Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:26:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234143.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_SRR6234143 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234143.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:26:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234143.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	889,693
Mapped reads	477,886 / 53.71%
Unmapped reads	411,807 / 46.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,232 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	24,726 / 2.78%
Duplication rate	4.31%
Clipped reads	264,647 / 29.75%

2.2. ACGT Content

Number/percentage of A's	8,459,097 / 27.94%
Number/percentage of C's	5,056,641 / 16.7%
Number/percentage of T's	10,121,834 / 33.44%
Number/percentage of G's	6,628,313 / 21.9%
Number/percentage of N's	5,808 / 0.02%
GC Percentage	38.6%

2.3. Coverage

Mean	0.0098

Standard Deviation	0.1508

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

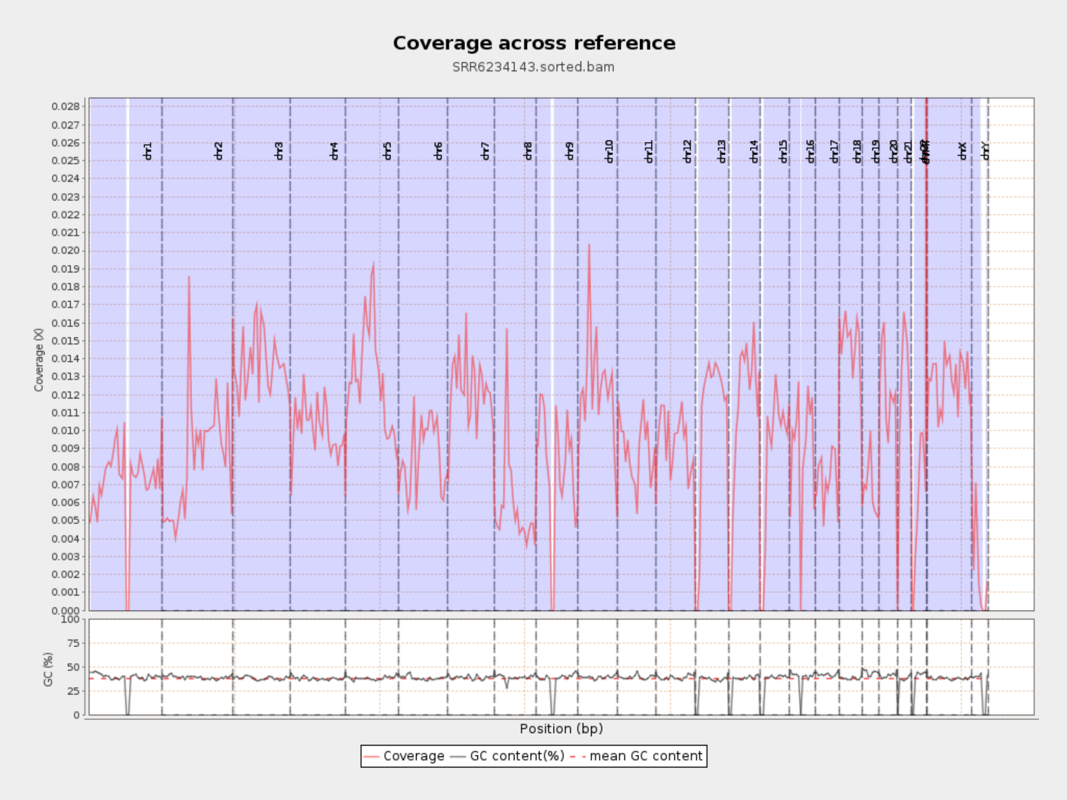
General error rate	1.03%
Mismatches	305,513
Insertions	2,747
Mapped reads with at least one insertion	0.57%
Deletions	15,486
Mapped reads with at least one deletion	3.17%
Homopolymer indels	42.26%

2.6. Chromosome stats

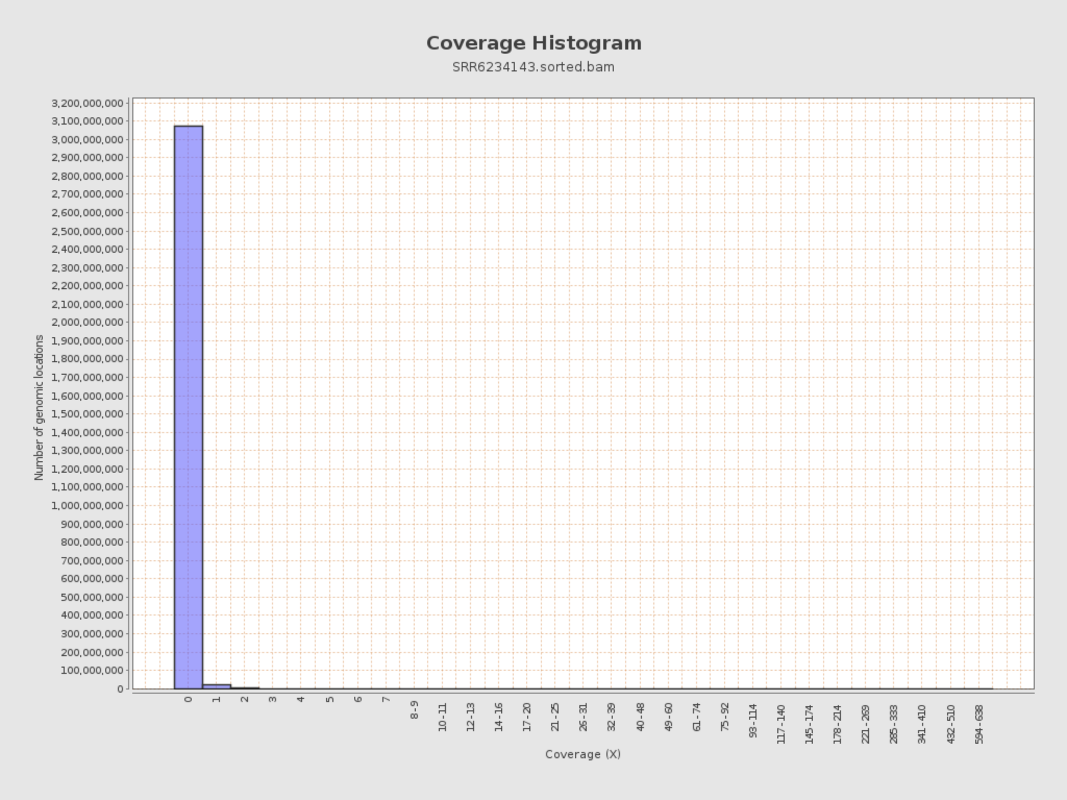
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1768451	0.0071	0.1364
chr2	243199373	2038478	0.0084	0.1324
chr3	198022430	2719575	0.0137	0.1378
chr4	191154276	1934648	0.0101	0.1197
chr5	180915260	2343112	0.013	0.1346
chr6	171115067	1473881	0.0086	0.1131
chr7	159138663	1975852	0.0124	0.1532

chr8	146364022	839885	0.0057	0.3784
chr9	141213431	1125441	0.008	0.1177
chr10	135534747	1687357	0.0124	0.1451
chr11	135006516	1197402	0.0089	0.1164
chr12	133851895	1255332	0.0094	0.1155
chr13	115169878	1213264	0.0105	0.1217
chr14	107349540	1164468	0.0108	0.1251
chr15	102531392	880909	0.0086	0.1092
chr16	90354753	810111	0.009	0.1125
chr17	81195210	582918	0.0072	0.0989
chr18	78077248	1166831	0.0149	0.2163
chr19	59128983	404695	0.0068	0.123
chr20	63025520	762275	0.0121	0.13
chr21	48129895	566455	0.0118	0.1277
chr22	51304566	290835	0.0057	0.0866
chrMT	16571	3847	0.2322	0.6575
chrX	155270560	1970356	0.0127	0.1347
chrY	59373566	122648	0.0021	0.062

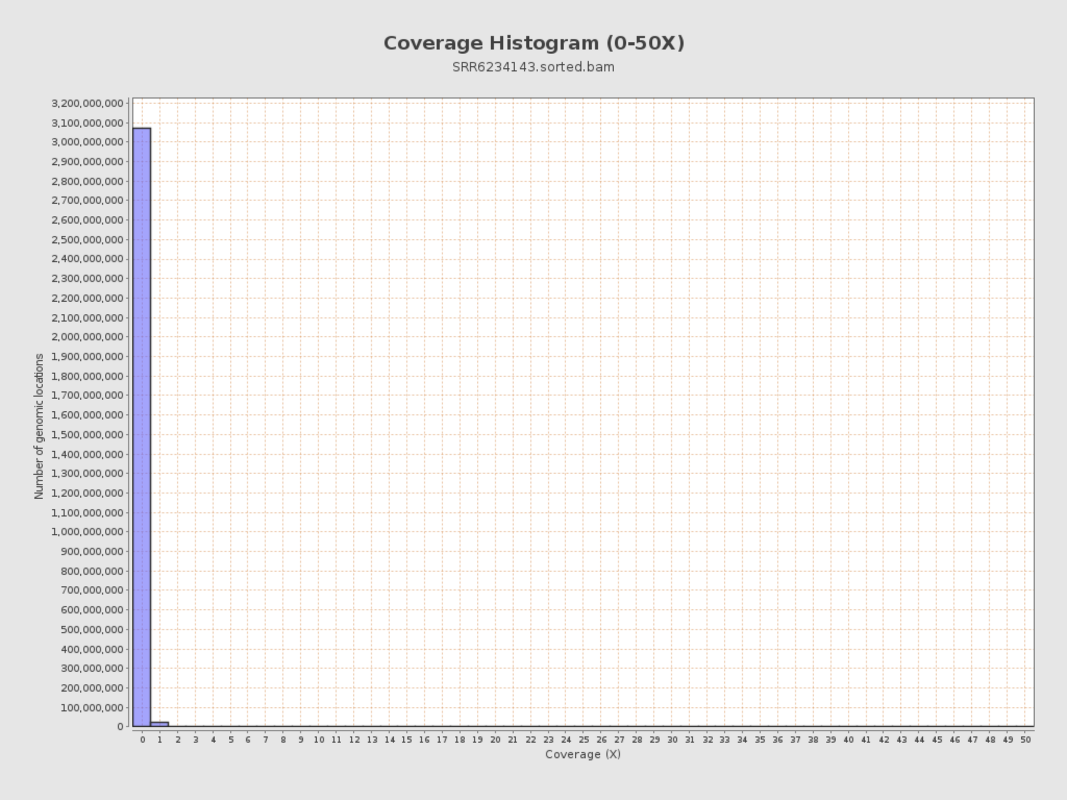
3. Results : Coverage across reference



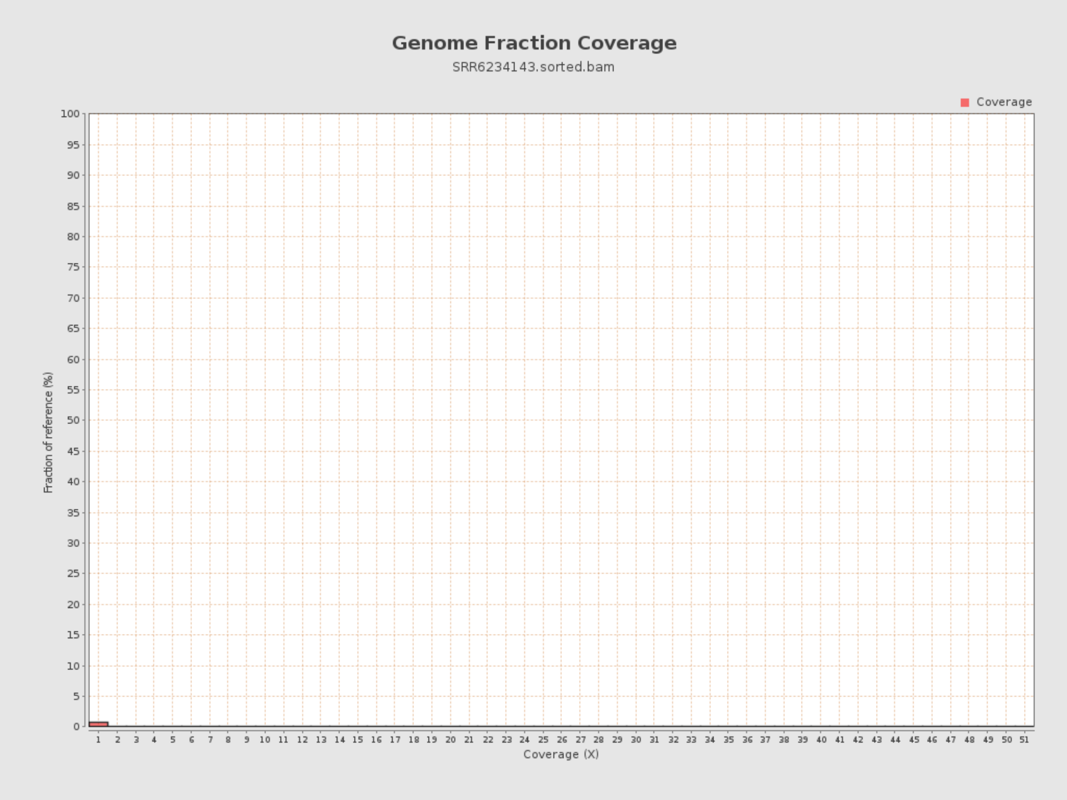
4. Results : Coverage Histogram



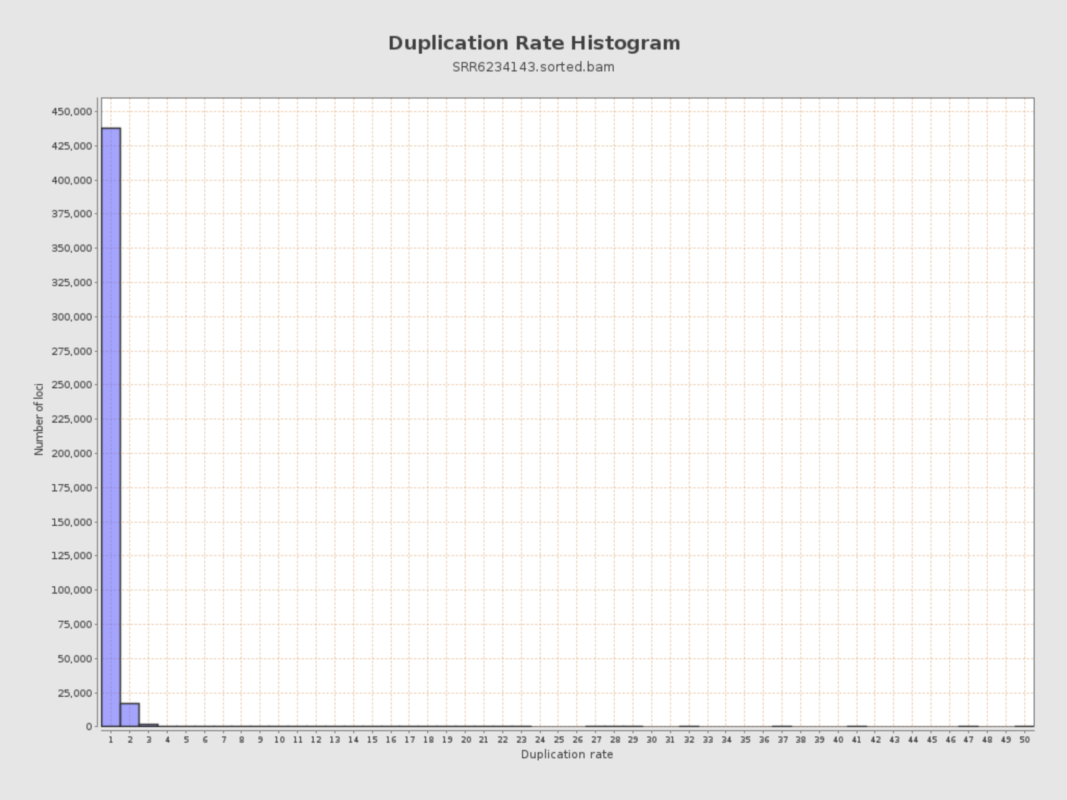
5. Results : Coverage Histogram (0-50X)



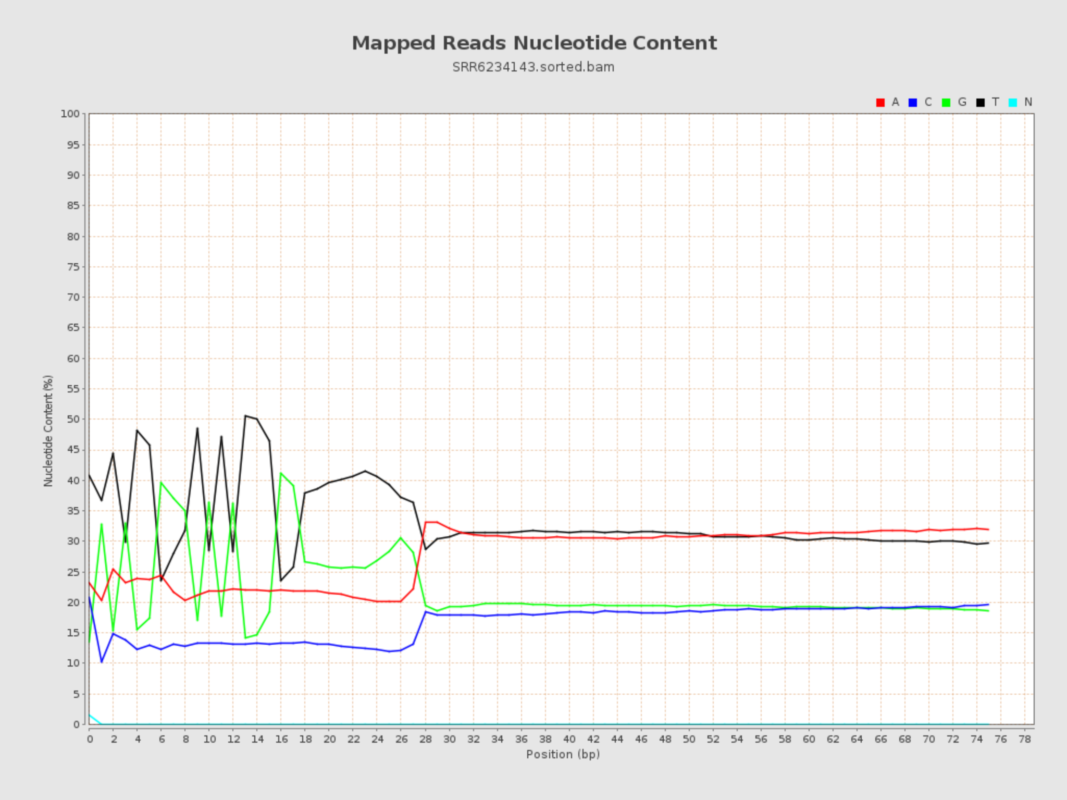
6. Results : Genome Fraction Coverage



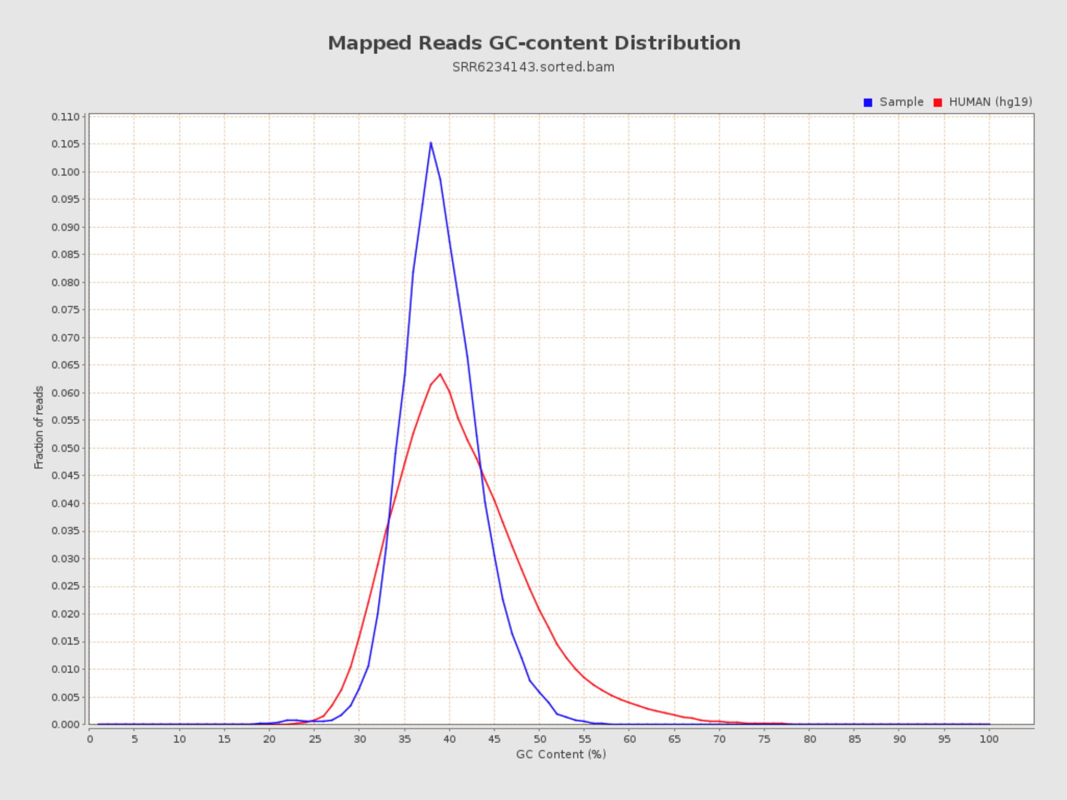
7. Results : Duplication Rate Histogram



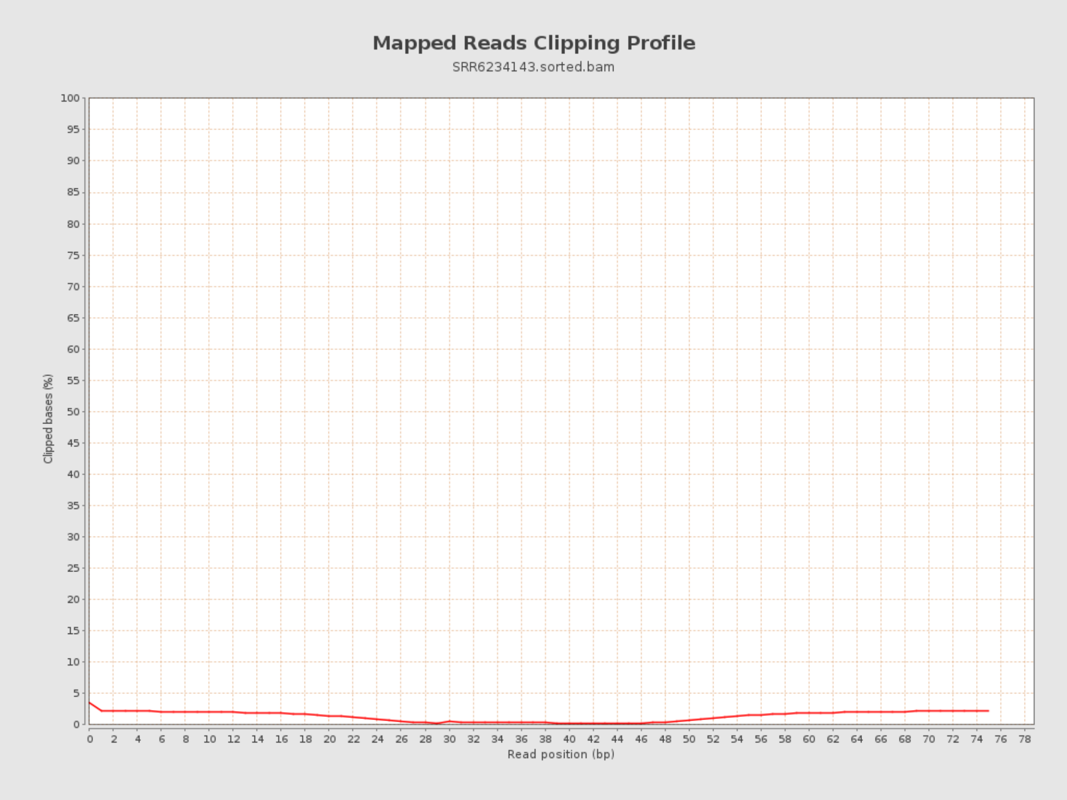
8. Results : Mapped Reads Nucleotide Content



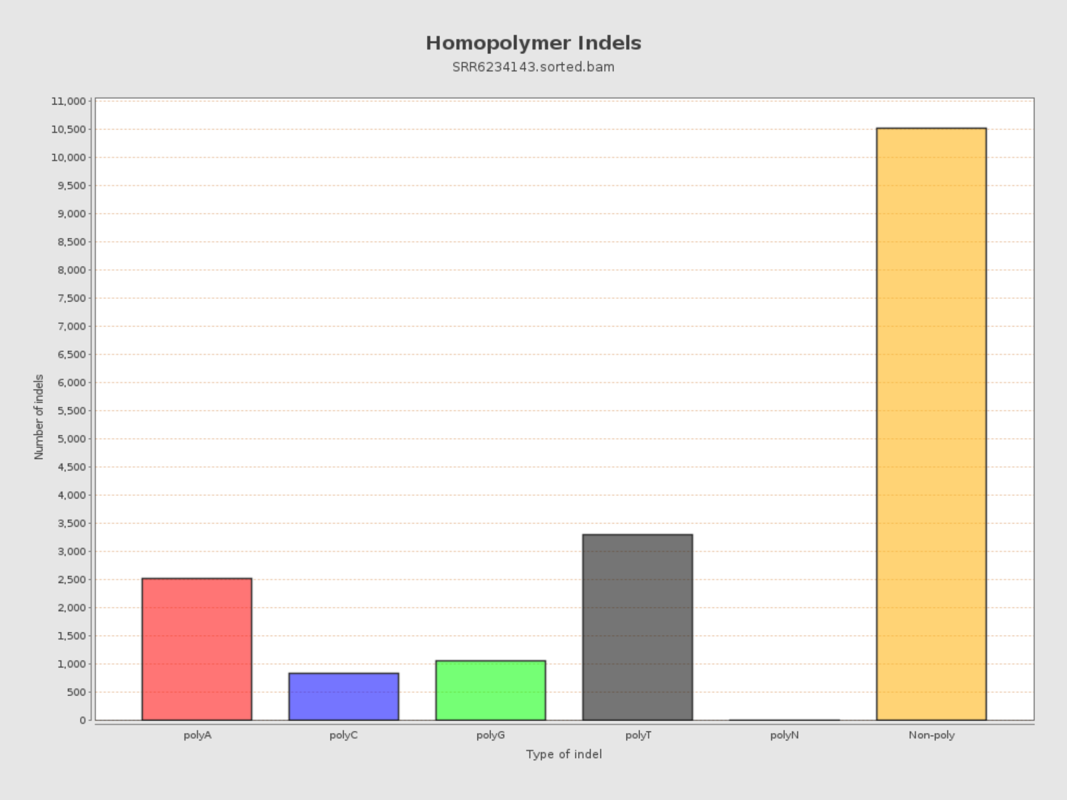
9. Results : Mapped Reads GC-content Distribution



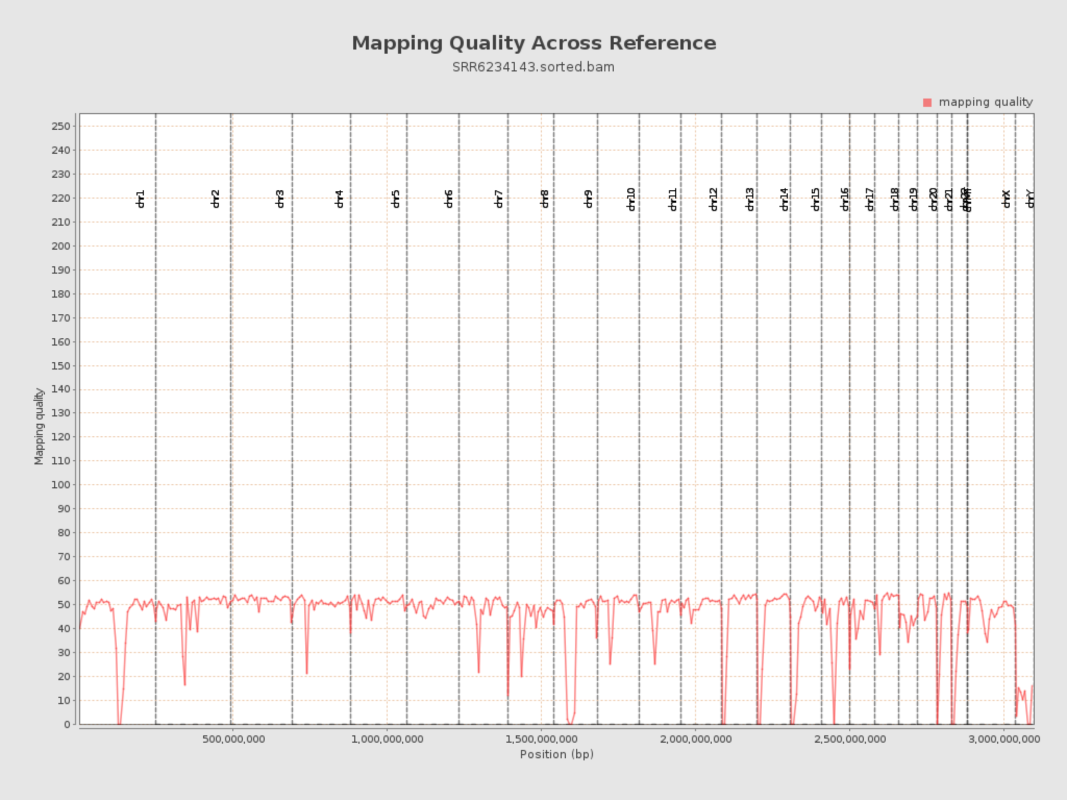
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram