Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:08:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234047.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_SRR6234047 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234047.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:08:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,009,227
Mapped reads	2,762,971 / 91.82%
Unmapped reads	246,256 / 8.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,129 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	180,203 / 5.99%
Duplication rate	4.87%
Clipped reads	1,411,052 / 46.89%

2.2. ACGT Content

Number/percentage of A's	46,317,008 / 25.79%
Number/percentage of C's	33,531,564 / 18.67%
Number/percentage of T's	56,565,394 / 31.5%
Number/percentage of G's	43,086,298 / 23.99%
Number/percentage of N's	68,229 / 0.04%
GC Percentage	42.67%

2.3. Coverage

Mean	0.058

Standard Deviation	0.7228

2.4. Mapping Quality

Mean Mapping Quality	41.21

2.5. Mismatches and indels

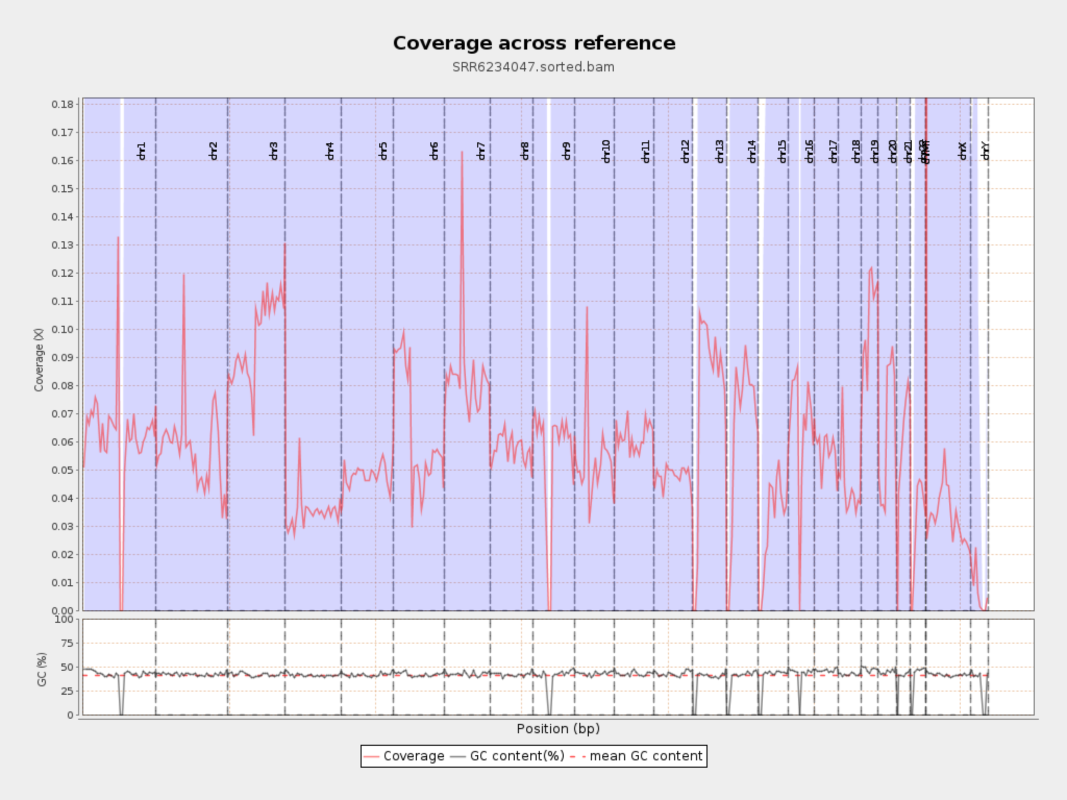
General error rate	0.68%
Mismatches	1,202,183
Insertions	13,170
Mapped reads with at least one insertion	0.47%
Deletions	43,017
Mapped reads with at least one deletion	1.54%
Homopolymer indels	43.88%

2.6. Chromosome stats

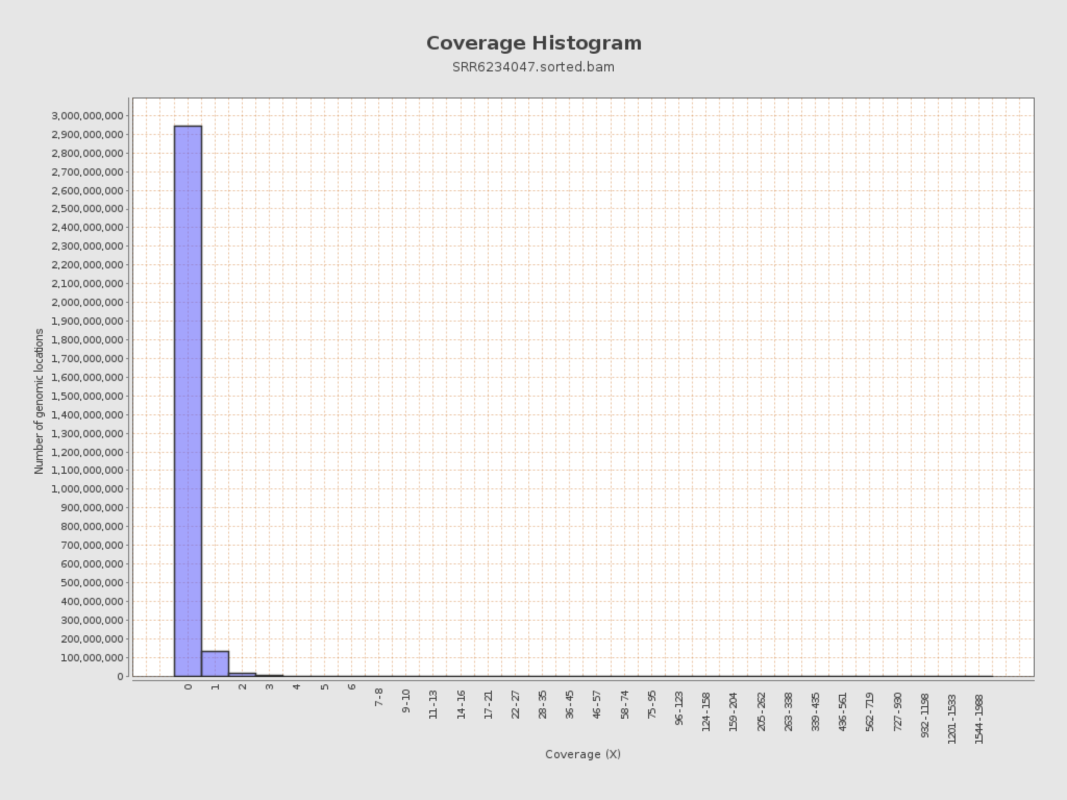
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15403003	0.0618	1.6764
chr2	243199373	13935982	0.0573	0.772
chr3	198022430	19142269	0.0967	0.3613
chr4	191154276	6733169	0.0352	0.253
chr5	180915260	8726116	0.0482	0.2584
chr6	171115067	10913380	0.0638	0.3901
chr7	159138663	13439043	0.0844	1.3179

chr8	146364022	8418894	0.0575	0.5956
chr9	141213431	7821967	0.0554	0.4776
chr10	135534747	7182733	0.053	0.6491
chr11	135006516	8271518	0.0613	0.4377
chr12	133851895	6436130	0.0481	0.266
chr13	115169878	8885121	0.0771	0.3286
chr14	107349540	7033556	0.0655	0.3509
chr15	102531392	3123675	0.0305	0.2349
chr16	90354753	5831361	0.0645	0.3722
chr17	81195210	4650105	0.0573	0.301
chr18	78077248	3479172	0.0446	1.1574
chr19	59128983	6128776	0.1037	0.984
chr20	63025520	4020761	0.0638	0.3482
chr21	48129895	2837448	0.059	0.3015
chr22	51304566	1555674	0.0303	0.196
chrMT	16571	68569	4.1379	3.163
chrX	155270560	5193505	0.0334	0.2855
chrY	59373566	413553	0.007	0.1592

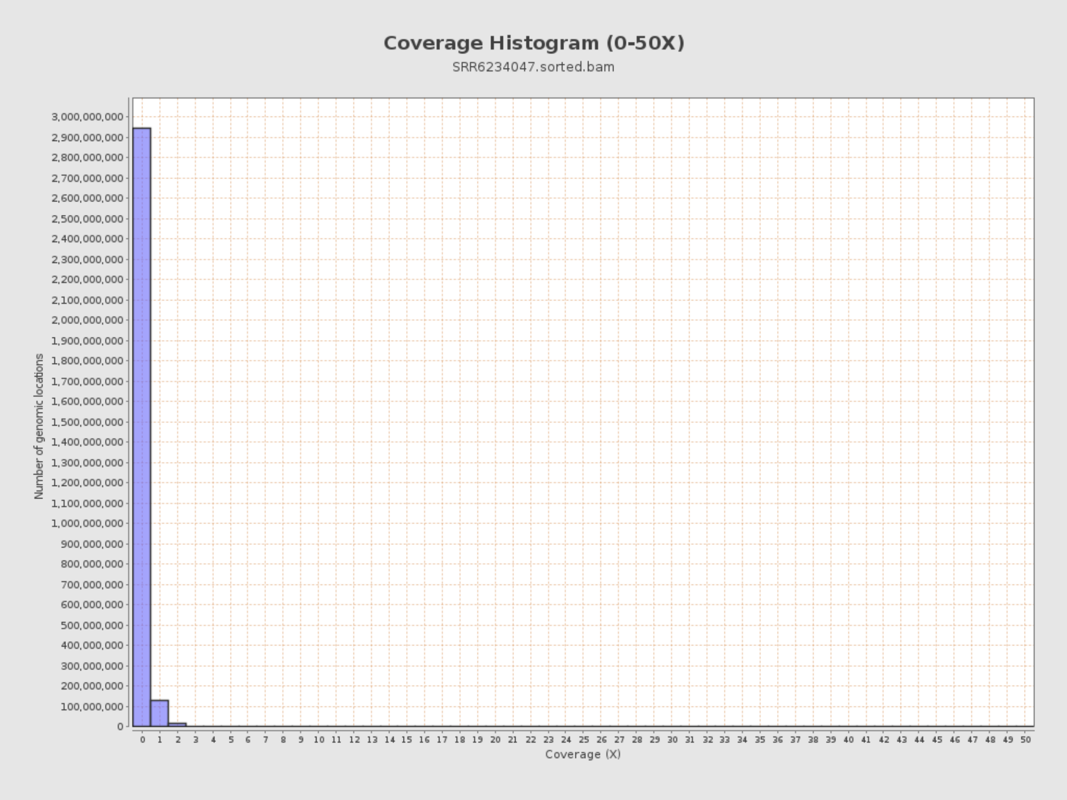
3. Results : Coverage across reference



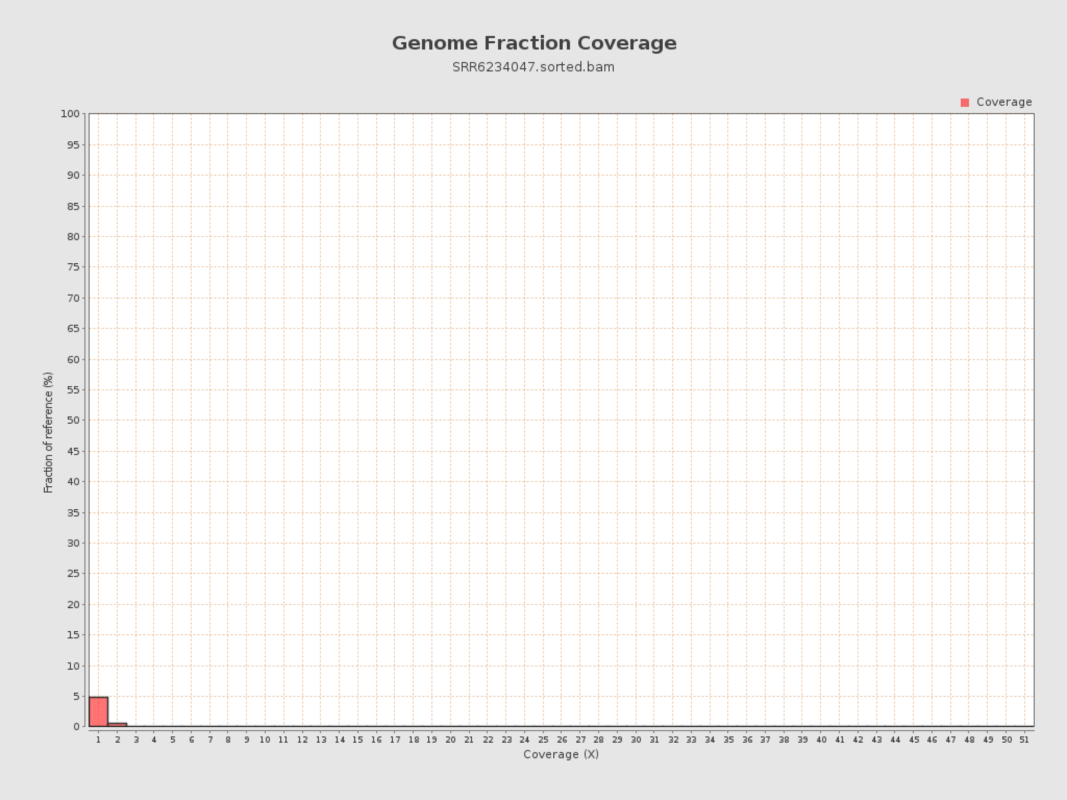
4. Results : Coverage Histogram



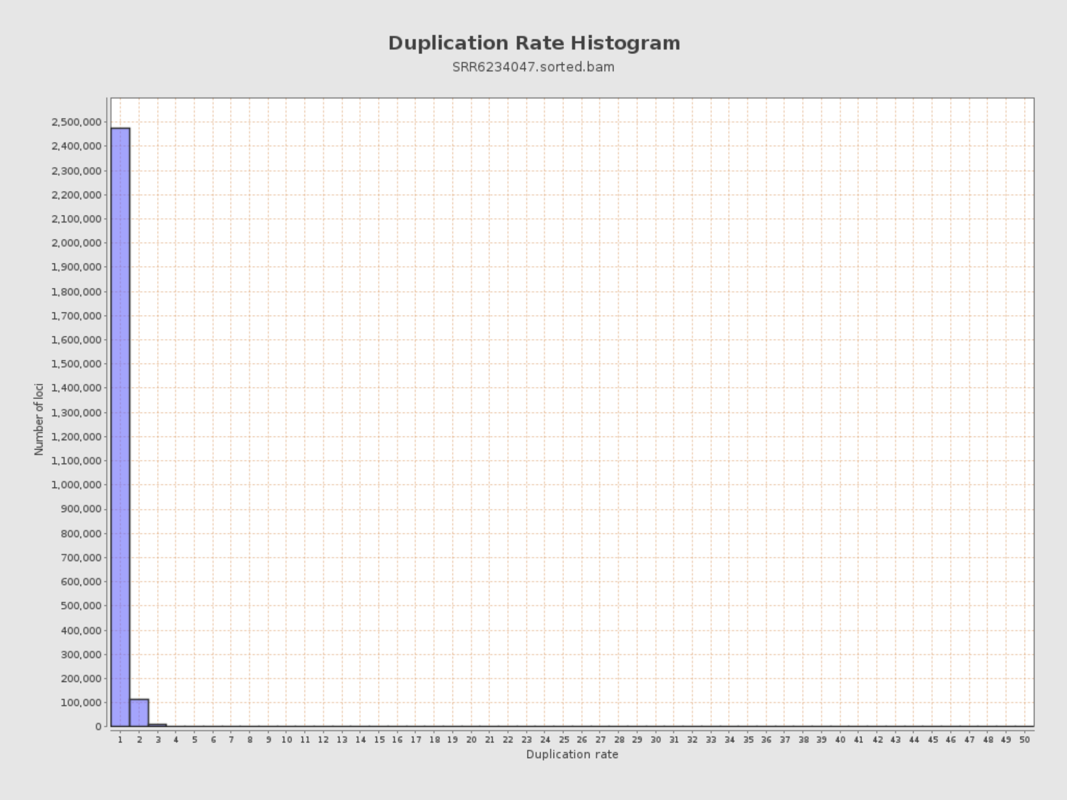
5. Results : Coverage Histogram (0-50X)



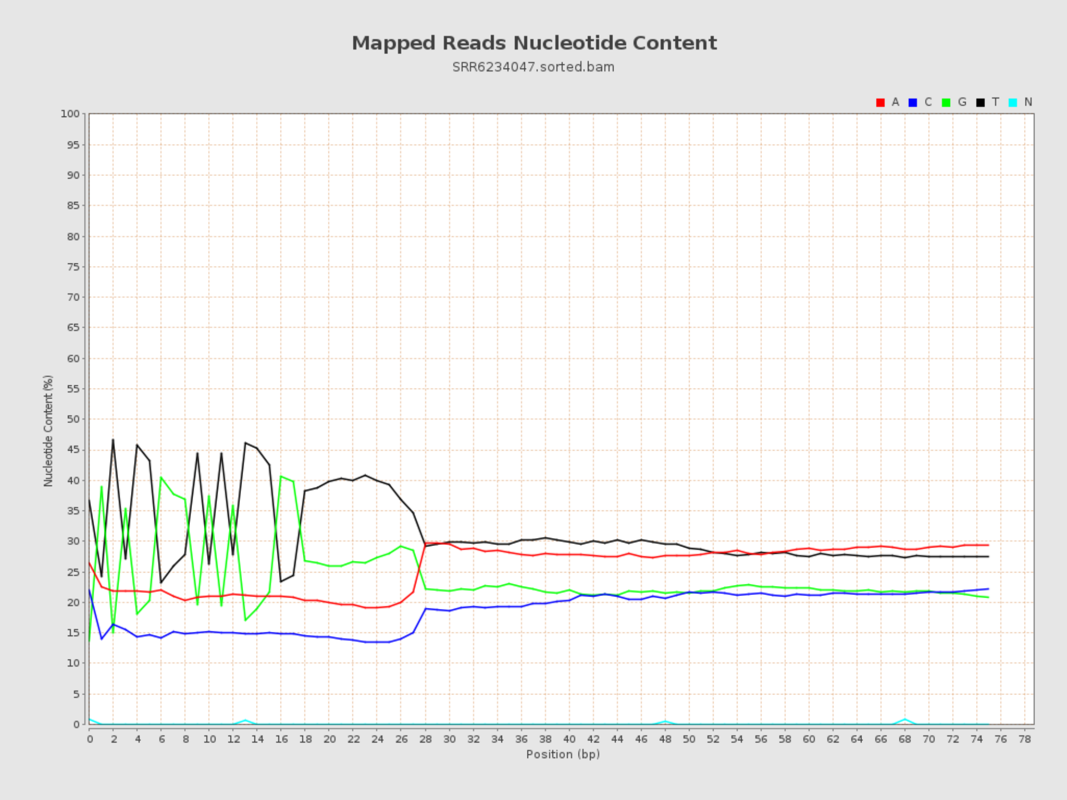
6. Results : Genome Fraction Coverage



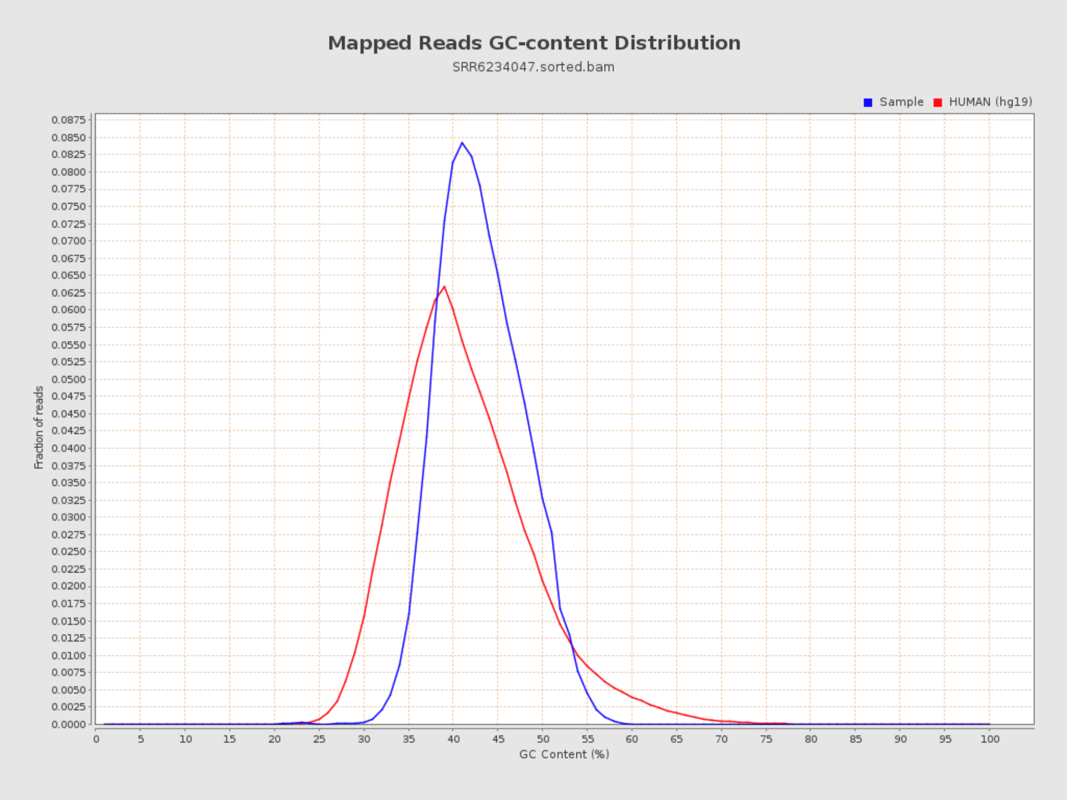
7. Results : Duplication Rate Histogram



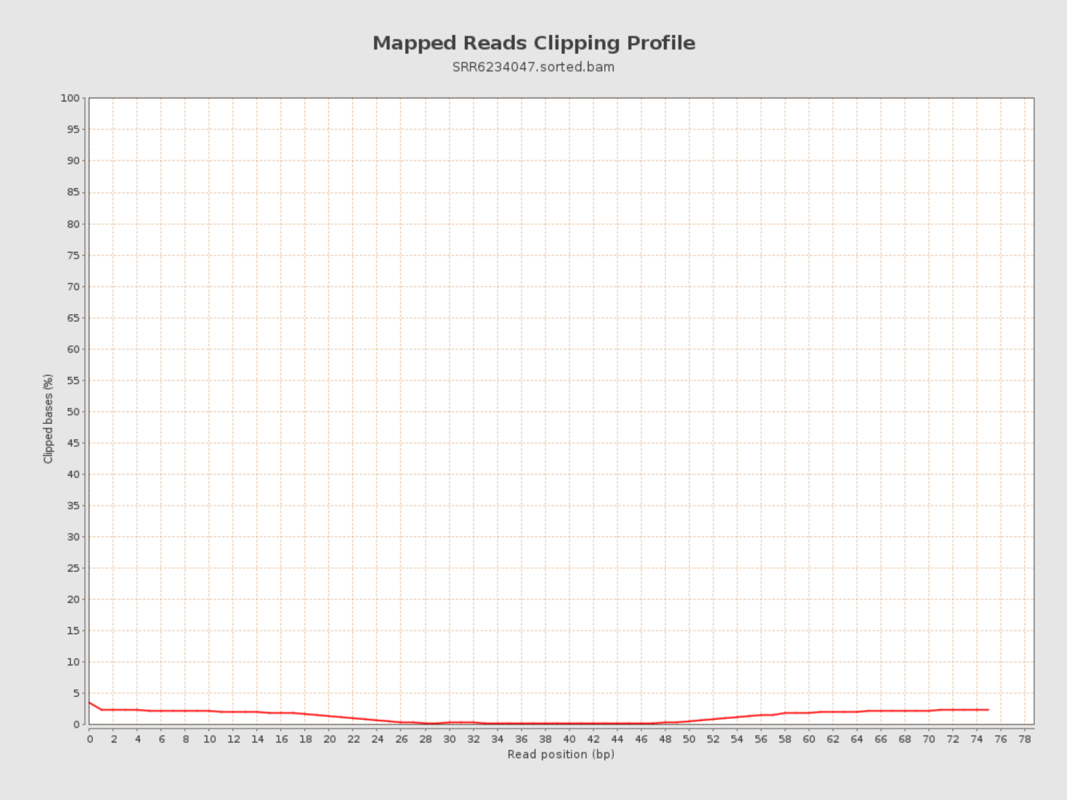
8. Results : Mapped Reads Nucleotide Content



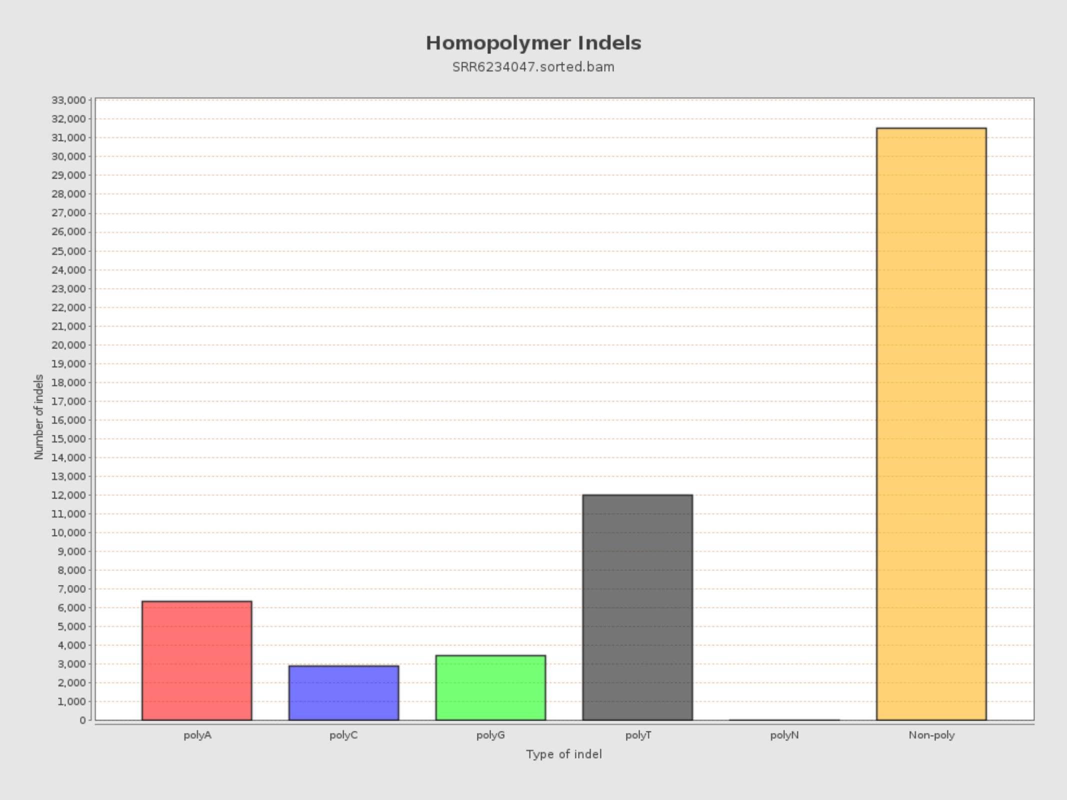
9. Results : Mapped Reads GC-content Distribution



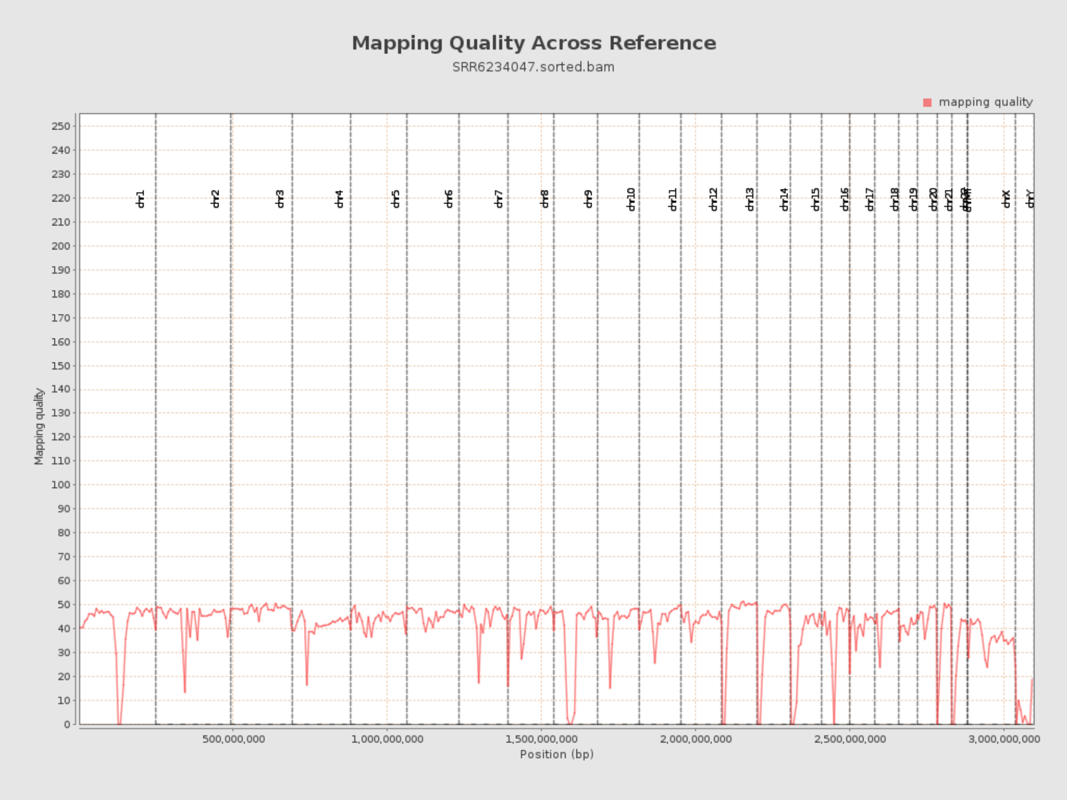
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram