Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 15:29:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234096.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_SRR6234096 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234096.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 15:29:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234096.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,956,514
Mapped reads	3,746,057 / 94.68%
Unmapped reads	210,457 / 5.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,277 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	400,183 / 10.11%
Duplication rate	8.93%
Clipped reads	2,006,313 / 50.71%

2.2. ACGT Content

Number/percentage of A's	60,023,529 / 25.05%
Number/percentage of C's	43,381,060 / 18.1%
Number/percentage of T's	78,540,506 / 32.77%
Number/percentage of G's	57,695,208 / 24.07%
Number/percentage of N's	22,396 / 0.01%
GC Percentage	42.17%

2.3. Coverage

Mean	0.0775

Standard Deviation	0.8266

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

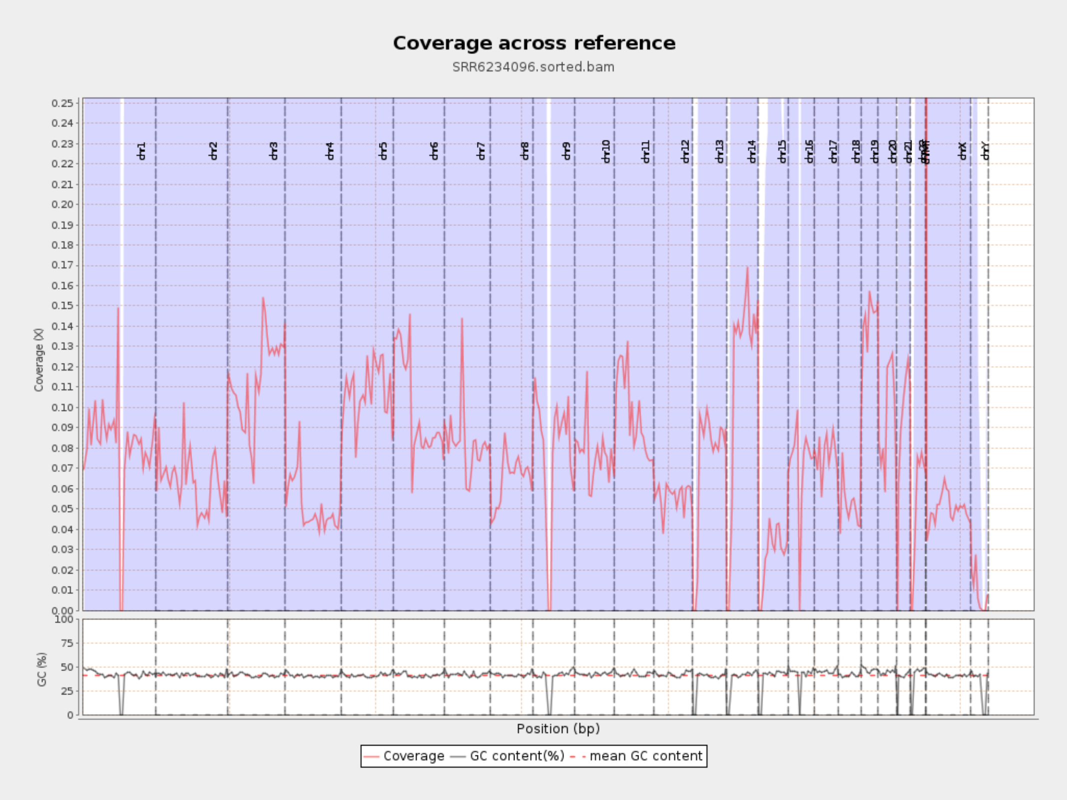
General error rate	0.56%
Mismatches	1,319,707
Insertions	15,660
Mapped reads with at least one insertion	0.41%
Deletions	58,197
Mapped reads with at least one deletion	1.54%
Homopolymer indels	43.59%

2.6. Chromosome stats

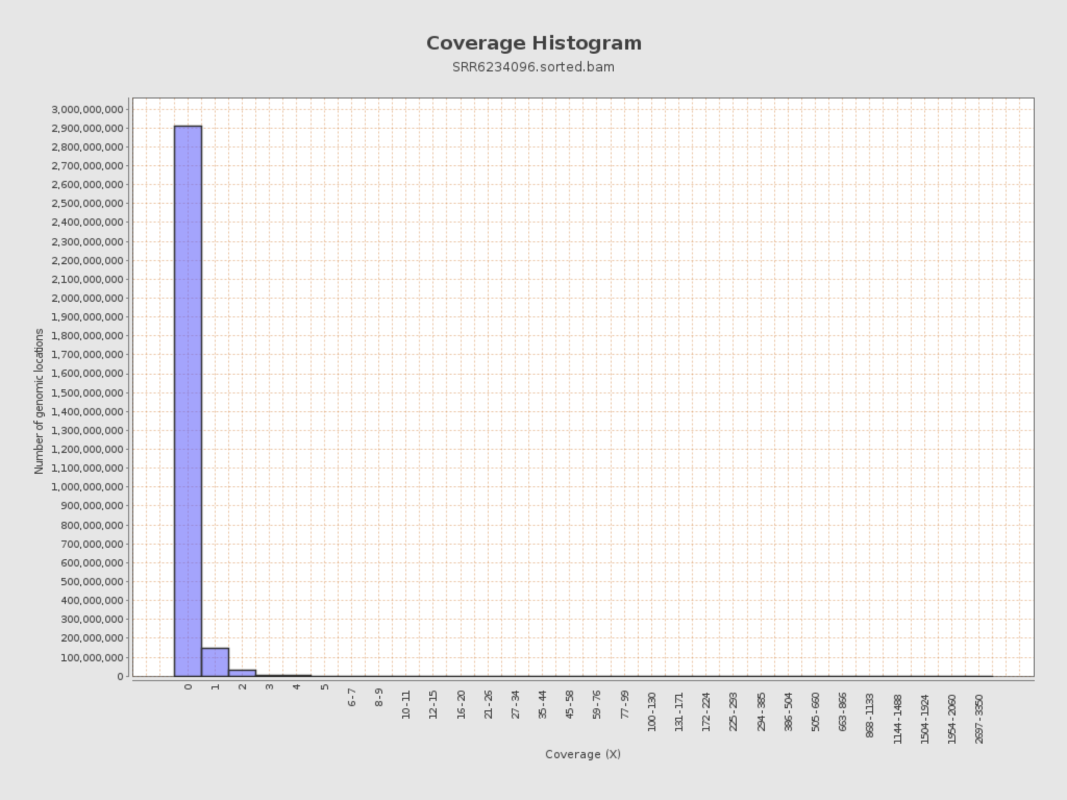
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20311934	0.0815	1.7537
chr2	243199373	15356761	0.0631	1.4969
chr3	198022430	22405319	0.1131	0.4229
chr4	191154276	9804679	0.0513	0.307
chr5	180915260	19423390	0.1074	0.4168
chr6	171115067	17029685	0.0995	0.6441
chr7	159138663	13245536	0.0832	1.0248

chr8	146364022	9459111	0.0646	0.5613
chr9	141213431	11117705	0.0787	0.5045
chr10	135534747	10373697	0.0765	0.5981
chr11	135006516	13082419	0.0969	0.5452
chr12	133851895	7559741	0.0565	0.314
chr13	115169878	8448540	0.0734	0.3929
chr14	107349540	12655740	0.1179	0.4533
chr15	102531392	2791474	0.0272	0.2585
chr16	90354753	6427751	0.0711	0.3864
chr17	81195210	6285205	0.0774	0.382
chr18	78077248	4042671	0.0518	1.2004
chr19	59128983	8454314	0.143	1.0462
chr20	63025520	6019558	0.0955	0.4067
chr21	48129895	4392449	0.0913	0.3968
chr22	51304566	2635209	0.0514	0.2781
chrMT	16571	166549	10.0506	6.0155
chrX	155270560	7753400	0.0499	0.3449
chrY	59373566	523247	0.0088	0.2119

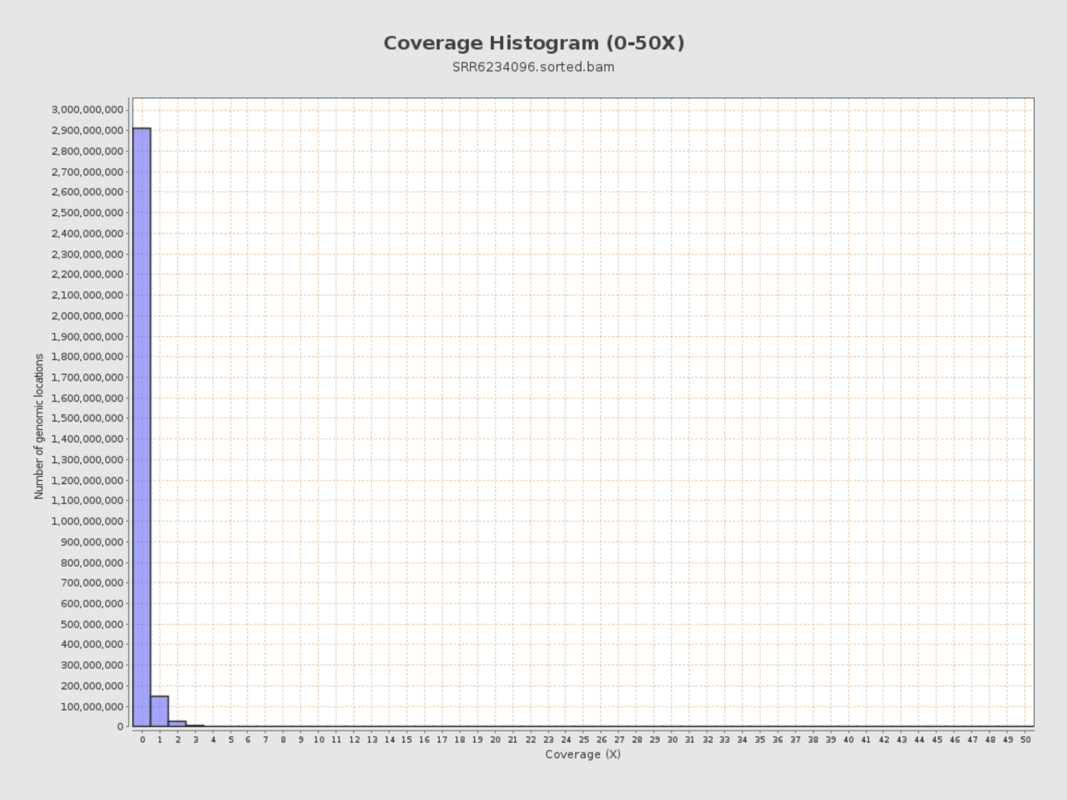
3. Results : Coverage across reference



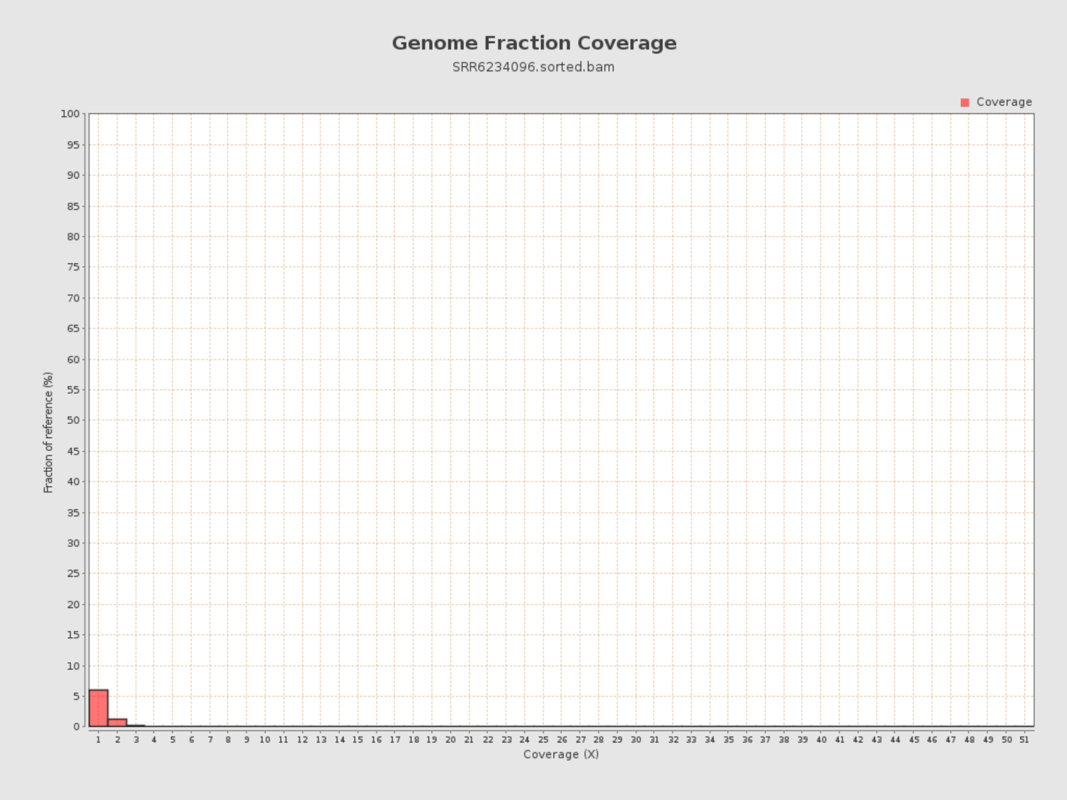
4. Results : Coverage Histogram



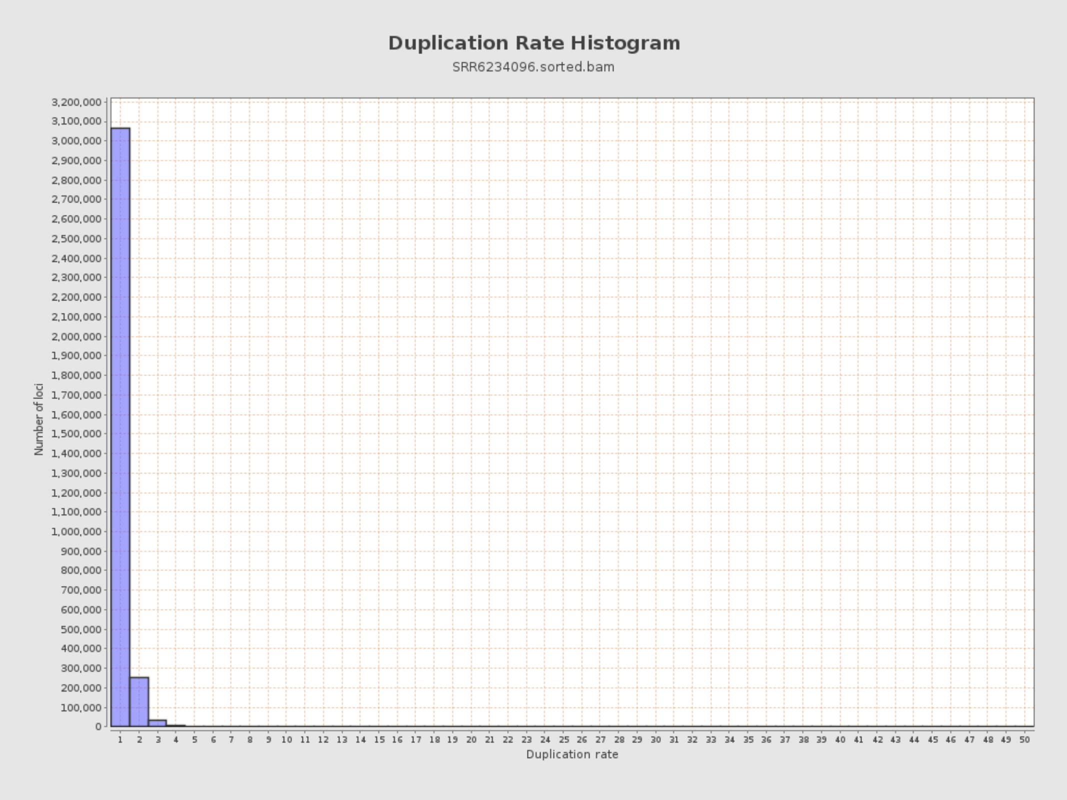
5. Results : Coverage Histogram (0-50X)



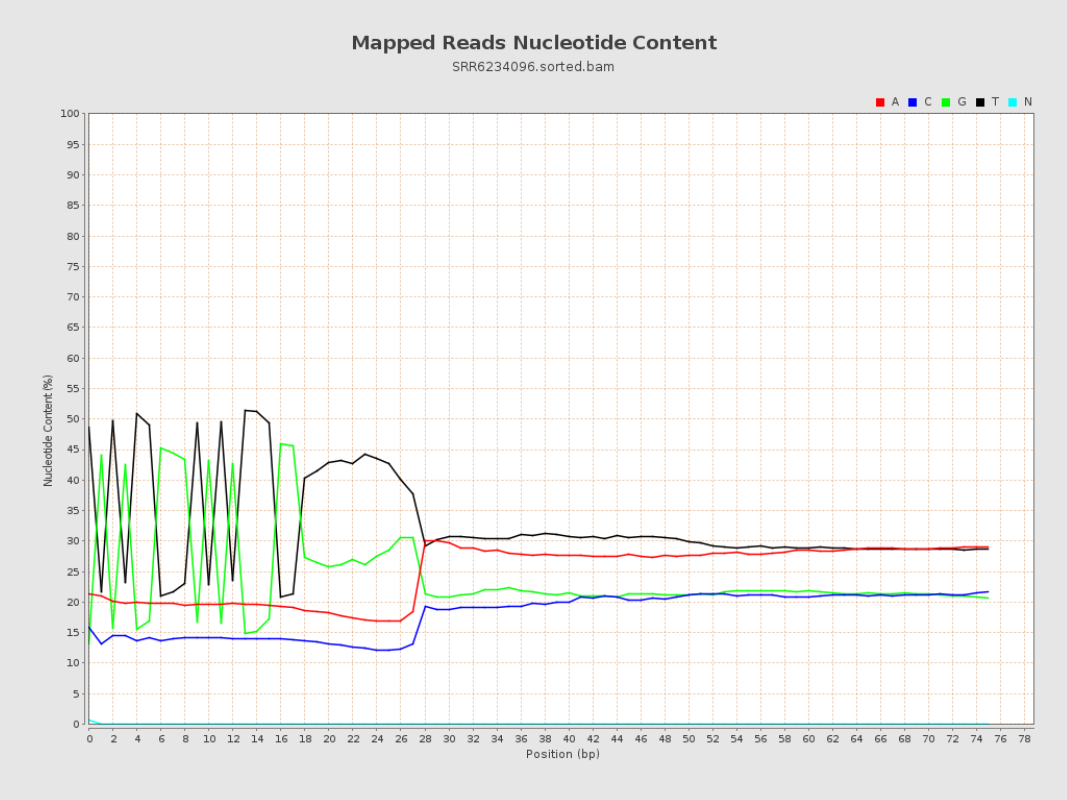
6. Results : Genome Fraction Coverage



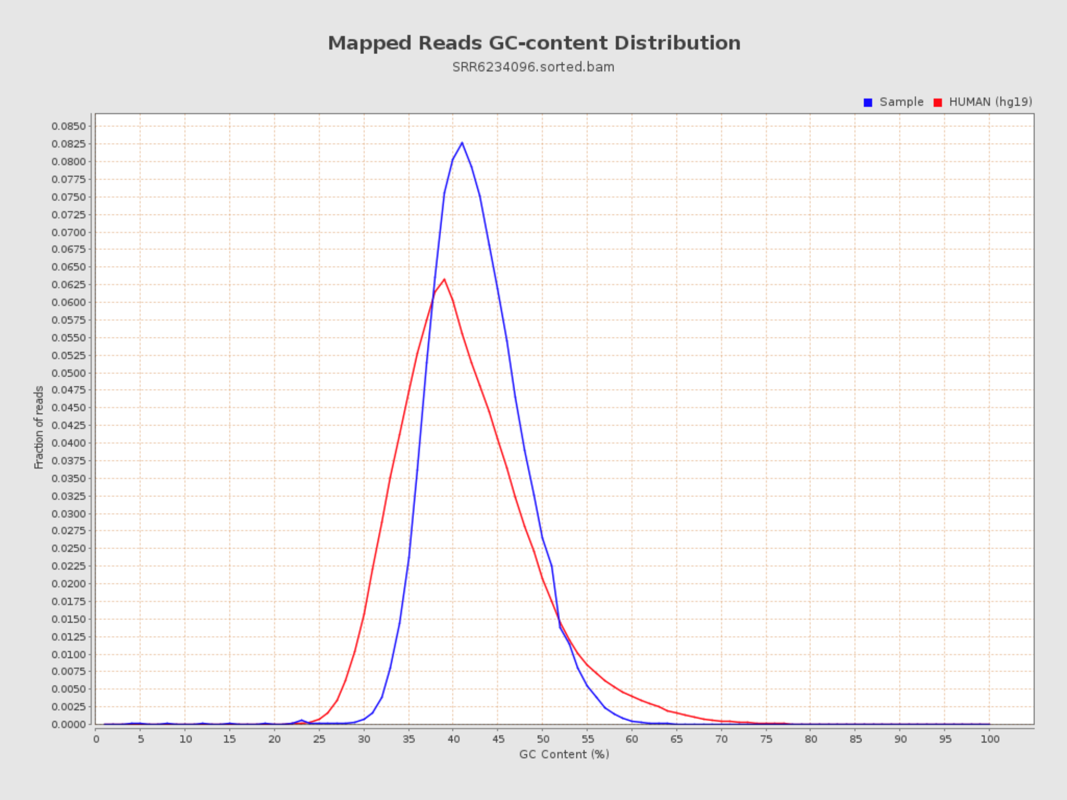
7. Results : Duplication Rate Histogram



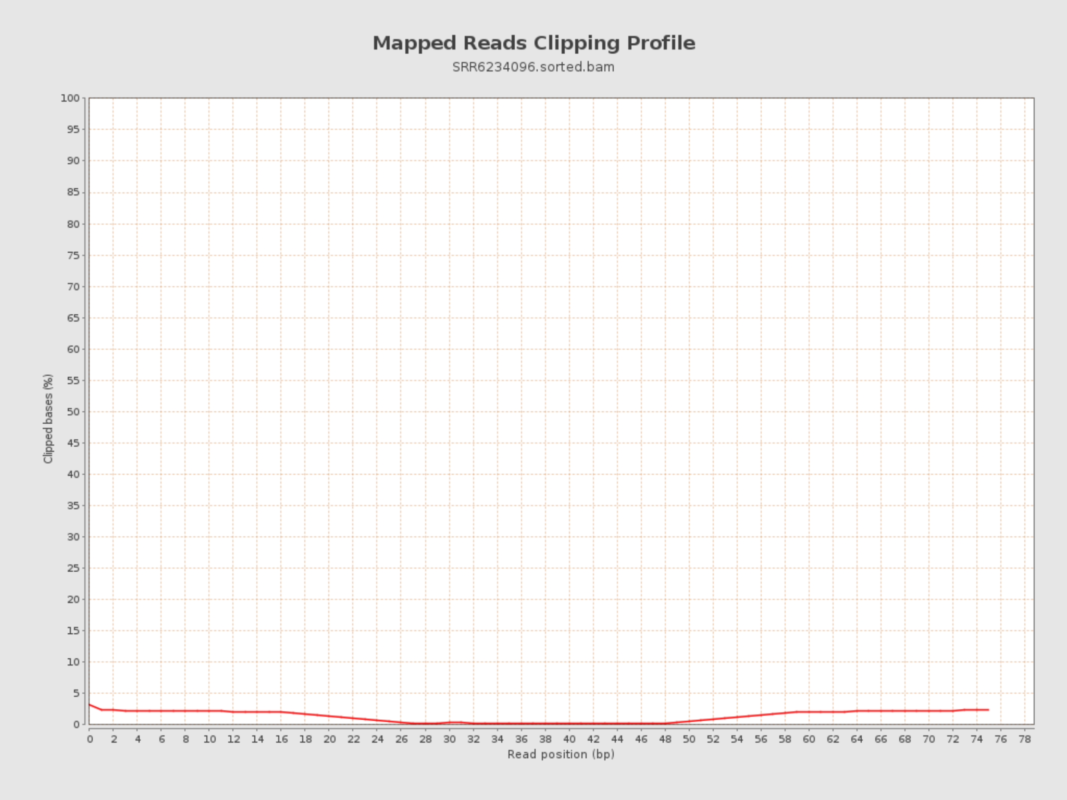
8. Results : Mapped Reads Nucleotide Content



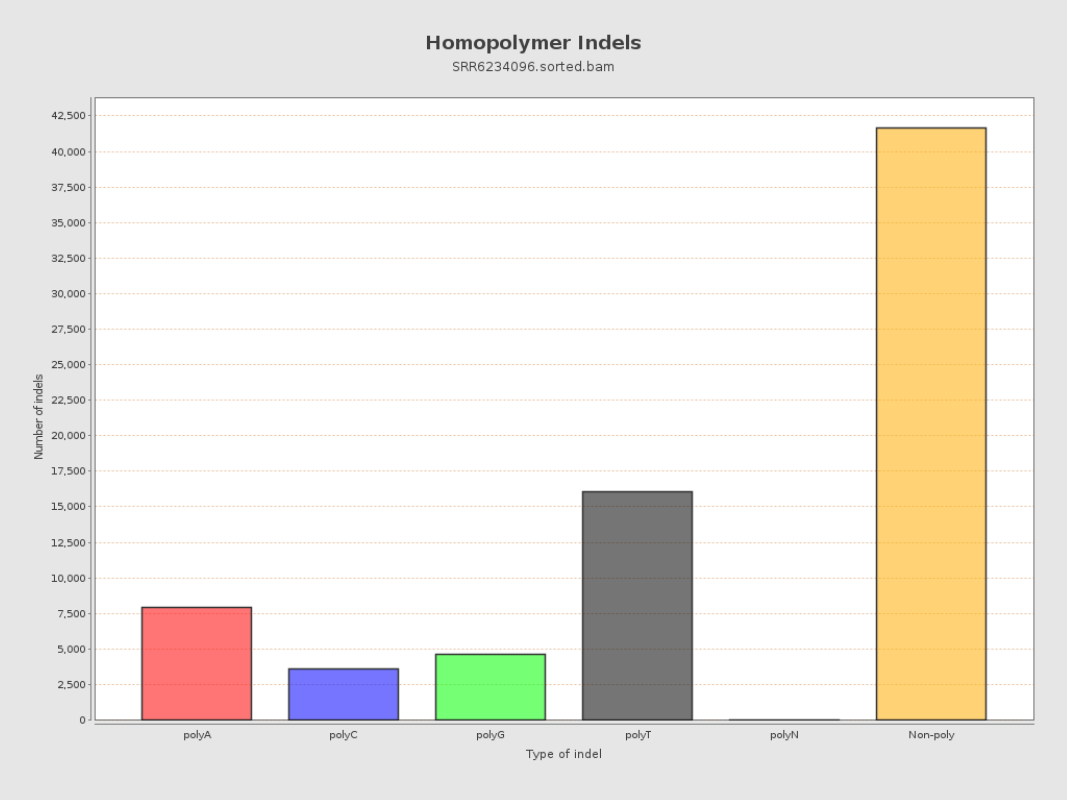
9. Results : Mapped Reads GC-content Distribution



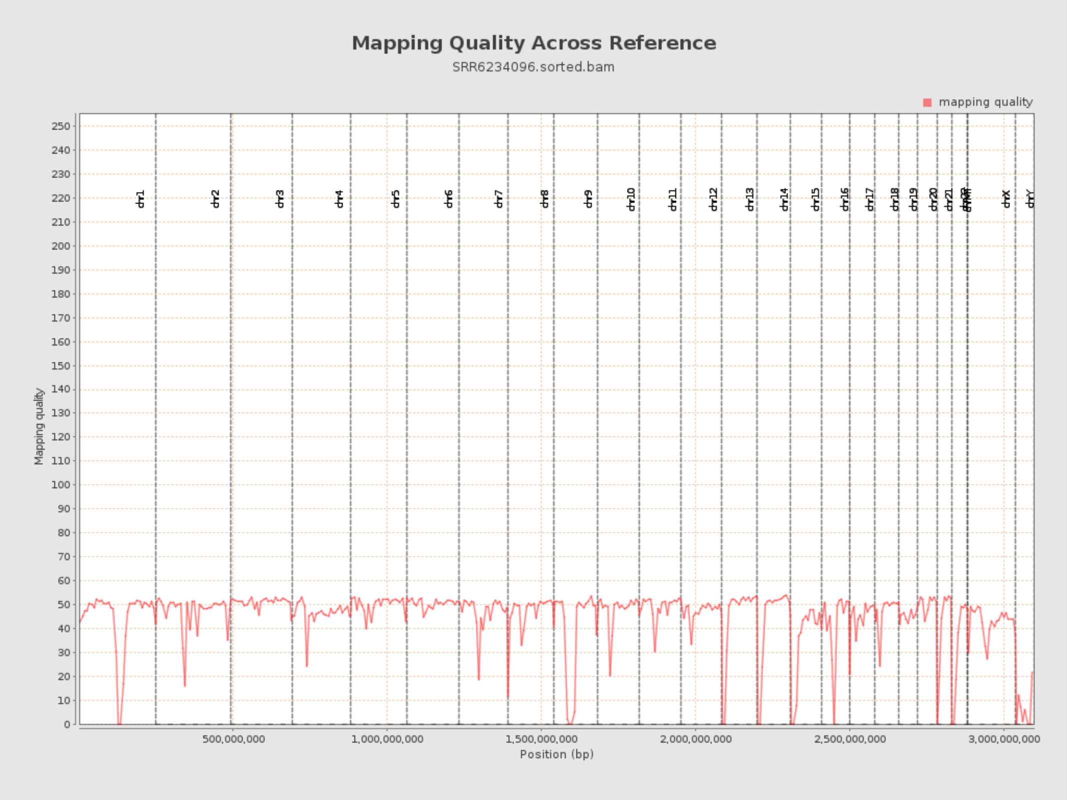
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram