Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:51:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234086.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_SRR6234086 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234086.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:51:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,909,907
Mapped reads	778,267 / 40.75%
Unmapped reads	1,131,640 / 59.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,683 / 0.19%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	68,104 / 3.57%
Duplication rate	7.18%
Clipped reads	554,786 / 29.05%

2.2. ACGT Content

Number/percentage of A's	12,309,403 / 26.63%
Number/percentage of C's	7,362,248 / 15.92%
Number/percentage of T's	15,539,072 / 33.61%
Number/percentage of G's	11,014,638 / 23.83%
Number/percentage of N's	5,844 / 0.01%
GC Percentage	39.75%

2.3. Coverage

Mean	0.0149

Standard Deviation	0.1843

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

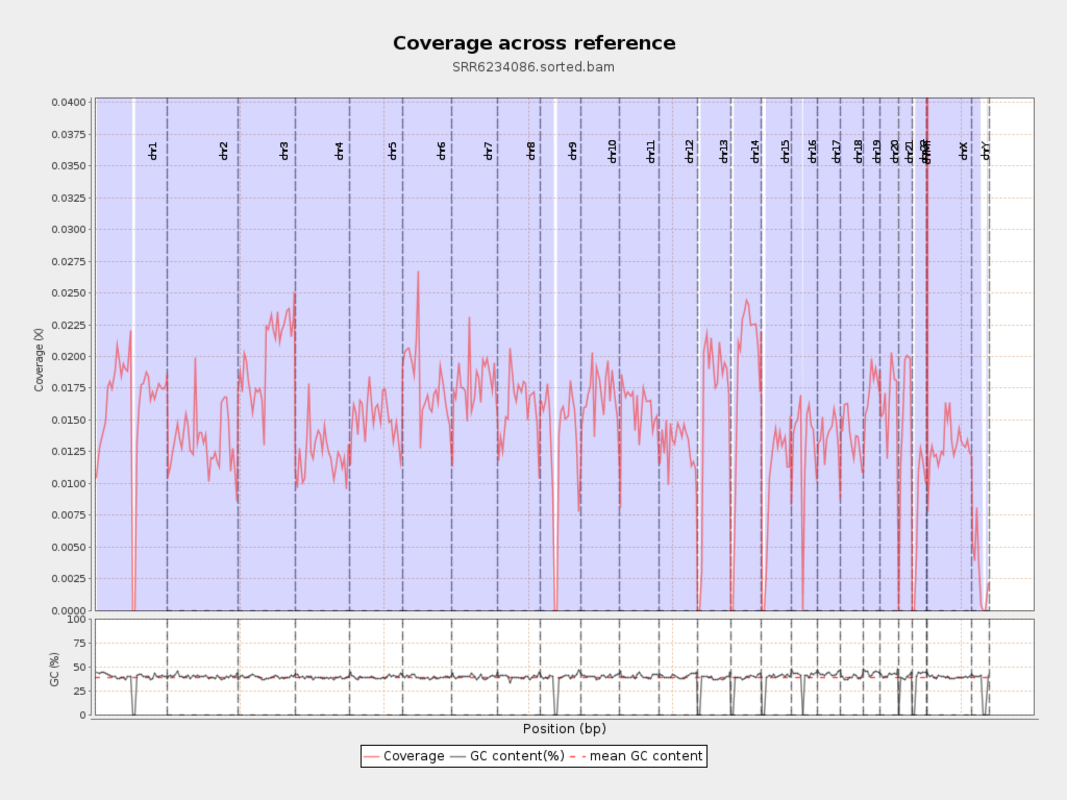
General error rate	1.12%
Mismatches	508,000
Insertions	4,216
Mapped reads with at least one insertion	0.54%
Deletions	18,675
Mapped reads with at least one deletion	2.36%
Homopolymer indels	45.59%

2.6. Chromosome stats

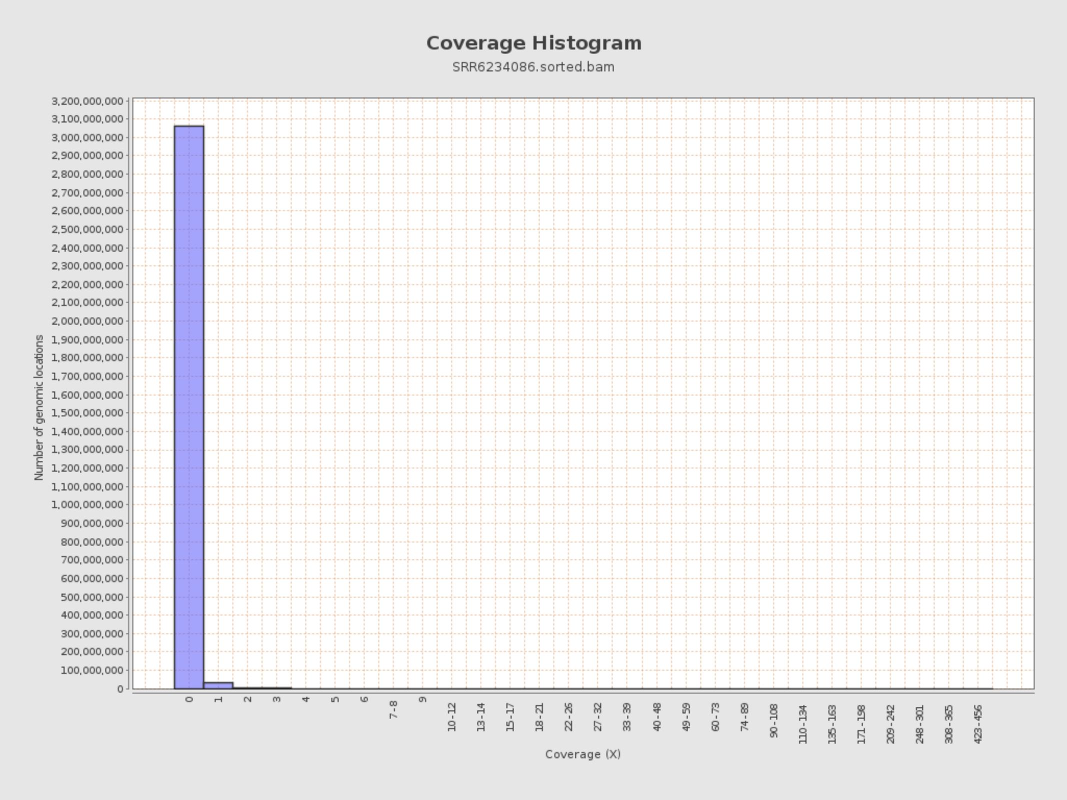
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4030028	0.0162	0.2101
chr2	243199373	3241037	0.0133	0.1866
chr3	198022430	3965385	0.02	0.1781
chr4	191154276	2355413	0.0123	0.1441
chr5	180915260	2766074	0.0153	0.1667
chr6	171115067	3046069	0.0178	0.1835
chr7	159138663	2836946	0.0178	0.2235

chr8	146364022	2345518	0.016	0.3112
chr9	141213431	1879536	0.0133	0.1595
chr10	135534747	2286228	0.0169	0.1748
chr11	135006516	2160191	0.016	0.1769
chr12	133851895	1749683	0.0131	0.1458
chr13	115169878	1847132	0.016	0.1639
chr14	107349540	1957342	0.0182	0.1719
chr15	102531392	1044677	0.0102	0.1316
chr16	90354753	1149452	0.0127	0.1427
chr17	81195210	1109191	0.0137	0.1511
chr18	78077248	1077572	0.0138	0.2961
chr19	59128983	1025161	0.0173	0.1826
chr20	63025520	1026668	0.0163	0.1603
chr21	48129895	735820	0.0153	0.1555
chr22	51304566	406808	0.0079	0.11
chrMT	16571	33439	2.0179	2.2567
chrX	155270560	2021191	0.013	0.1453
chrY	59373566	167633	0.0028	0.069

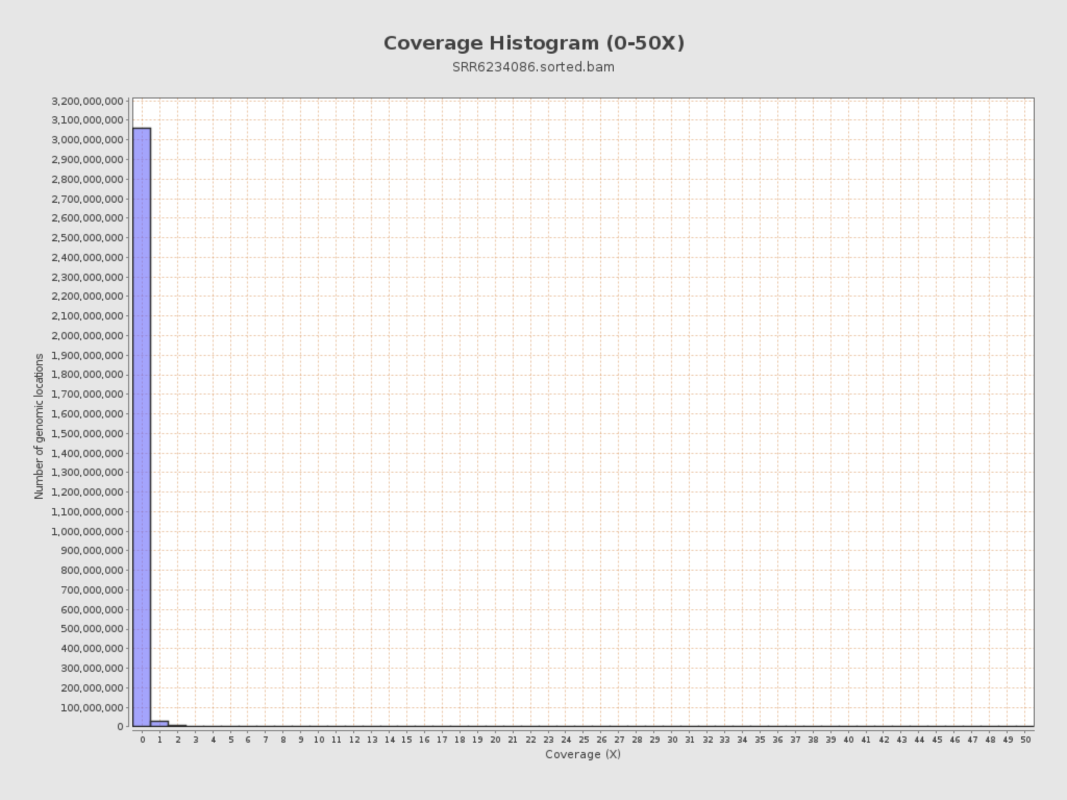
3. Results : Coverage across reference



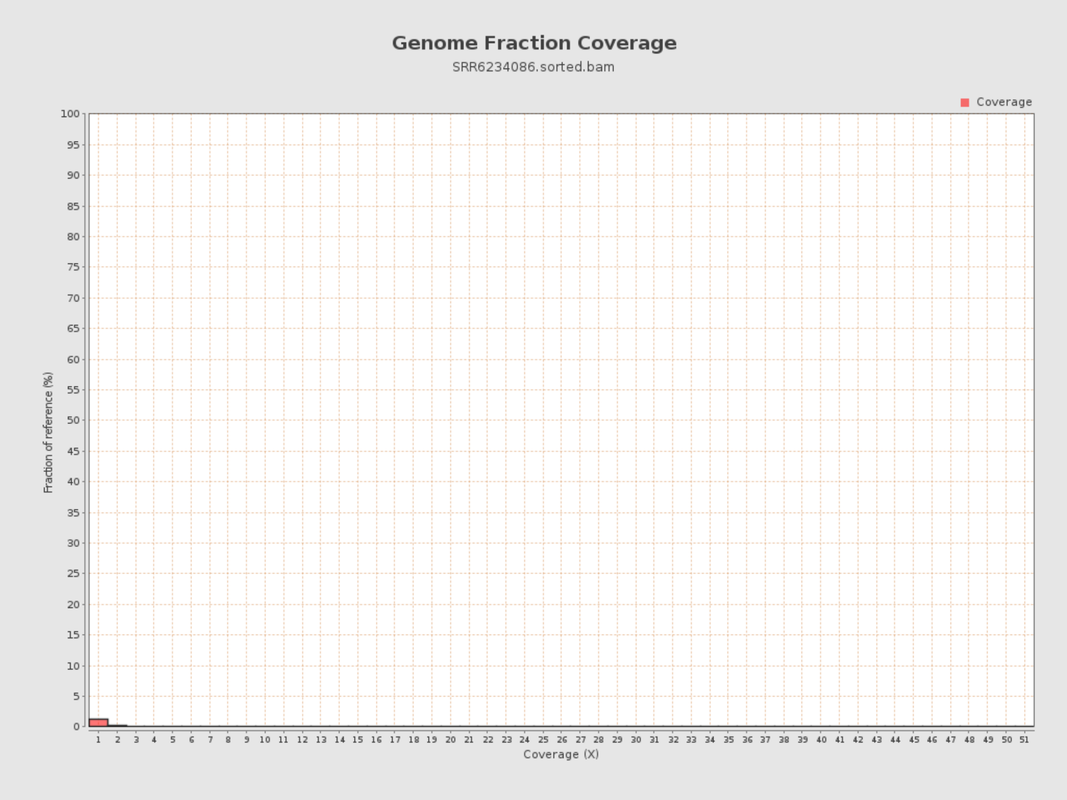
4. Results : Coverage Histogram



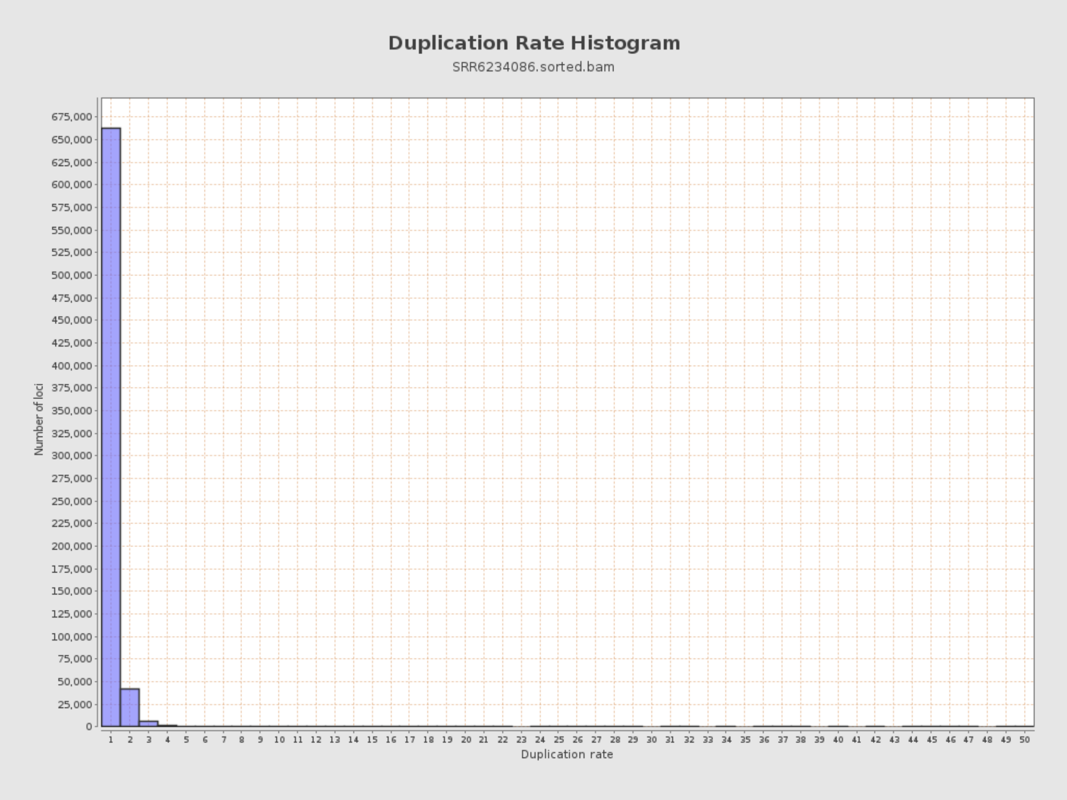
5. Results : Coverage Histogram (0-50X)



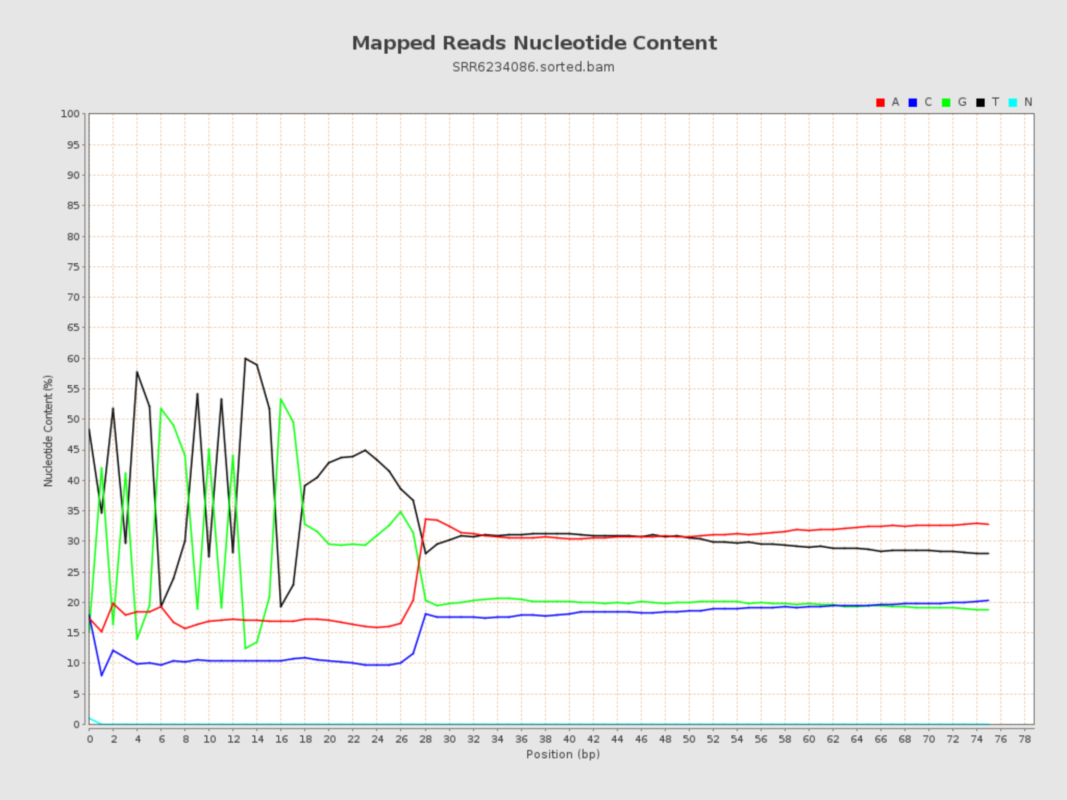
6. Results : Genome Fraction Coverage



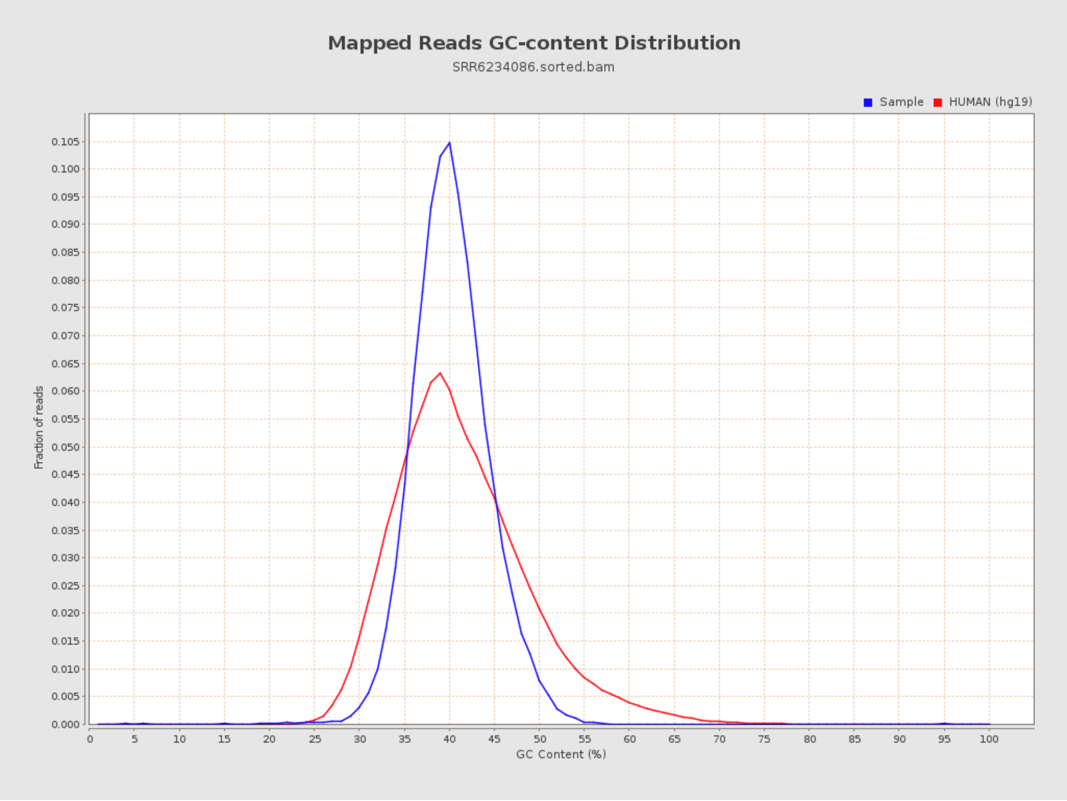
7. Results : Duplication Rate Histogram



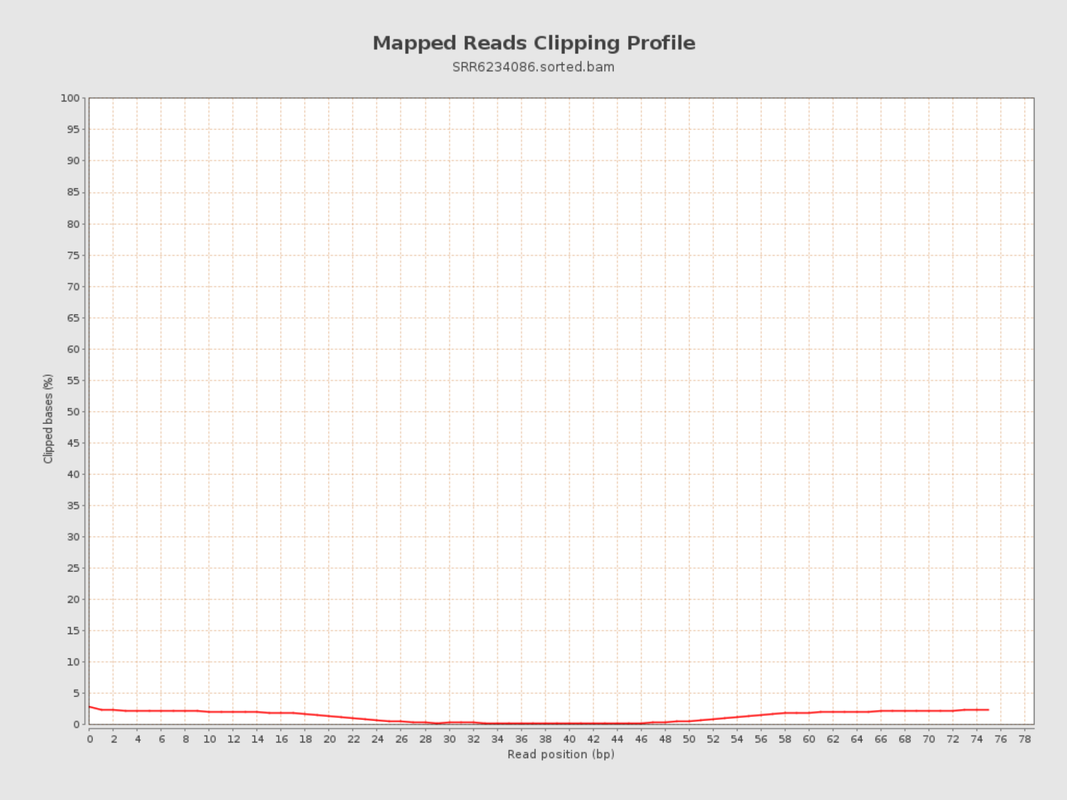
8. Results : Mapped Reads Nucleotide Content



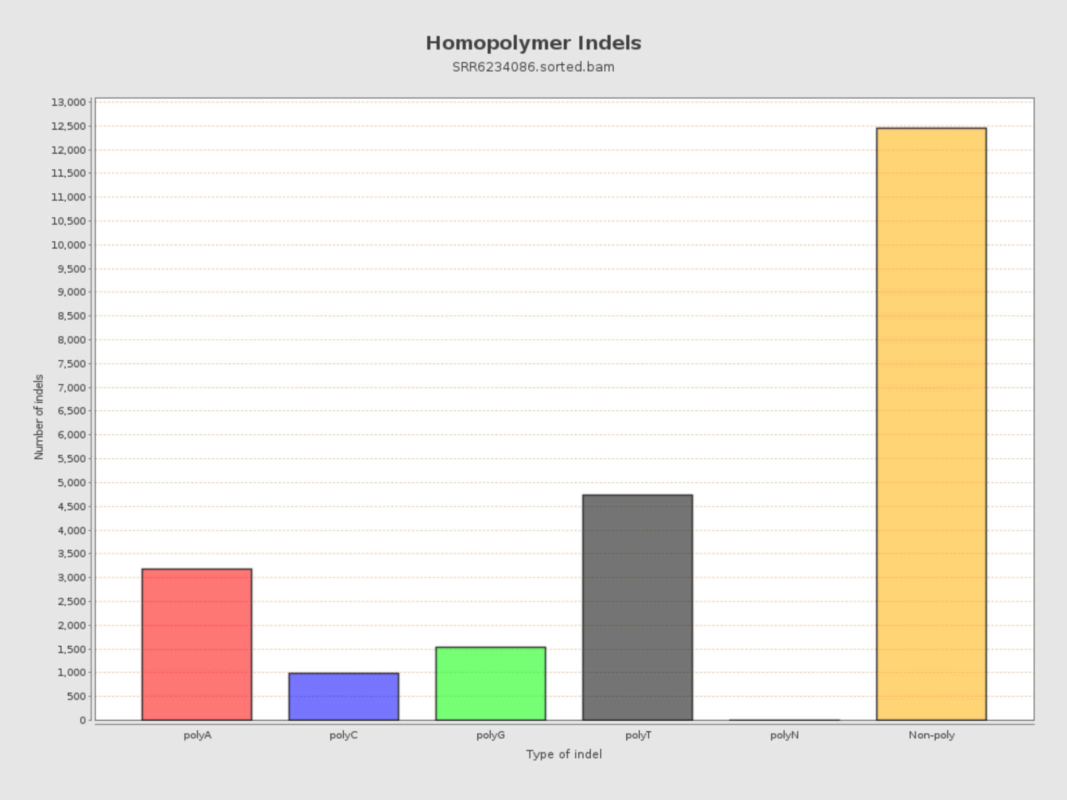
9. Results : Mapped Reads GC-content Distribution



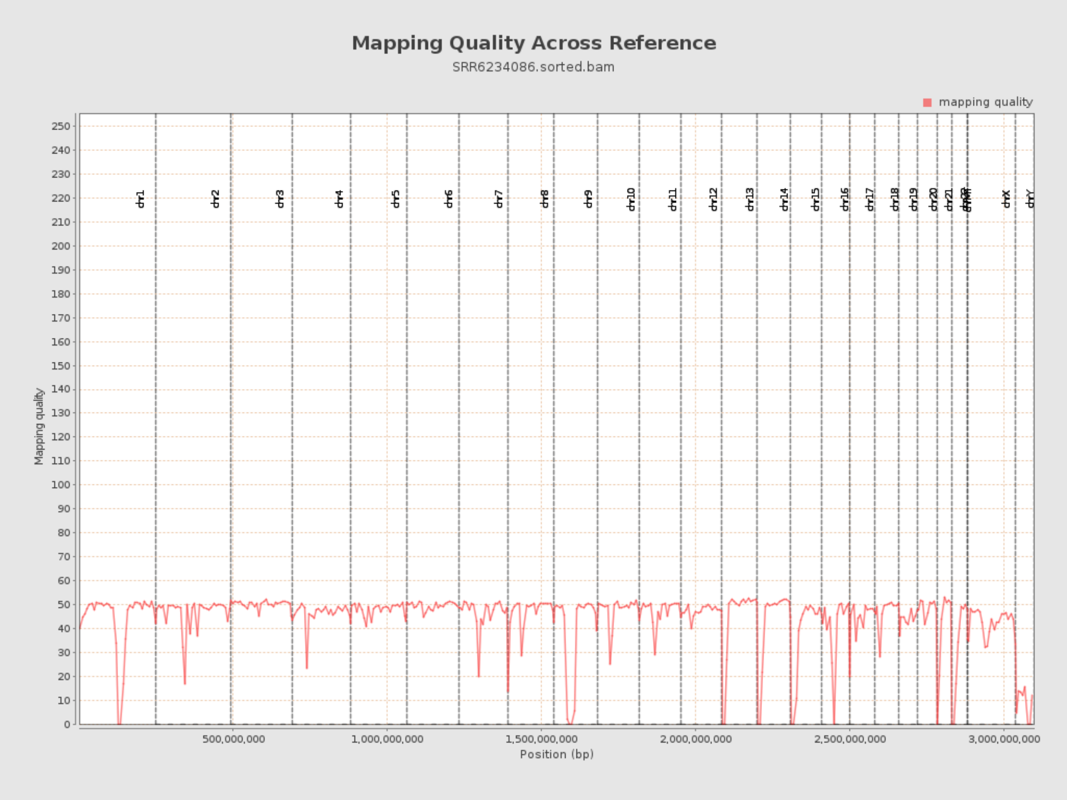
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram