Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:12:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234120.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_SRR6234120 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234120.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:11:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234120.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	935,405
Mapped reads	689,345 / 73.69%
Unmapped reads	246,060 / 26.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,775 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	15,304 / 1.64%
Duplication rate	1.72%
Clipped reads	300,476 / 32.12%

2.2. ACGT Content

Number/percentage of A's	13,160,888 / 28.83%
Number/percentage of C's	7,862,577 / 17.23%
Number/percentage of T's	14,539,267 / 31.85%
Number/percentage of G's	10,075,369 / 22.07%
Number/percentage of N's	8,022 / 0.02%
GC Percentage	39.3%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.1681

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

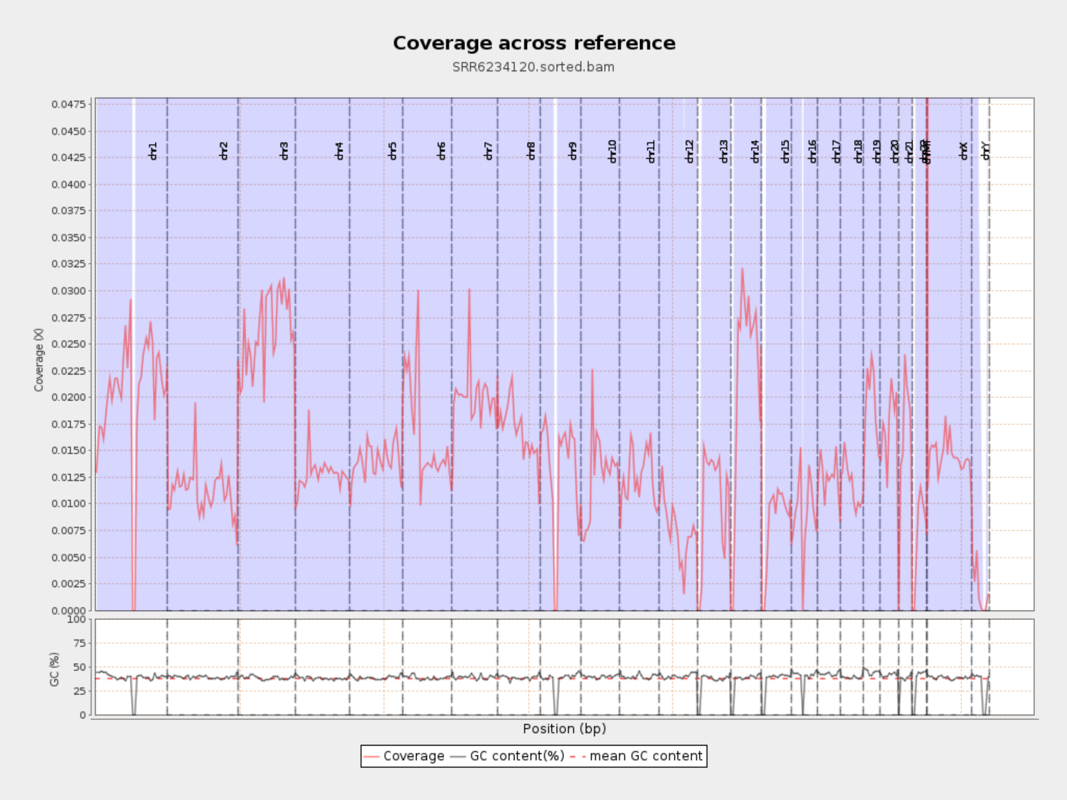
General error rate	0.9%
Mismatches	404,353
Insertions	3,779
Mapped reads with at least one insertion	0.54%
Deletions	12,900
Mapped reads with at least one deletion	1.85%
Homopolymer indels	45.91%

2.6. Chromosome stats

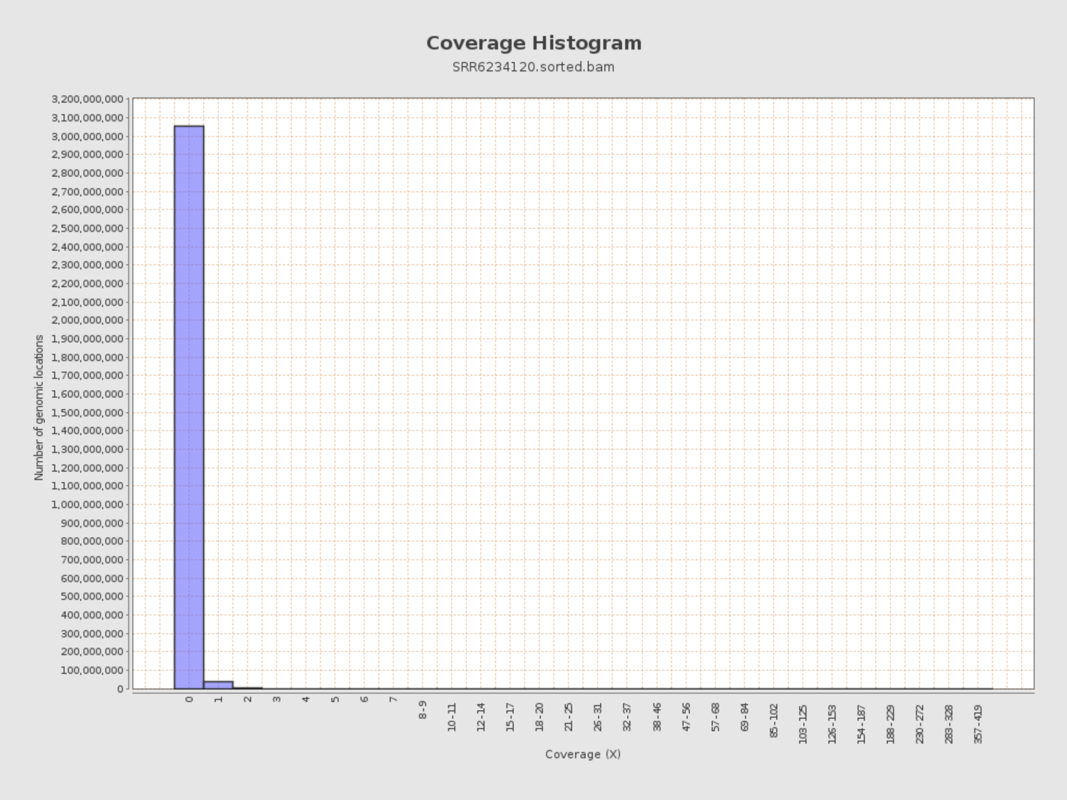
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5039792	0.0202	0.2652
chr2	243199373	2730104	0.0112	0.1581
chr3	198022430	5209649	0.0263	0.171
chr4	191154276	2450964	0.0128	0.1211
chr5	180915260	2564475	0.0142	0.1246
chr6	171115067	2843823	0.0166	0.1508
chr7	159138663	3190910	0.0201	0.2325

chr8	146364022	2462826	0.0168	0.2871
chr9	141213431	1876556	0.0133	0.1404
chr10	135534747	1693185	0.0125	0.1471
chr11	135006516	1690175	0.0125	0.1317
chr12	133851895	1013756	0.0076	0.0914
chr13	115169878	1169726	0.0102	0.1052
chr14	107349540	2370516	0.0221	0.1601
chr15	102531392	841586	0.0082	0.0948
chr16	90354753	815720	0.009	0.1072
chr17	81195210	1019657	0.0126	0.1227
chr18	78077248	917080	0.0117	0.2274
chr19	59128983	1147045	0.0194	0.1877
chr20	63025520	1083372	0.0172	0.1386
chr21	48129895	783726	0.0163	0.1373
chr22	51304566	367551	0.0072	0.0884
chrMT	16571	13152	0.7937	1.1019
chrX	155270560	2260305	0.0146	0.13
chrY	59373566	113552	0.0019	0.053

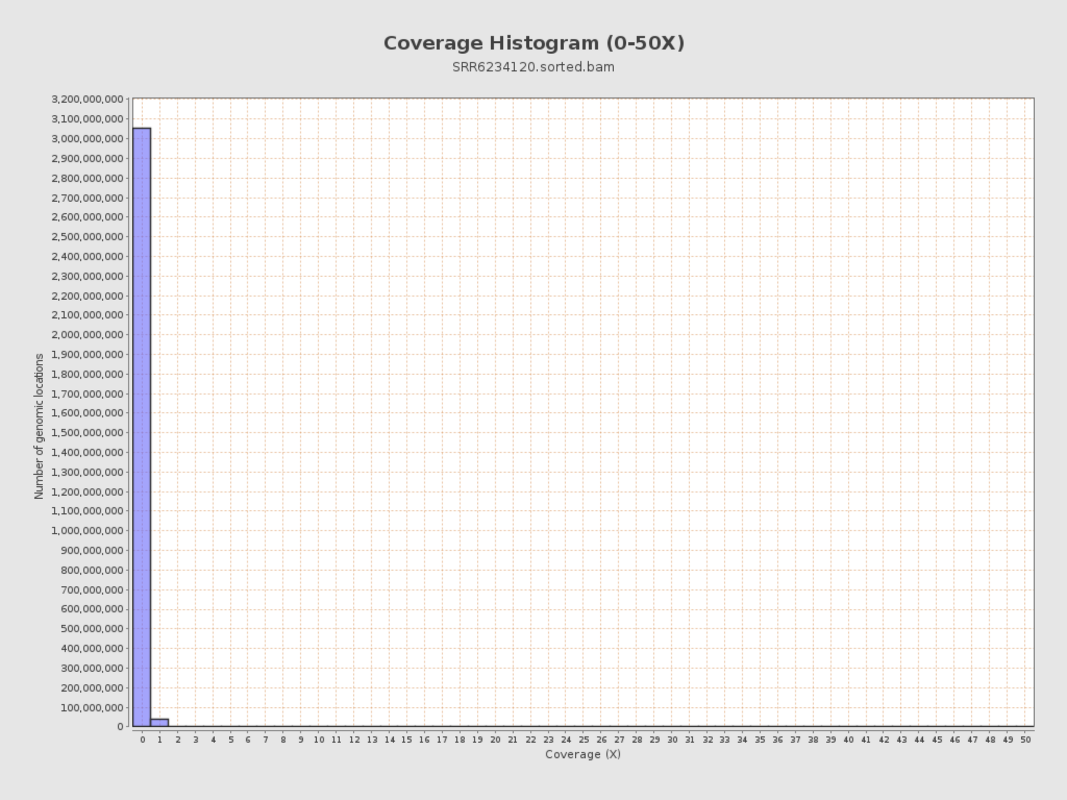
3. Results : Coverage across reference



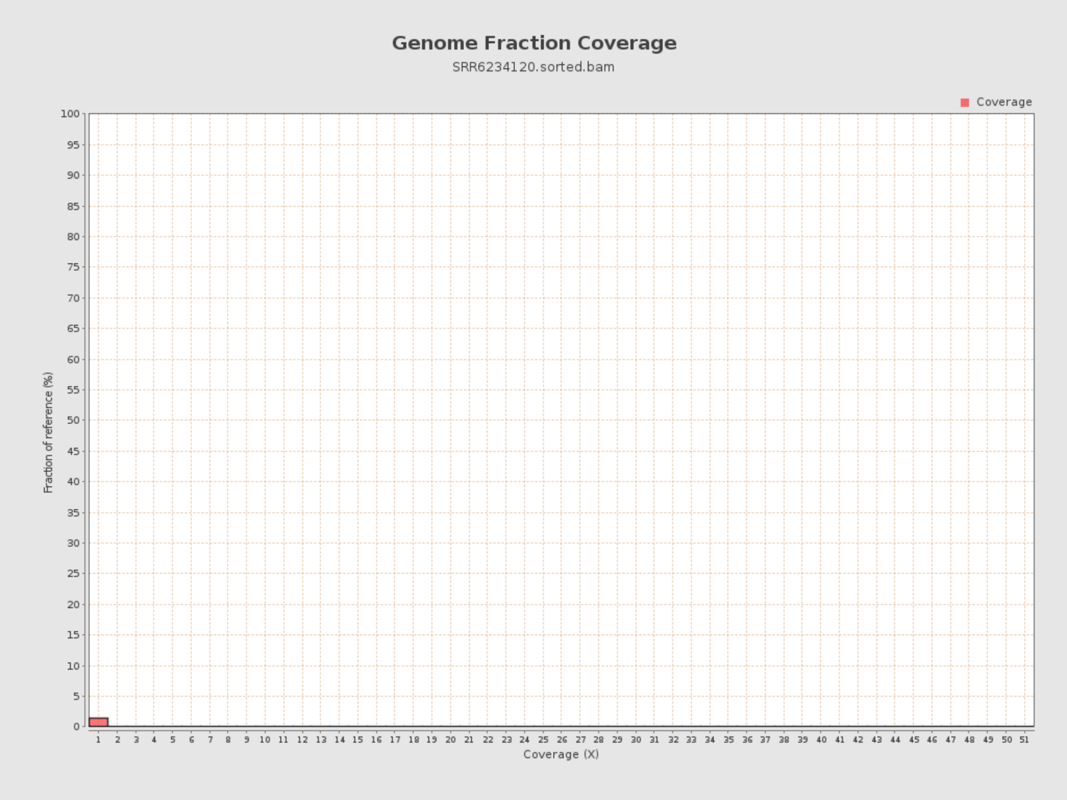
4. Results : Coverage Histogram



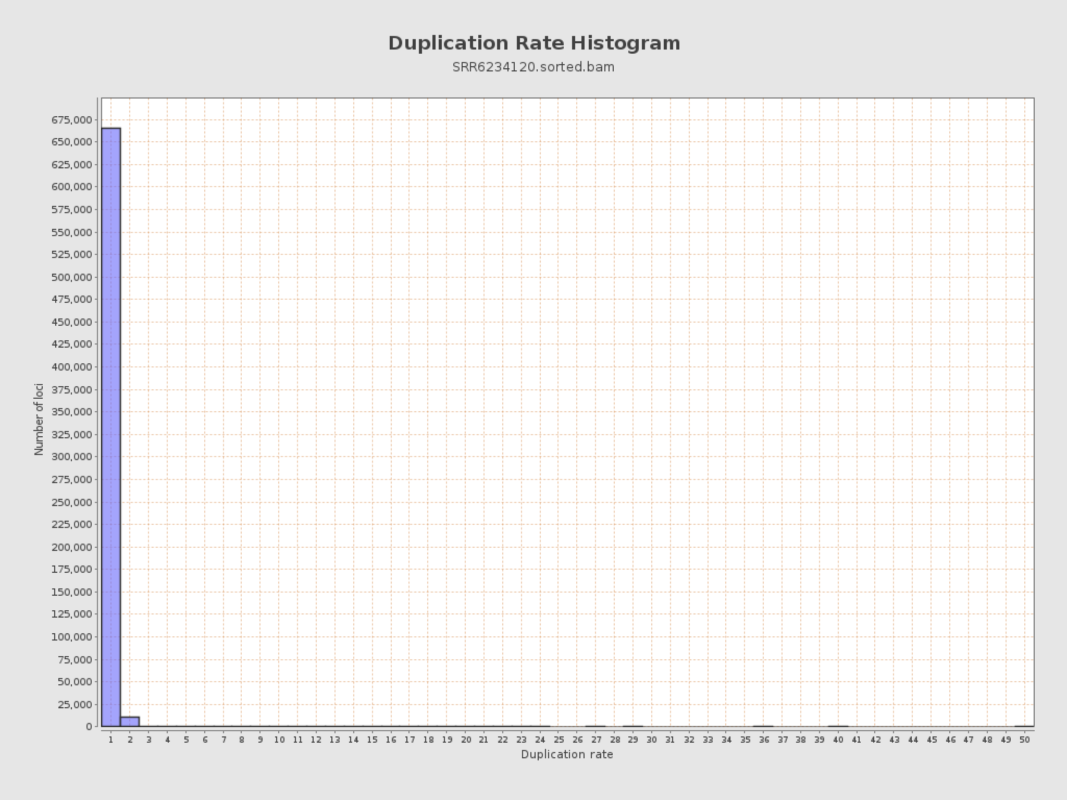
5. Results : Coverage Histogram (0-50X)



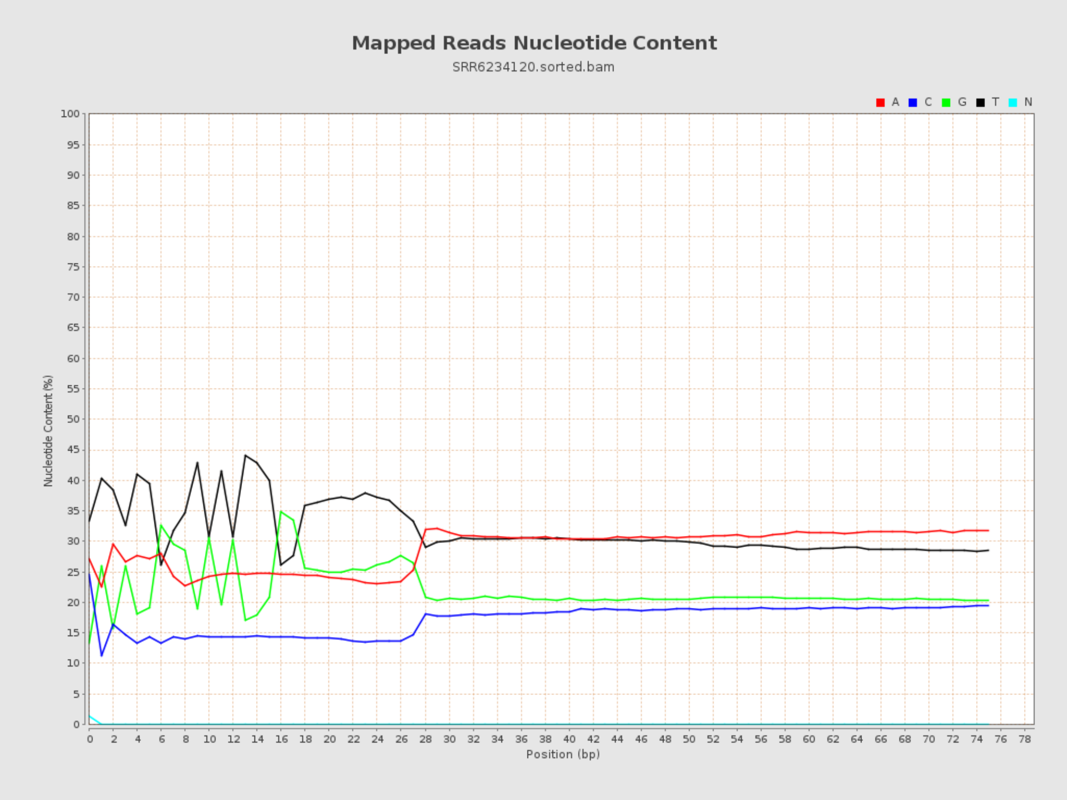
6. Results : Genome Fraction Coverage



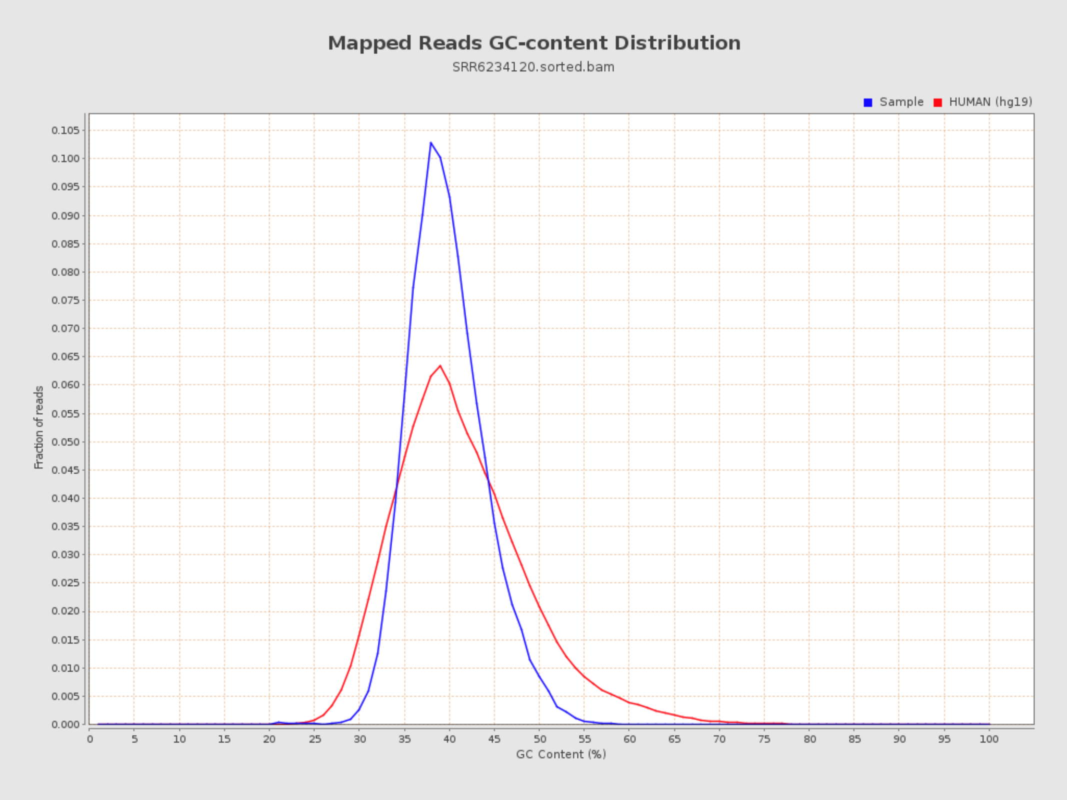
7. Results : Duplication Rate Histogram



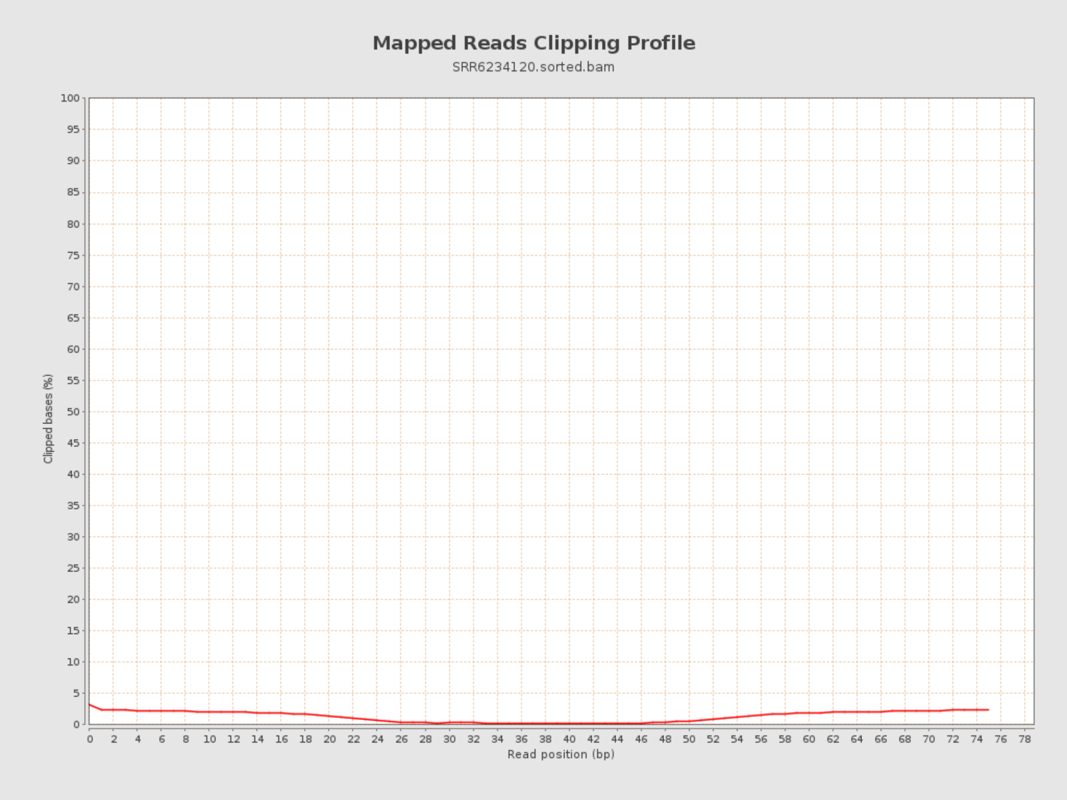
8. Results : Mapped Reads Nucleotide Content



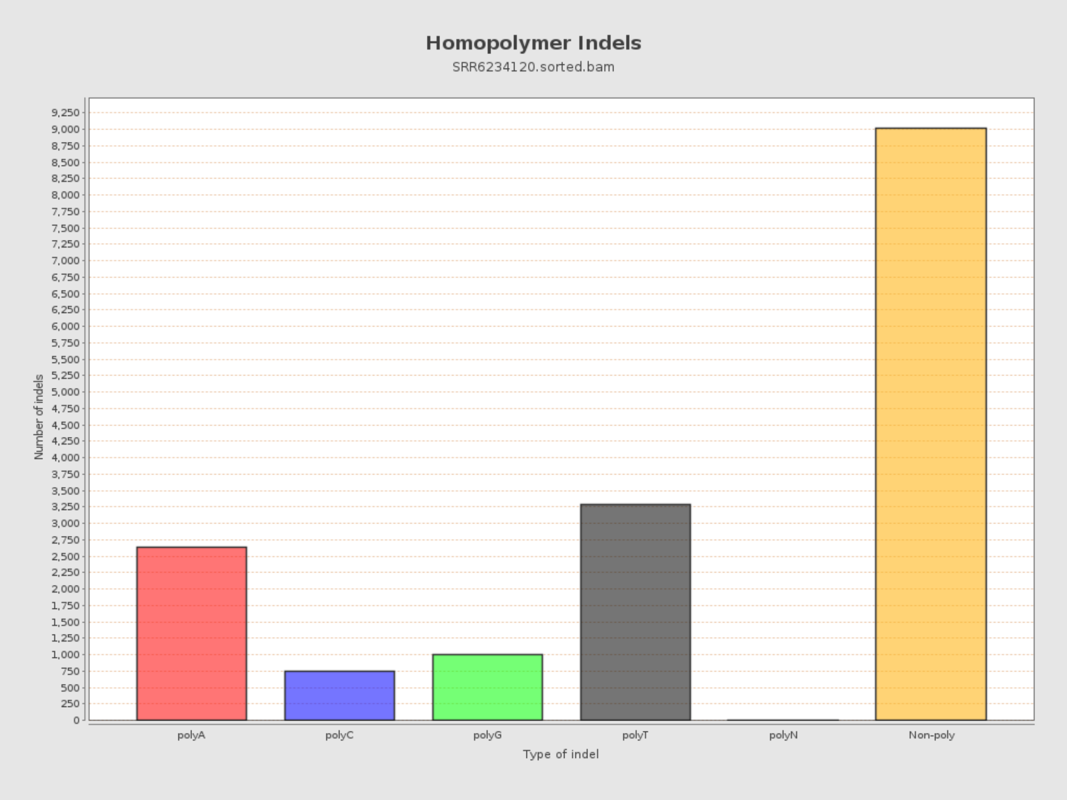
9. Results : Mapped Reads GC-content Distribution



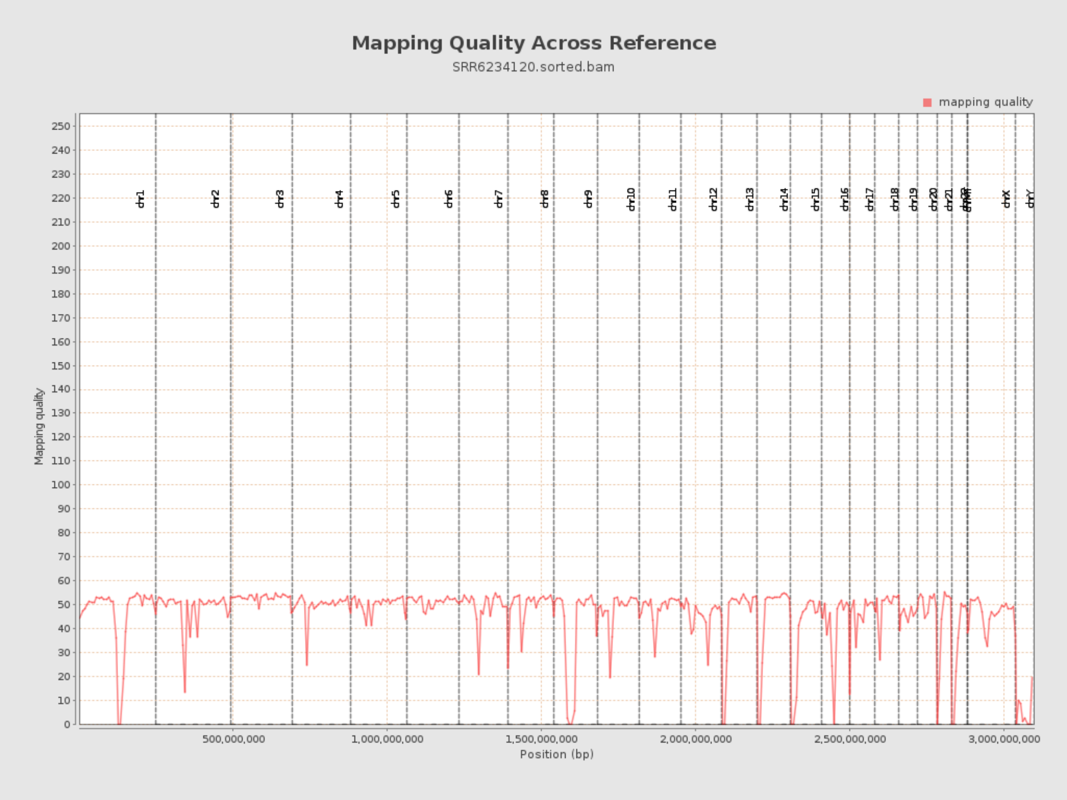
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram