Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 15:56:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234101.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_SRR6234101 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234101.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 15:56:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234101.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,321,703
Mapped reads	5,022,518 / 94.38%
Unmapped reads	299,185 / 5.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,937 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	535,688 / 10.07%
Duplication rate	8.71%
Clipped reads	2,679,145 / 50.34%

2.2. ACGT Content

Number/percentage of A's	83,423,882 / 25.82%
Number/percentage of C's	58,351,796 / 18.06%
Number/percentage of T's	104,924,977 / 32.47%
Number/percentage of G's	76,390,903 / 23.64%
Number/percentage of N's	30,602 / 0.01%
GC Percentage	41.7%

2.3. Coverage

Mean	0.1044

Standard Deviation	1.1505

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

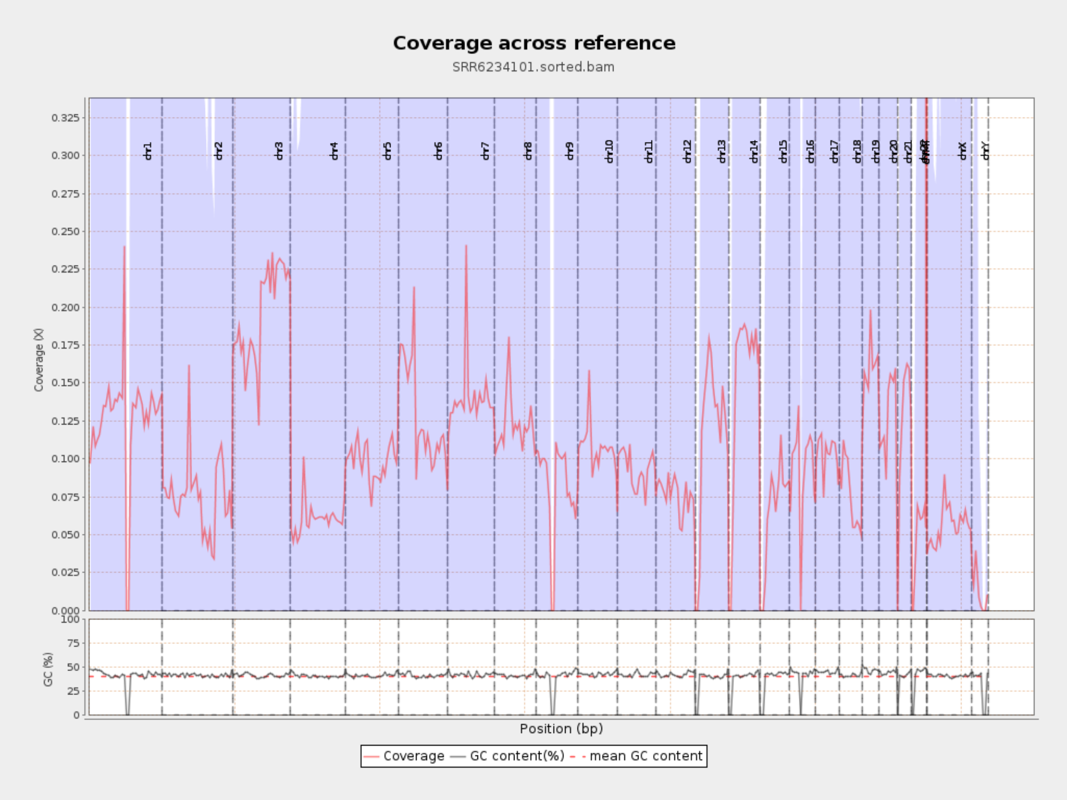
General error rate	0.56%
Mismatches	1,782,642
Insertions	20,893
Mapped reads with at least one insertion	0.41%
Deletions	74,170
Mapped reads with at least one deletion	1.46%
Homopolymer indels	44.04%

2.6. Chromosome stats

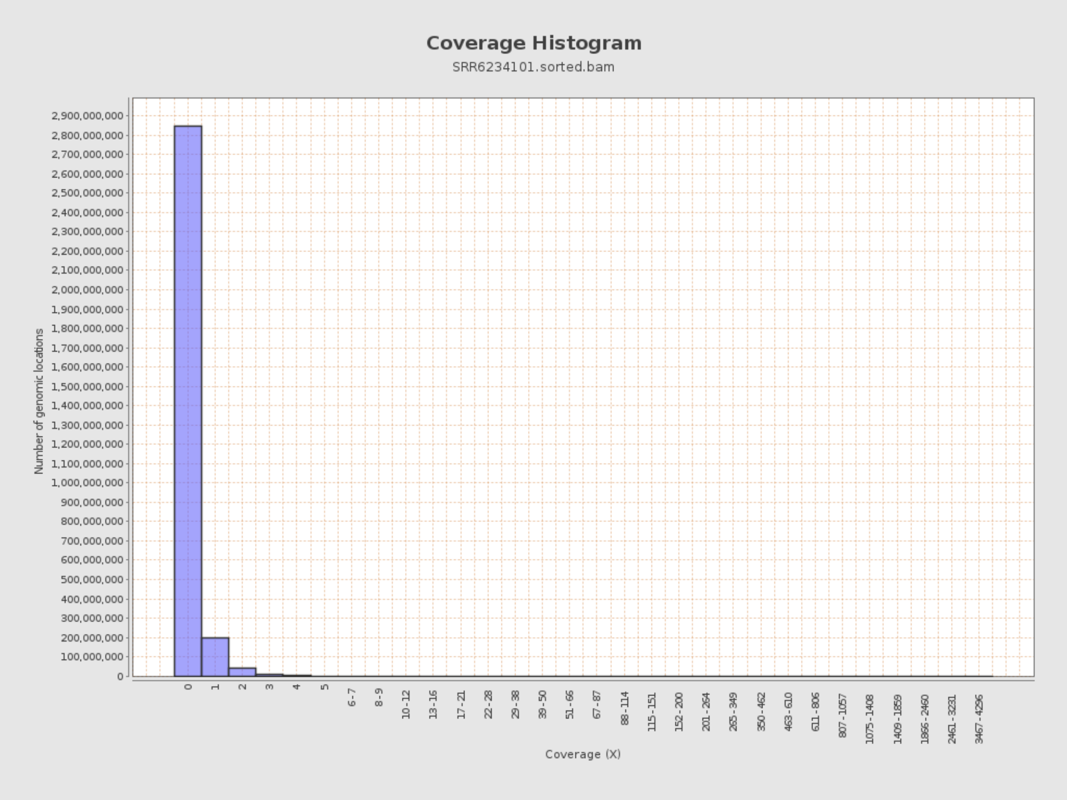
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31378698	0.1259	2.5004
chr2	243199373	18271205	0.0751	1.9602
chr3	198022430	38695326	0.1954	0.5586
chr4	191154276	11509436	0.0602	0.385
chr5	180915260	17782465	0.0983	0.4128
chr6	171115067	22145507	0.1294	0.8146
chr7	159138663	22501757	0.1414	1.6518

chr8	146364022	17947422	0.1226	1.0859
chr9	141213431	11331922	0.0802	0.7026
chr10	135534747	14662524	0.1082	0.7911
chr11	135006516	12533783	0.0928	0.6702
chr12	133851895	10146146	0.0758	0.3873
chr13	115169878	13466319	0.1169	0.4952
chr14	107349540	15938189	0.1485	0.5321
chr15	102531392	6722253	0.0656	0.3926
chr16	90354753	8477806	0.0938	0.4852
chr17	81195210	8348790	0.1028	0.4734
chr18	78077248	5958342	0.0763	1.7053
chr19	59128983	9453214	0.1599	1.3984
chr20	63025520	8022650	0.1273	0.4832
chr21	48129895	5921994	0.123	0.4735
chr22	51304566	2382098	0.0464	0.2587
chrMT	16571	220676	13.317	7.9759
chrX	155270560	8732102	0.0562	0.4419
chrY	59373566	701049	0.0118	0.2535

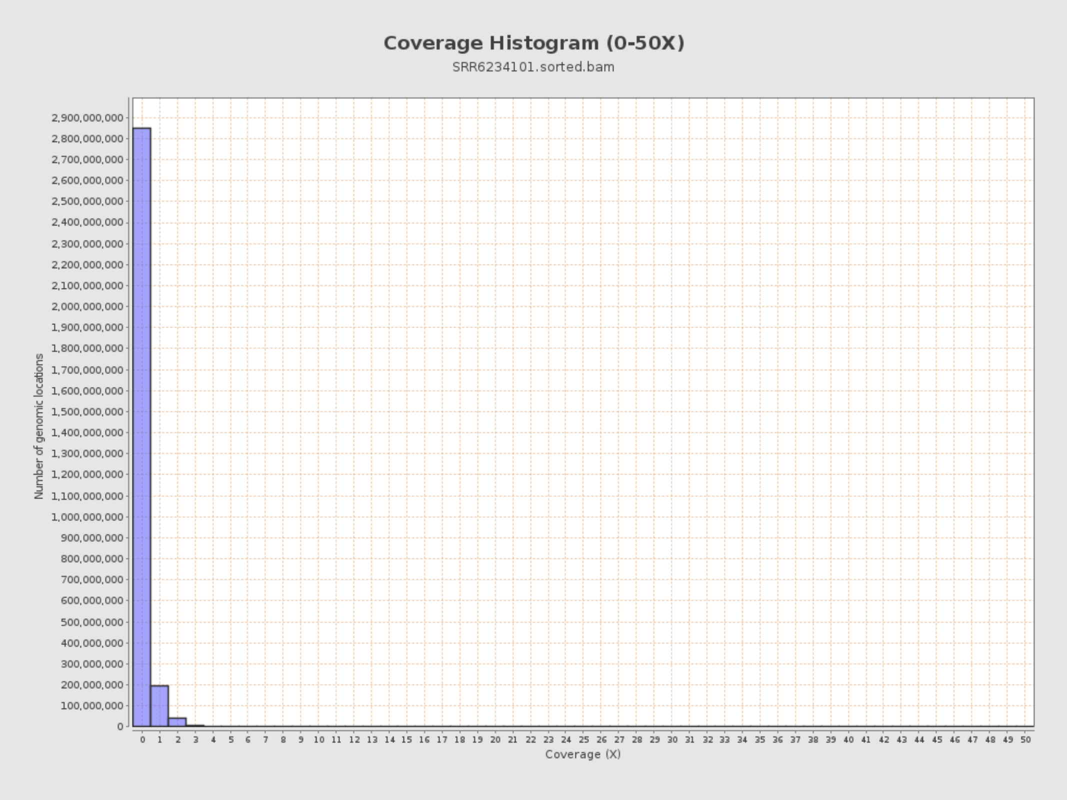
3. Results : Coverage across reference



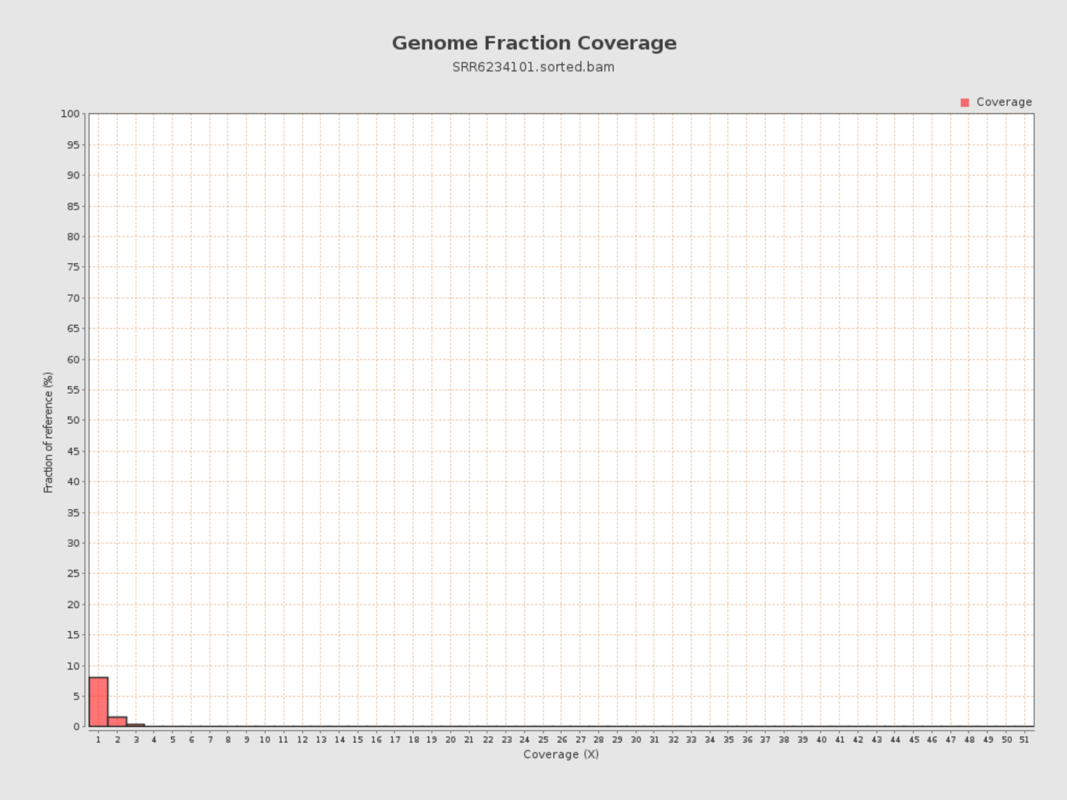
4. Results : Coverage Histogram



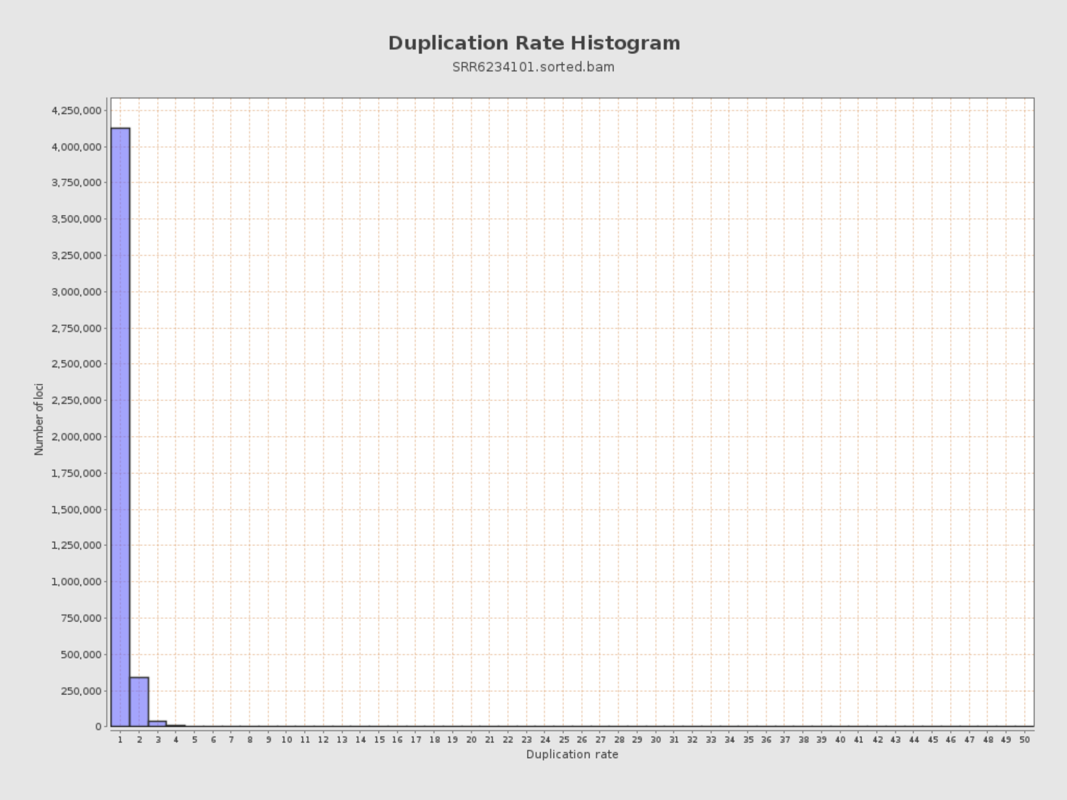
5. Results : Coverage Histogram (0-50X)



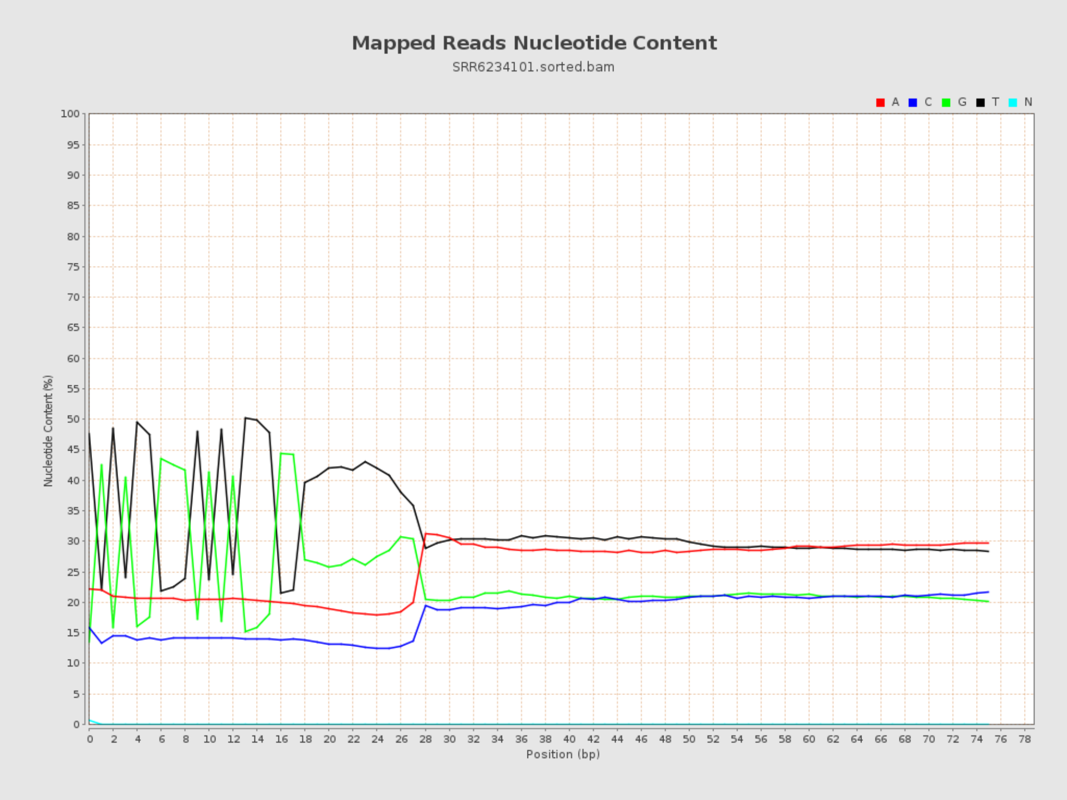
6. Results : Genome Fraction Coverage



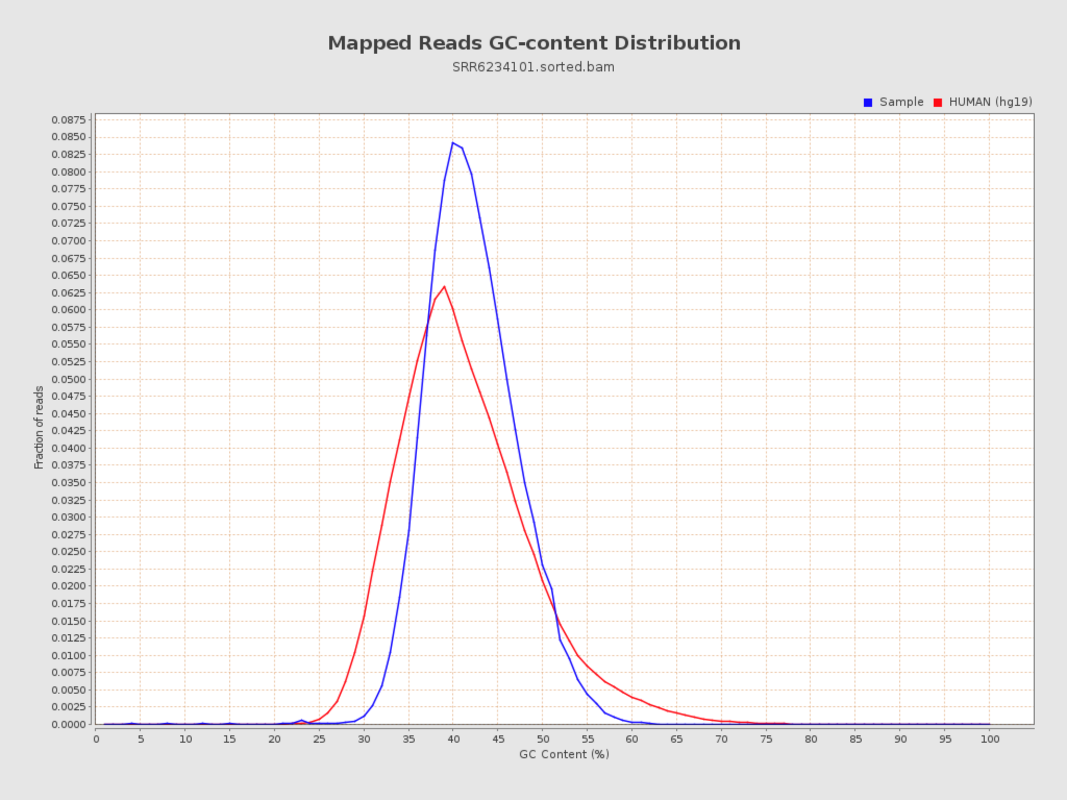
7. Results : Duplication Rate Histogram



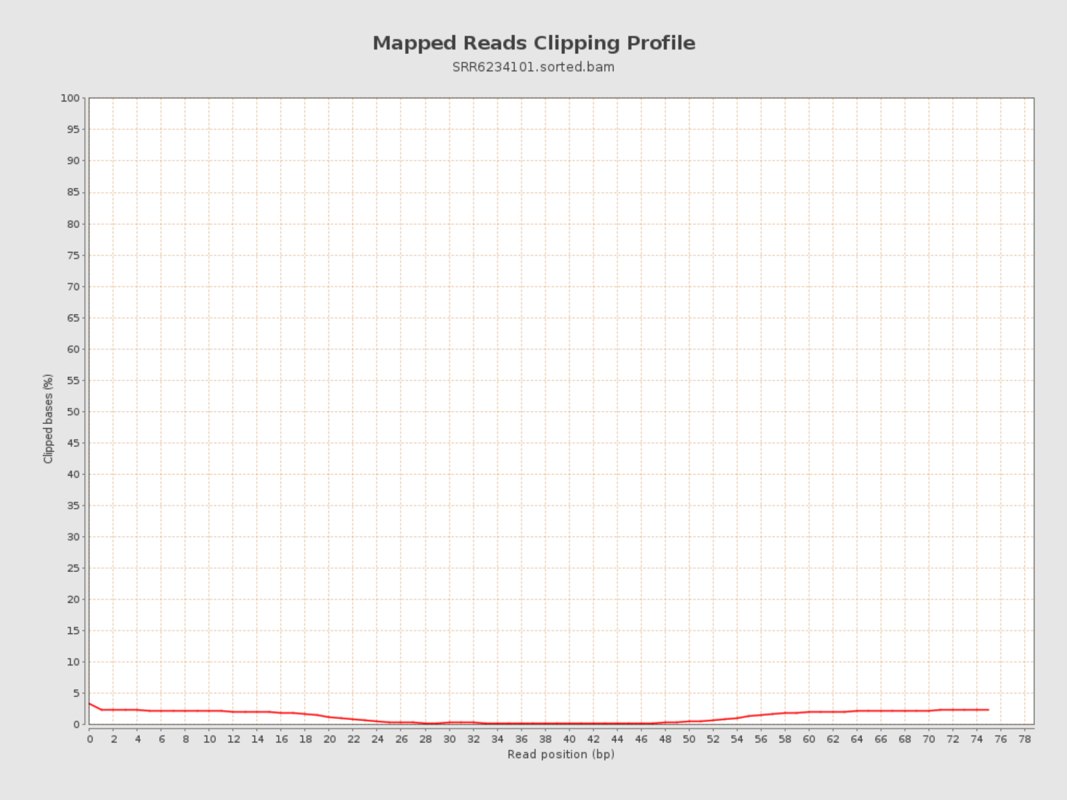
8. Results : Mapped Reads Nucleotide Content



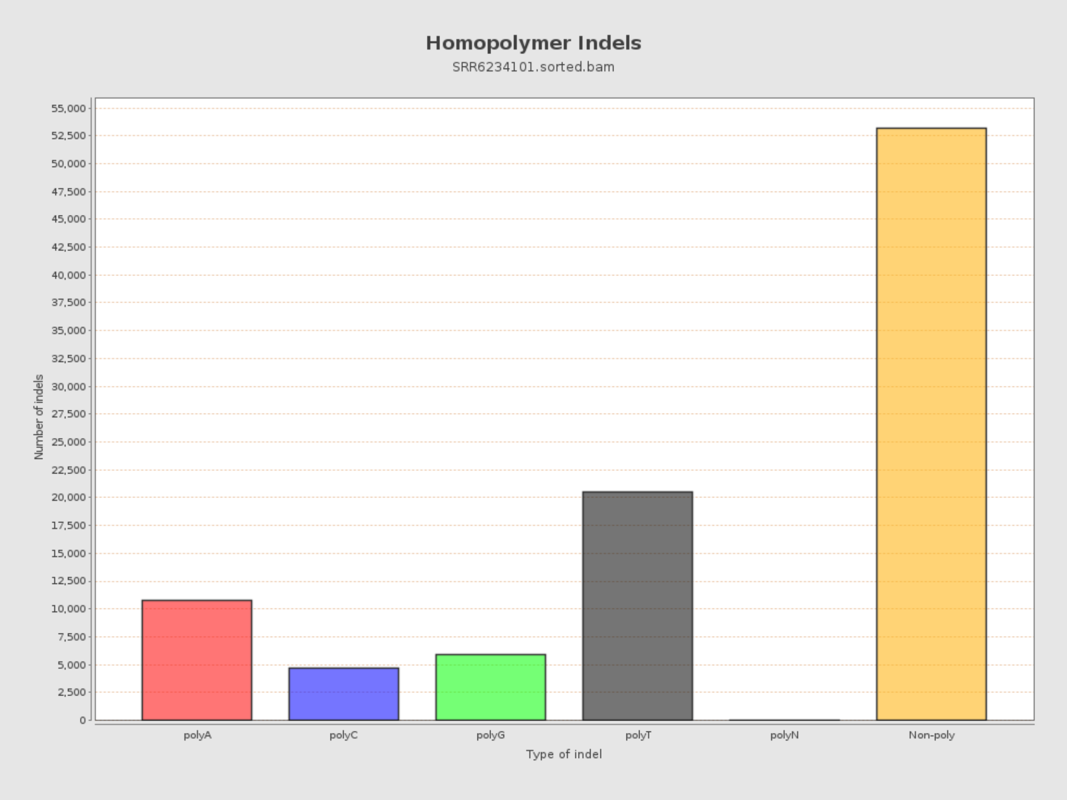
9. Results : Mapped Reads GC-content Distribution



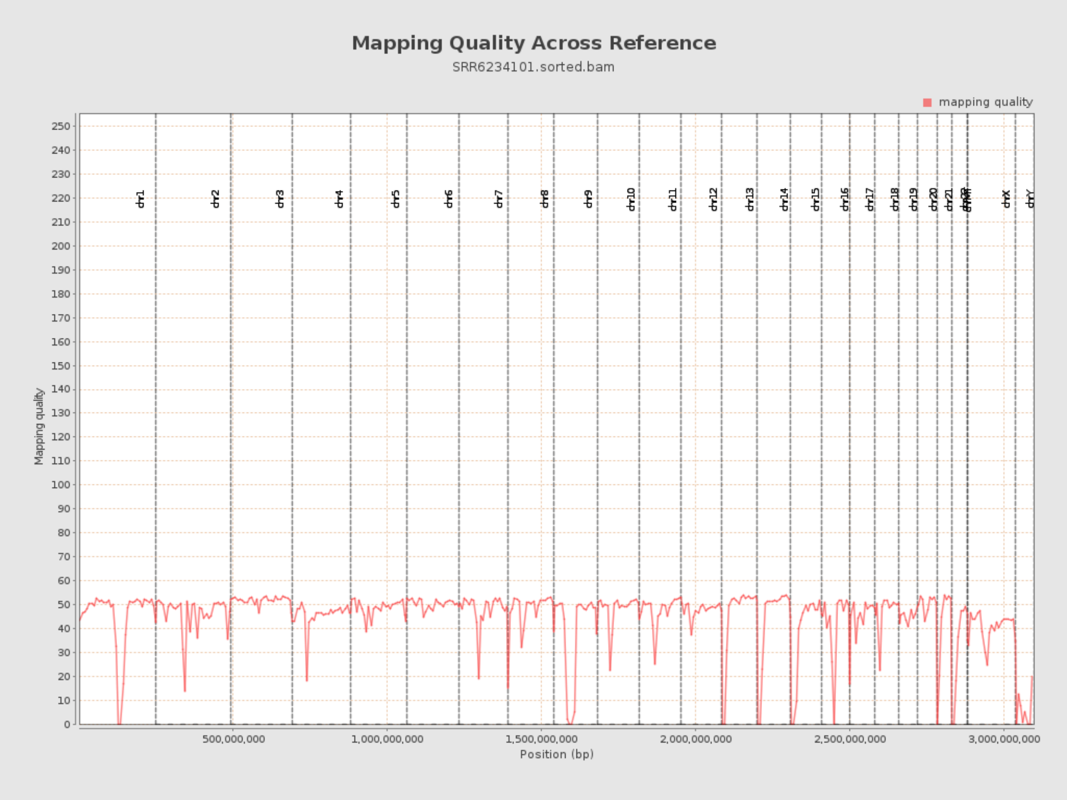
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram