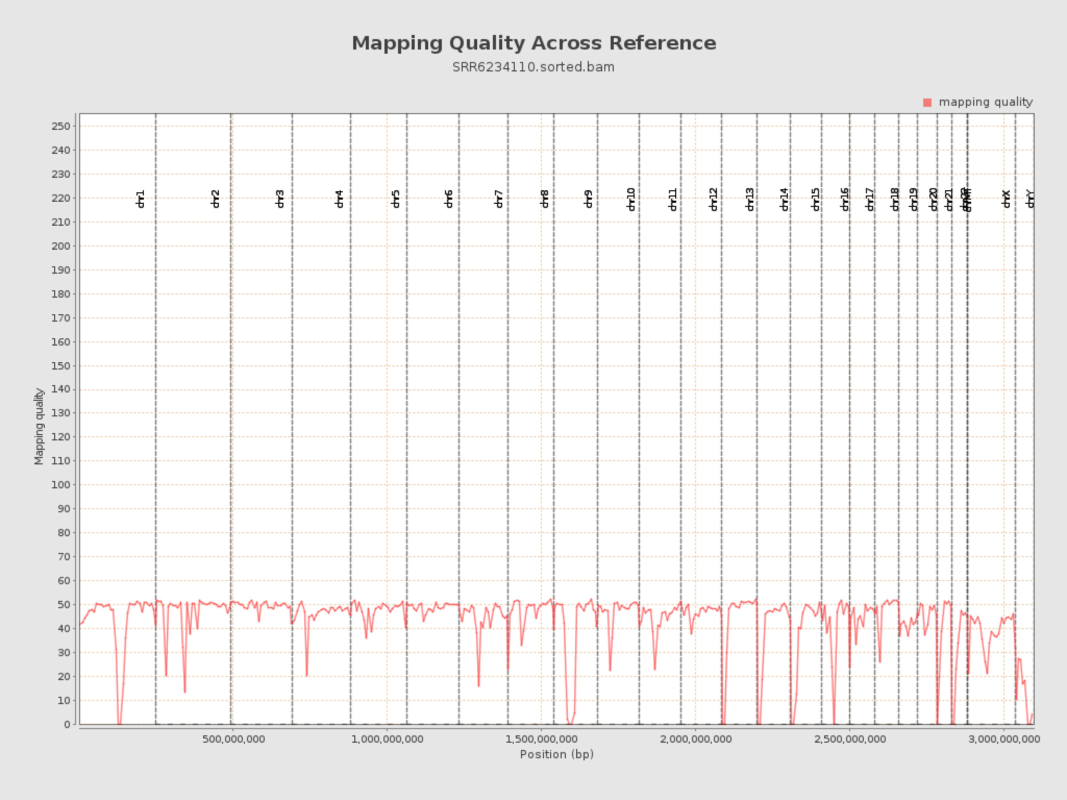
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram