Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:13:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234121.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_SRR6234121 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234121.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:13:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234121.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	719,092
Mapped reads	459,301 / 63.87%
Unmapped reads	259,791 / 36.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,286 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	11,104 / 1.54%
Duplication rate	1.95%
Clipped reads	207,000 / 28.79%

2.2. ACGT Content

Number/percentage of A's	8,659,706 / 28.58%
Number/percentage of C's	5,179,047 / 17.09%
Number/percentage of T's	9,848,492 / 32.5%
Number/percentage of G's	6,607,923 / 21.81%
Number/percentage of N's	4,358 / 0.01%
GC Percentage	38.9%

2.3. Coverage

Mean	0.0098

Standard Deviation	0.1297

2.4. Mapping Quality

Mean Mapping Quality	42.76

2.5. Mismatches and indels

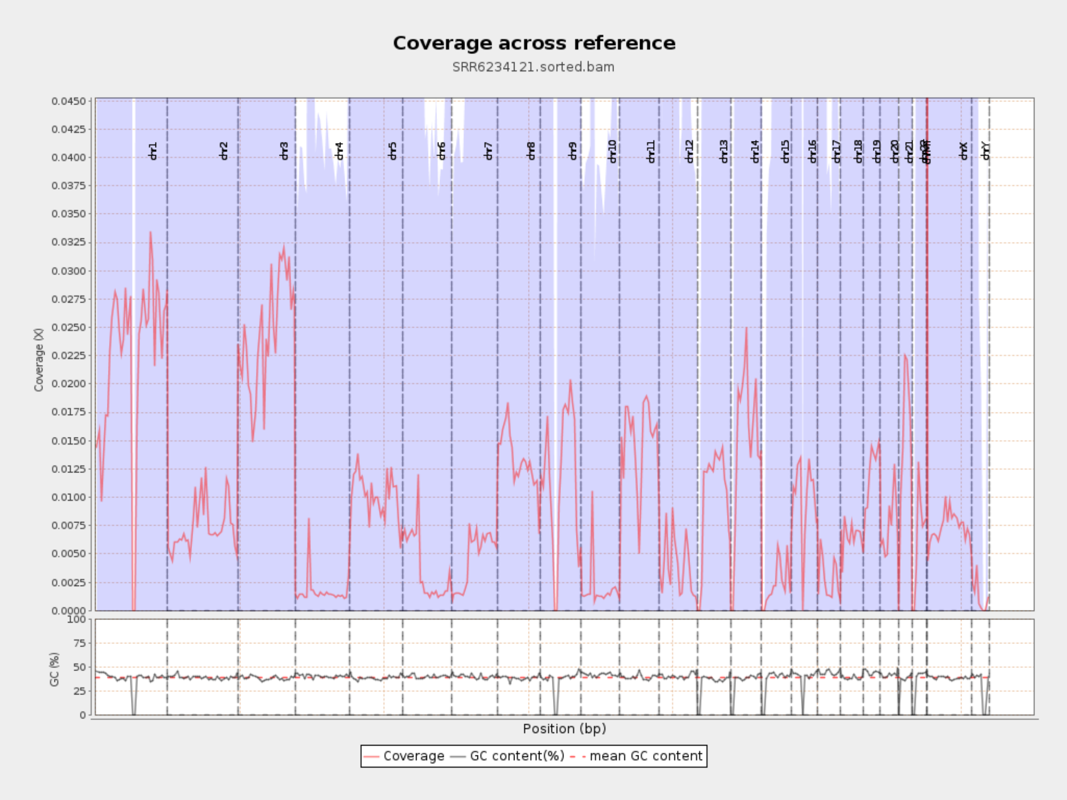
General error rate	0.9%
Mismatches	268,117
Insertions	2,577
Mapped reads with at least one insertion	0.56%
Deletions	8,647
Mapped reads with at least one deletion	1.86%
Homopolymer indels	46.64%

2.6. Chromosome stats

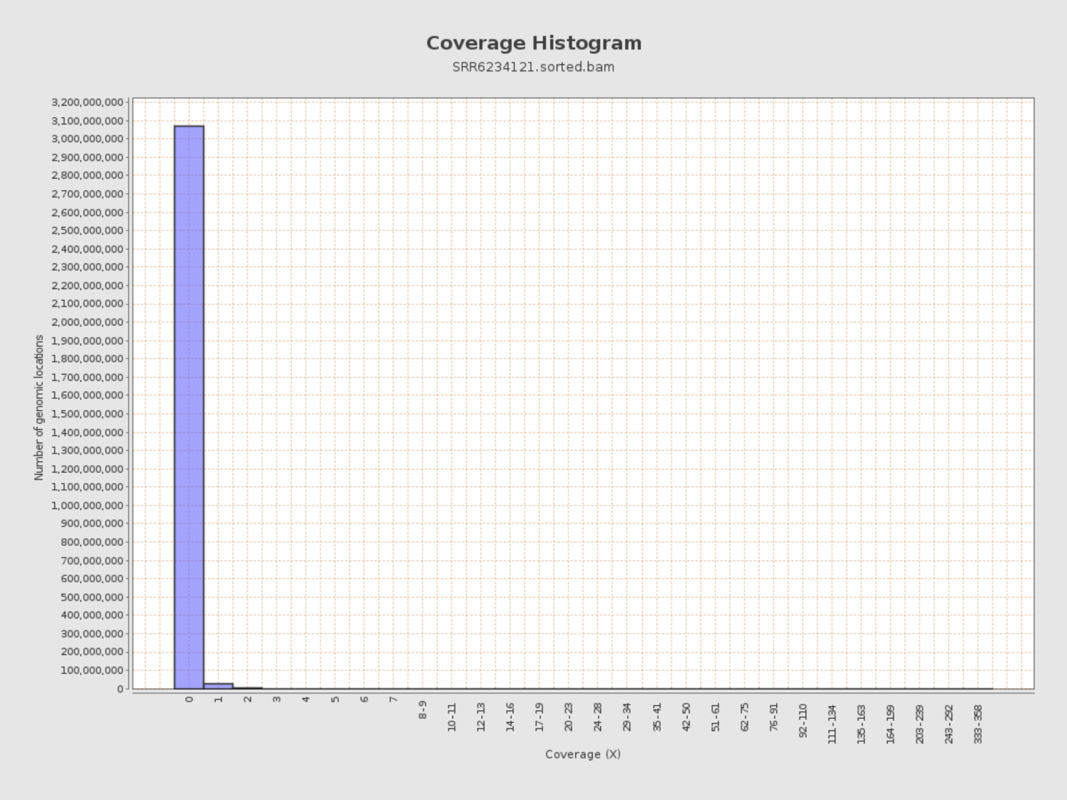
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5537066	0.0222	0.2222
chr2	243199373	1806380	0.0074	0.1119
chr3	198022430	4872282	0.0246	0.168
chr4	191154276	328938	0.0017	0.0473
chr5	180915260	1847714	0.0102	0.107
chr6	171115067	638442	0.0037	0.0732
chr7	159138663	728731	0.0046	0.0824

chr8	146364022	1953109	0.0133	0.2529
chr9	141213431	1670471	0.0118	0.1222
chr10	135534747	258805	0.0019	0.0741
chr11	135006516	2005707	0.0149	0.144
chr12	133851895	523593	0.0039	0.0666
chr13	115169878	1166587	0.0101	0.107
chr14	107349540	1612598	0.015	0.1312
chr15	102531392	249081	0.0024	0.053
chr16	90354753	881621	0.0098	0.1085
chr17	81195210	232453	0.0029	0.0644
chr18	78077248	509061	0.0065	0.1414
chr19	59128983	717609	0.0121	0.14
chr20	63025520	477435	0.0076	0.0924
chr21	48129895	735154	0.0153	0.1327
chr22	51304566	342831	0.0067	0.0964
chrMT	16571	3032	0.183	0.4891
chrX	155270560	1143510	0.0074	0.094
chrY	59373566	72521	0.0012	0.0426

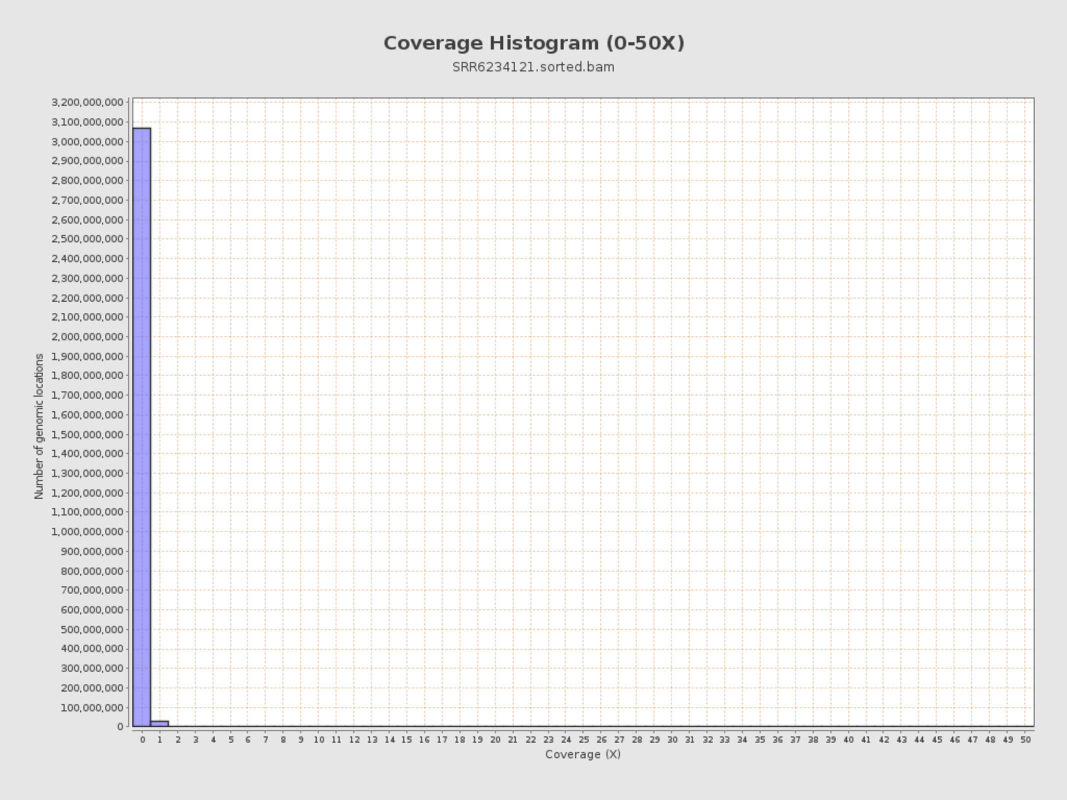
3. Results : Coverage across reference



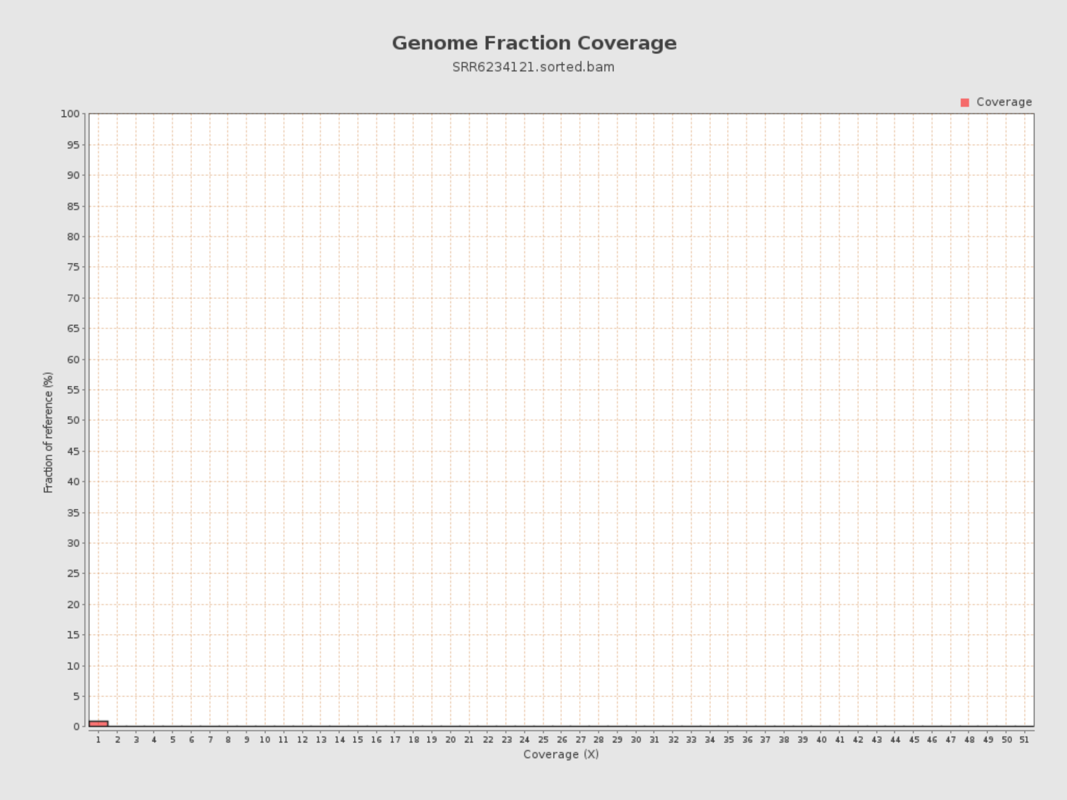
4. Results : Coverage Histogram



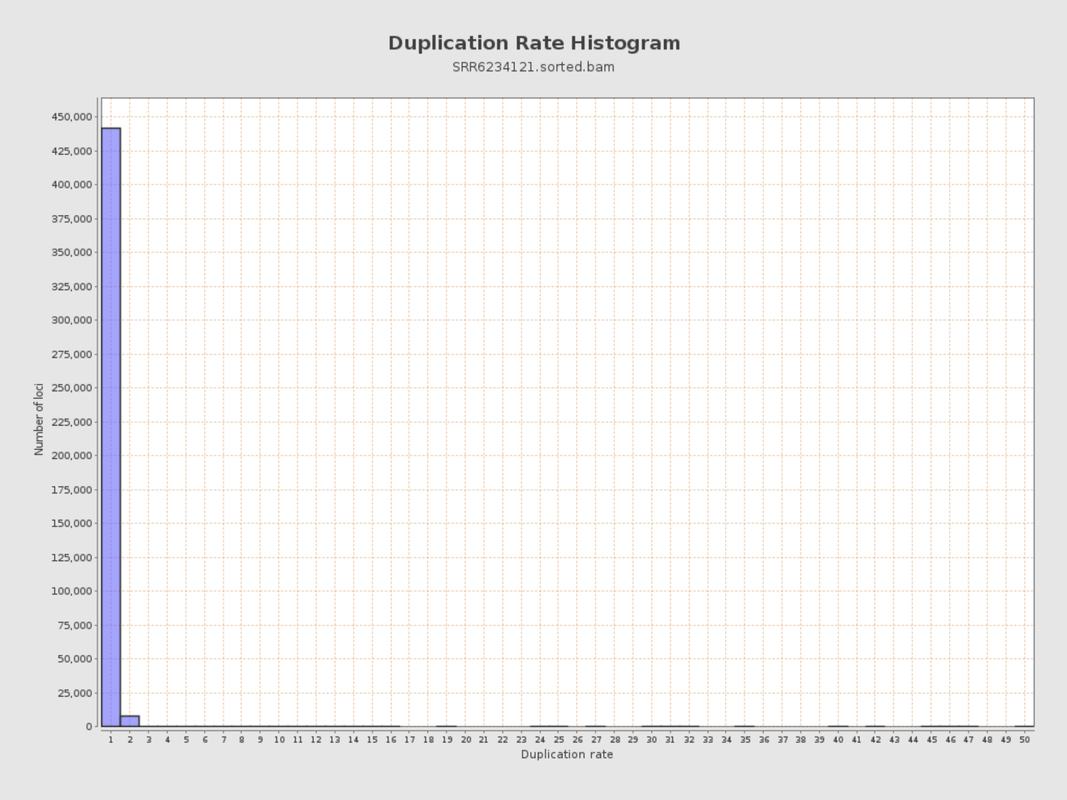
5. Results : Coverage Histogram (0-50X)



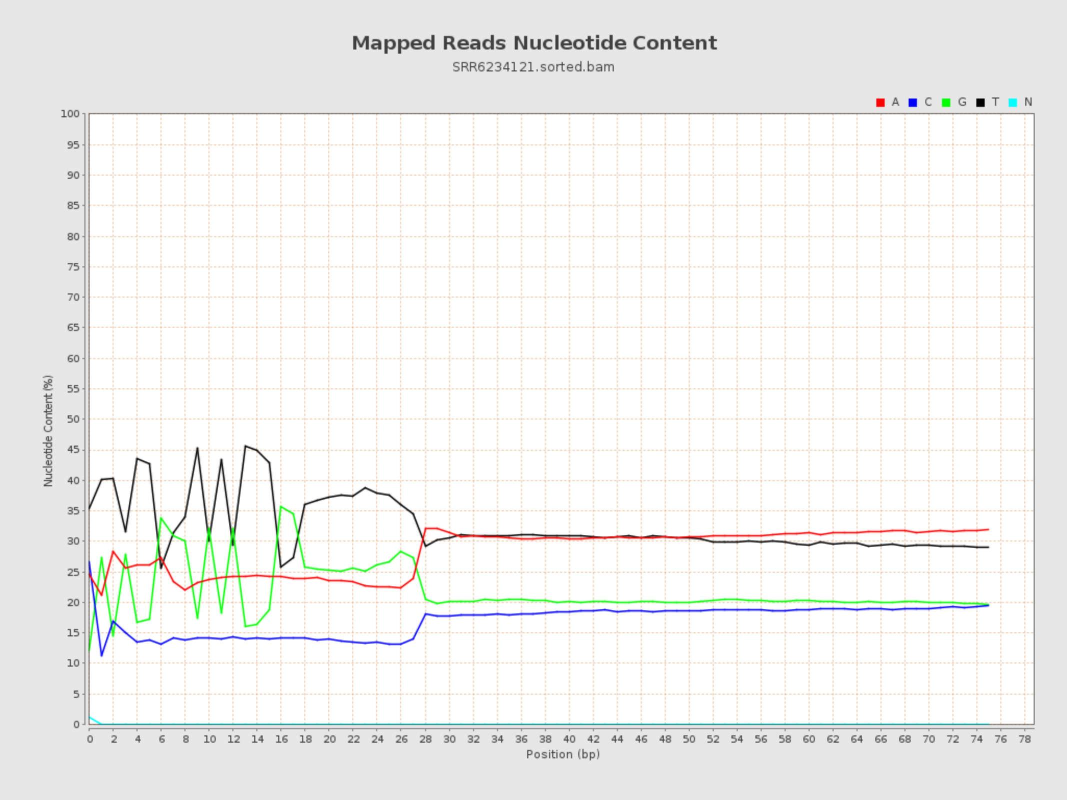
6. Results : Genome Fraction Coverage



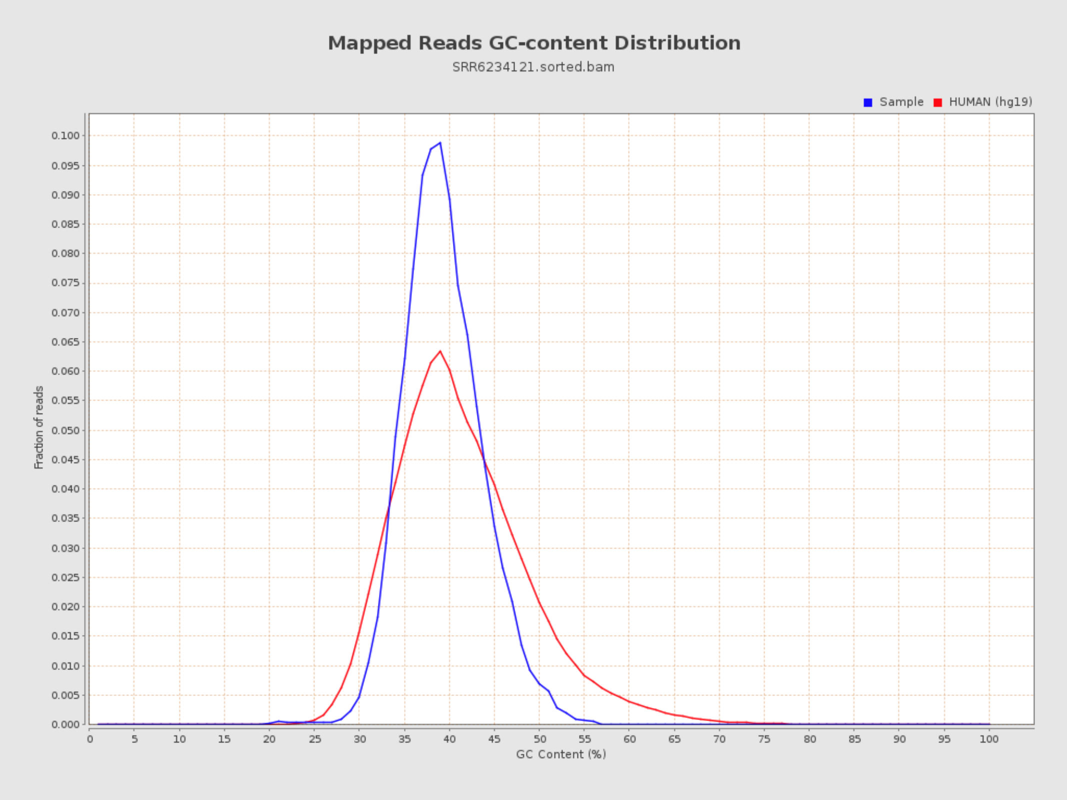
7. Results : Duplication Rate Histogram



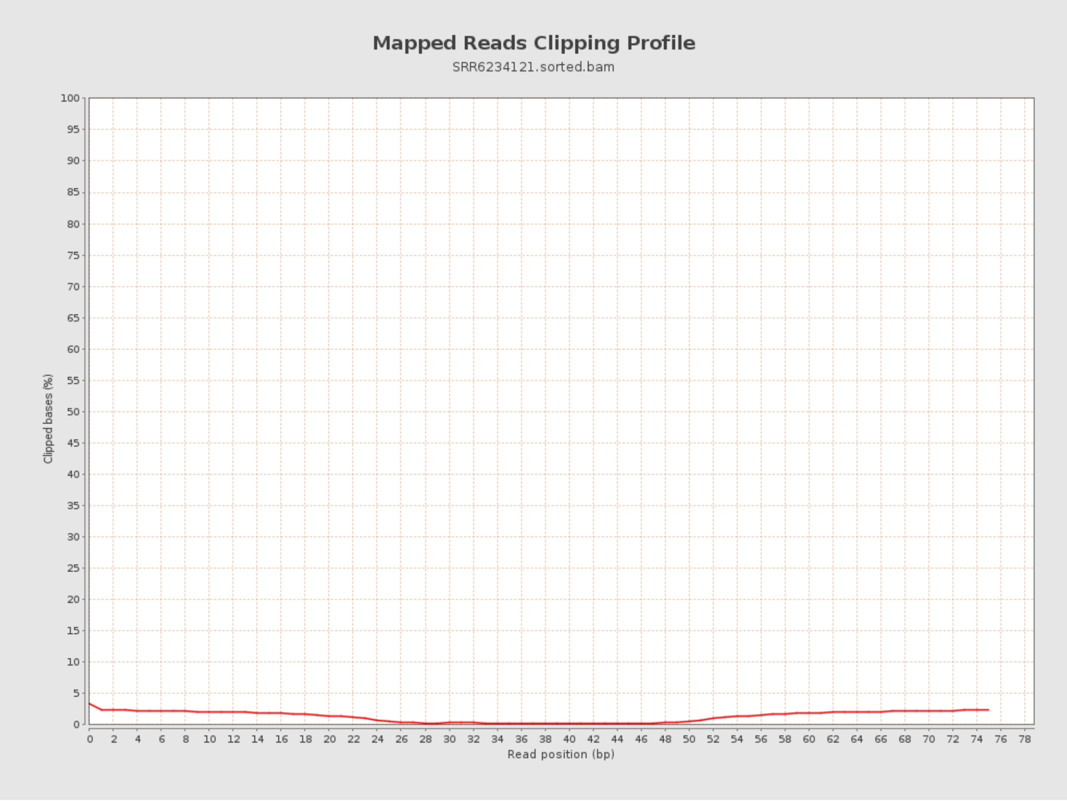
8. Results : Mapped Reads Nucleotide Content



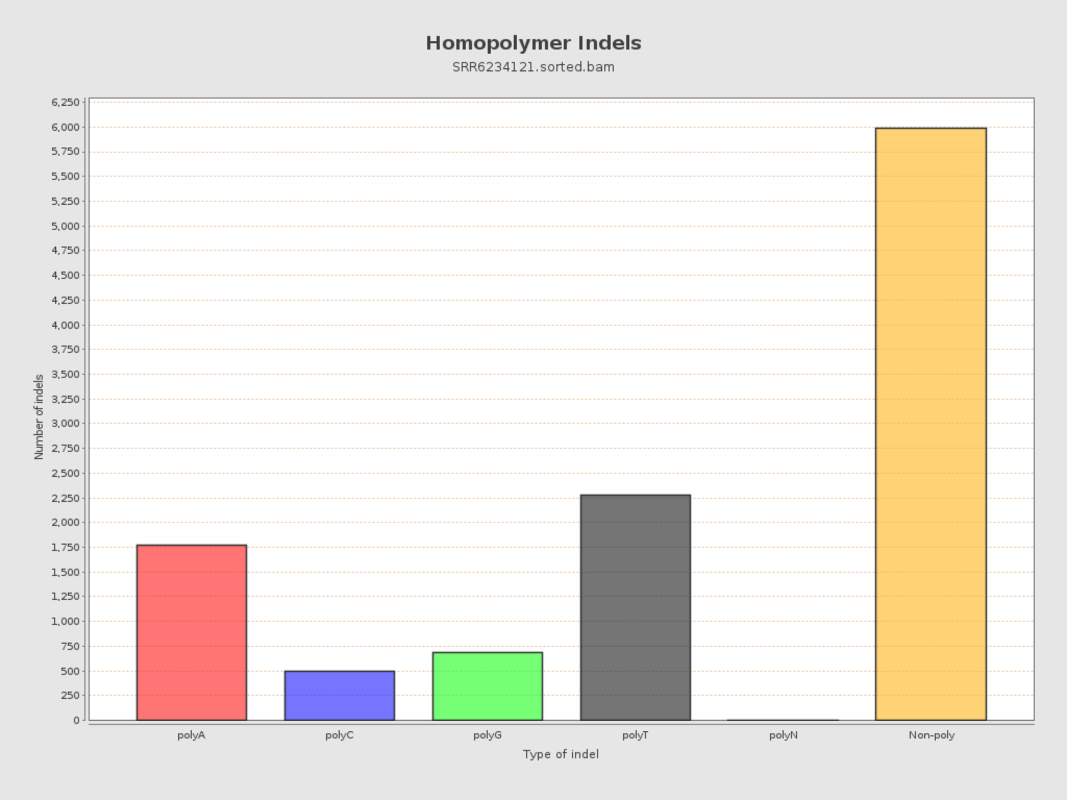
9. Results : Mapped Reads GC-content Distribution



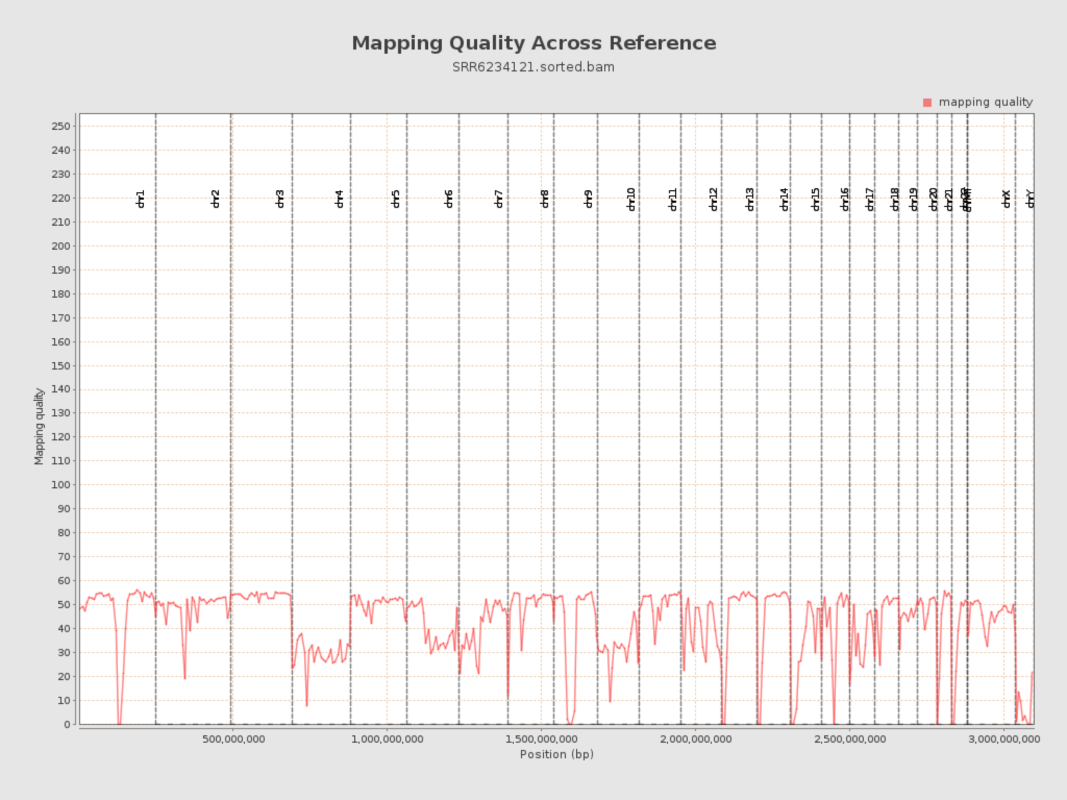
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram