Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 06:21:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231834.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_SRR6231834 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231834.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 06:21:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231834.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,152,676
Mapped reads	4,627,879 / 89.82%
Unmapped reads	524,797 / 10.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,314 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	440,215 / 8.54%
Duplication rate	7.57%
Clipped reads	2,546,775 / 49.43%

2.2. ACGT Content

Number/percentage of A's	74,684,724 / 25.36%
Number/percentage of C's	52,965,309 / 17.99%
Number/percentage of T's	96,013,327 / 32.61%
Number/percentage of G's	70,673,768 / 24%
Number/percentage of N's	111,263 / 0.04%
GC Percentage	41.99%

2.3. Coverage

Mean	0.0952

Standard Deviation	0.9625

2.4. Mapping Quality

Mean Mapping Quality	43.74

2.5. Mismatches and indels

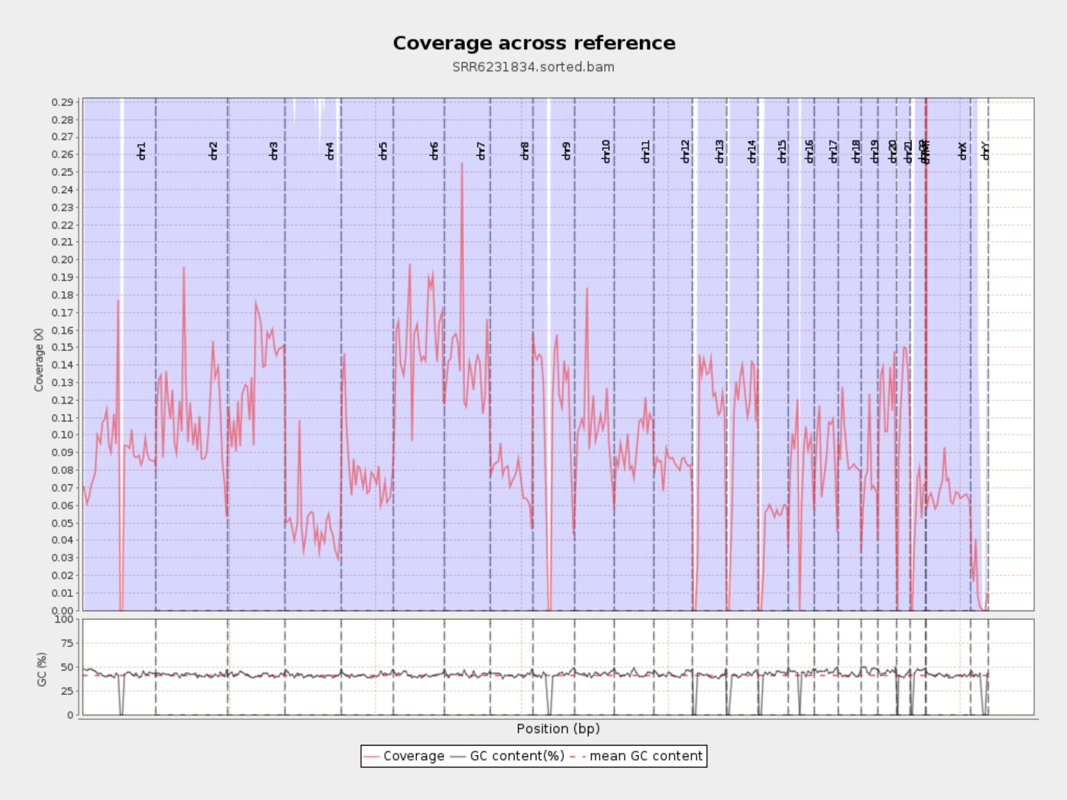
General error rate	0.64%
Mismatches	1,852,567
Insertions	19,409
Mapped reads with at least one insertion	0.42%
Deletions	66,720
Mapped reads with at least one deletion	1.43%
Homopolymer indels	43.98%

2.6. Chromosome stats

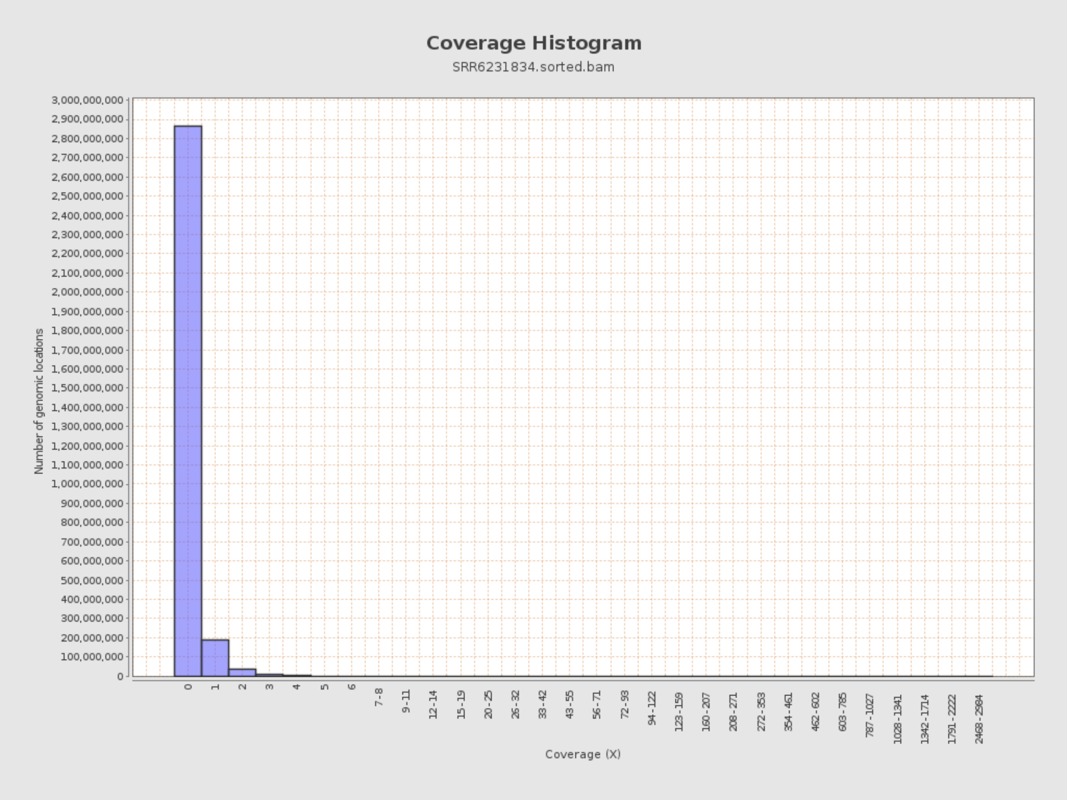
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21655170	0.0869	1.7143
chr2	243199373	27217133	0.1119	1.5217
chr3	198022430	26337720	0.133	0.455
chr4	191154276	9159613	0.0479	0.3462
chr5	180915260	14522892	0.0803	0.359
chr6	171115067	26571864	0.1553	0.8124
chr7	159138663	22719628	0.1428	1.8597

chr8	146364022	10993138	0.0751	0.7508
chr9	141213431	15729376	0.1114	0.7908
chr10	135534747	14354256	0.1059	0.8683
chr11	135006516	12805691	0.0949	0.652
chr12	133851895	11211444	0.0838	0.3876
chr13	115169878	12269764	0.1065	0.437
chr14	107349540	11216895	0.1045	0.473
chr15	102531392	4735052	0.0462	0.3421
chr16	90354753	7246200	0.0802	0.4796
chr17	81195210	7428612	0.0915	0.4407
chr18	78077248	7074735	0.0906	1.7529
chr19	59128983	4398627	0.0744	1.0591
chr20	63025520	7573317	0.1202	0.4682
chr21	48129895	5461628	0.1135	0.463
chr22	51304566	2605485	0.0508	0.2727
chrMT	16571	181162	10.9325	6.4603
chrX	155270560	10354260	0.0667	0.4552
chrY	59373566	743737	0.0125	0.2756

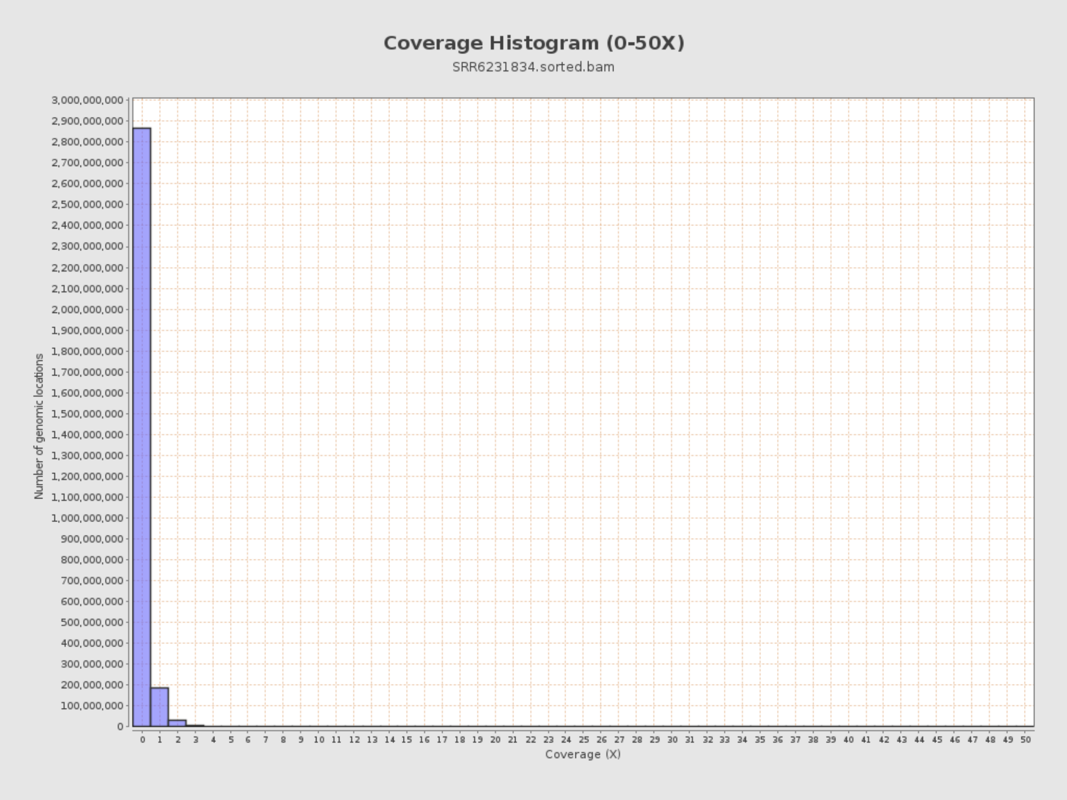
3. Results : Coverage across reference



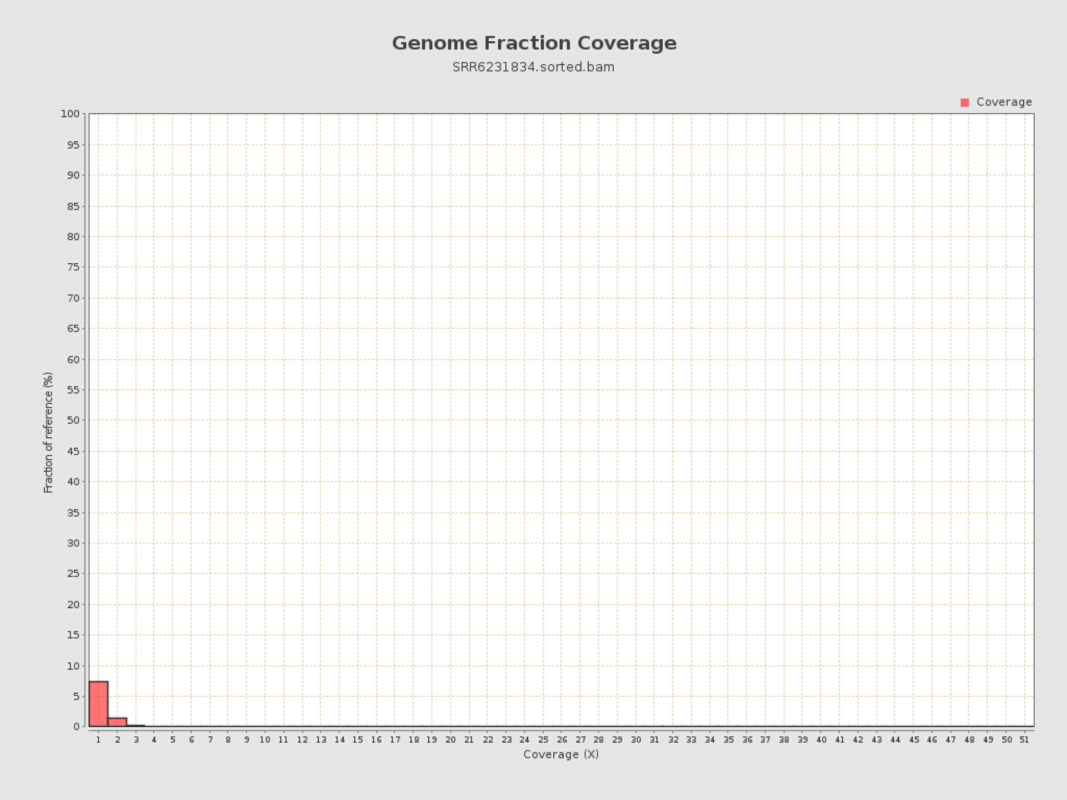
4. Results : Coverage Histogram



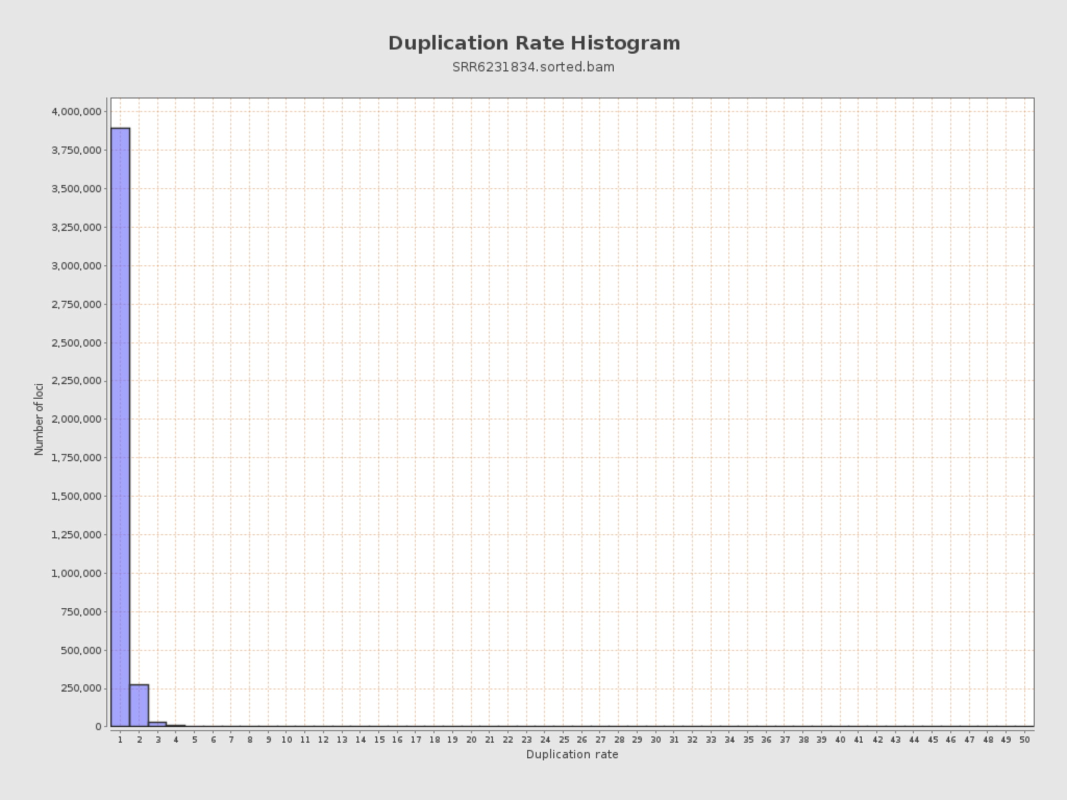
5. Results : Coverage Histogram (0-50X)



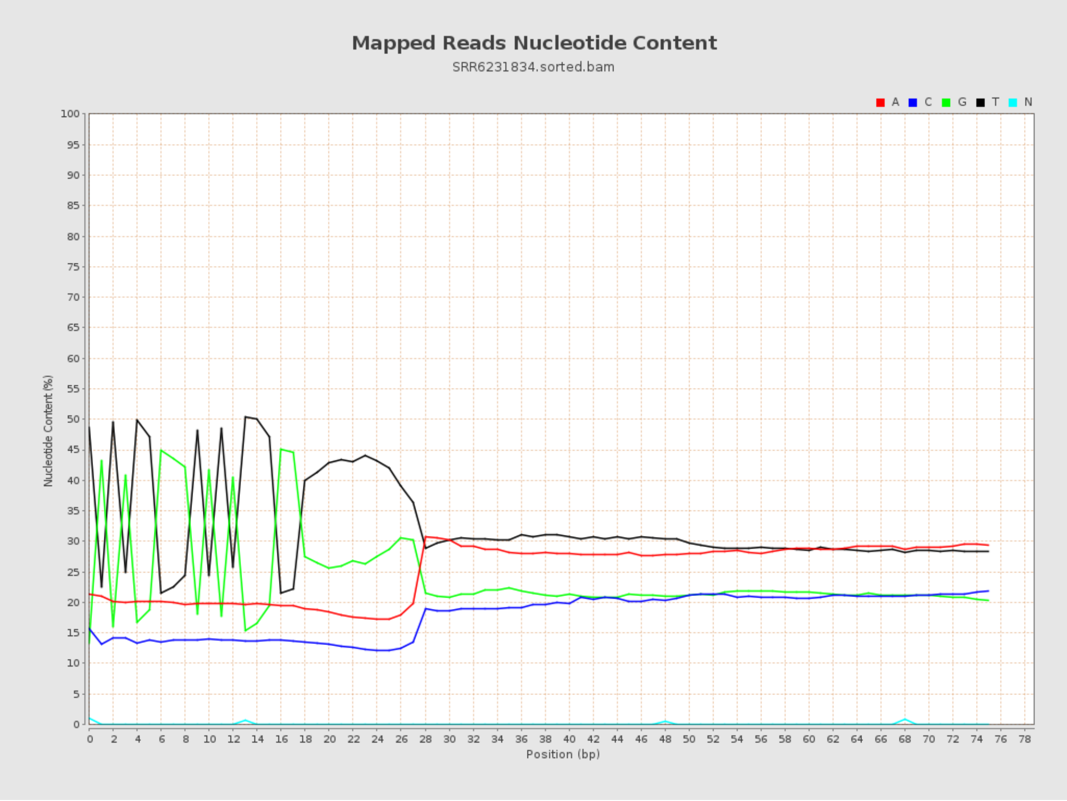
6. Results : Genome Fraction Coverage



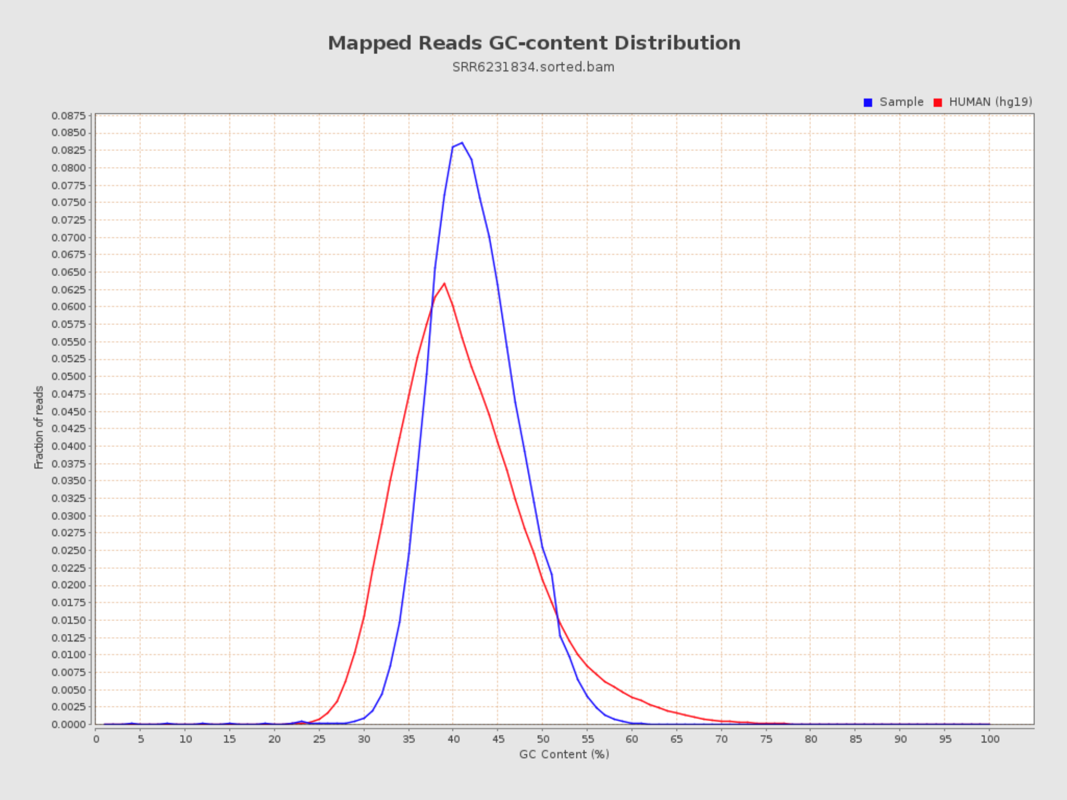
7. Results : Duplication Rate Histogram



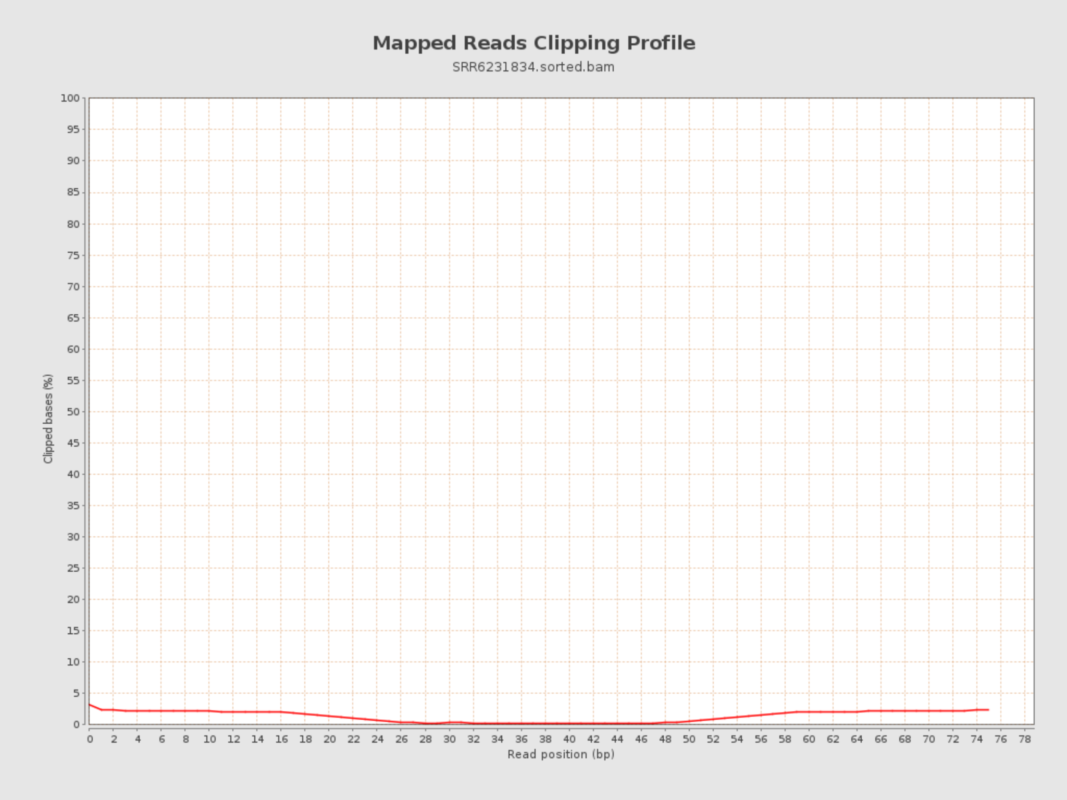
8. Results : Mapped Reads Nucleotide Content



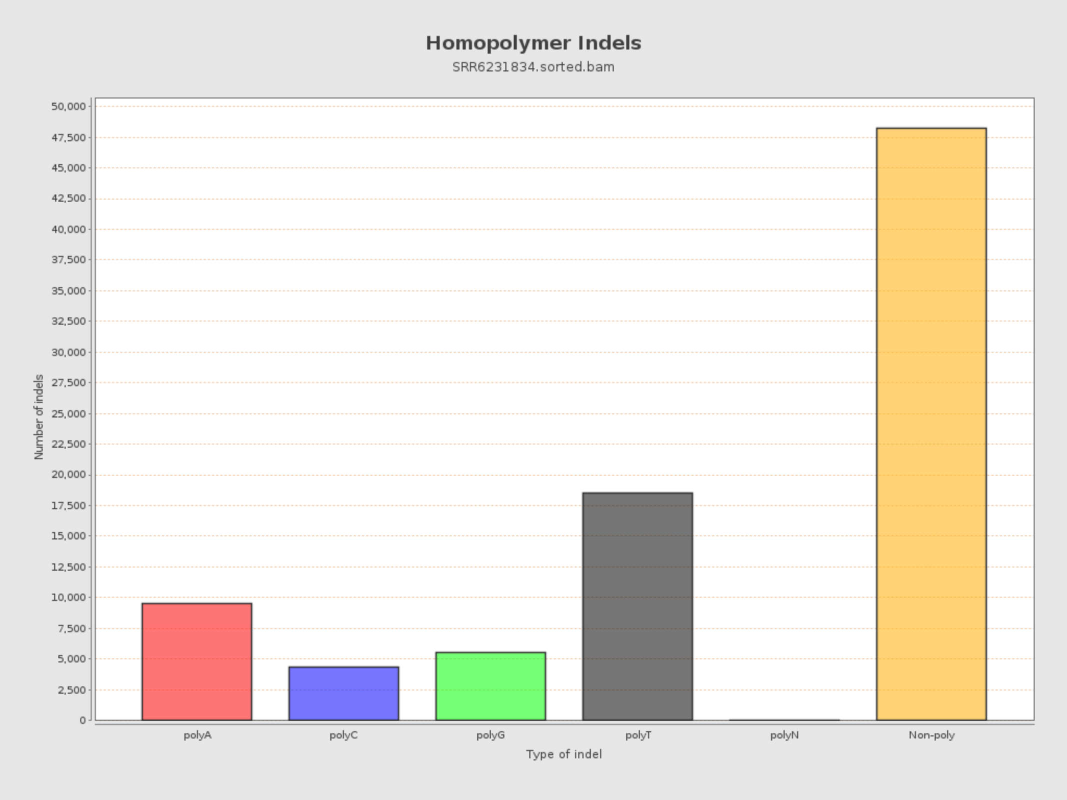
9. Results : Mapped Reads GC-content Distribution



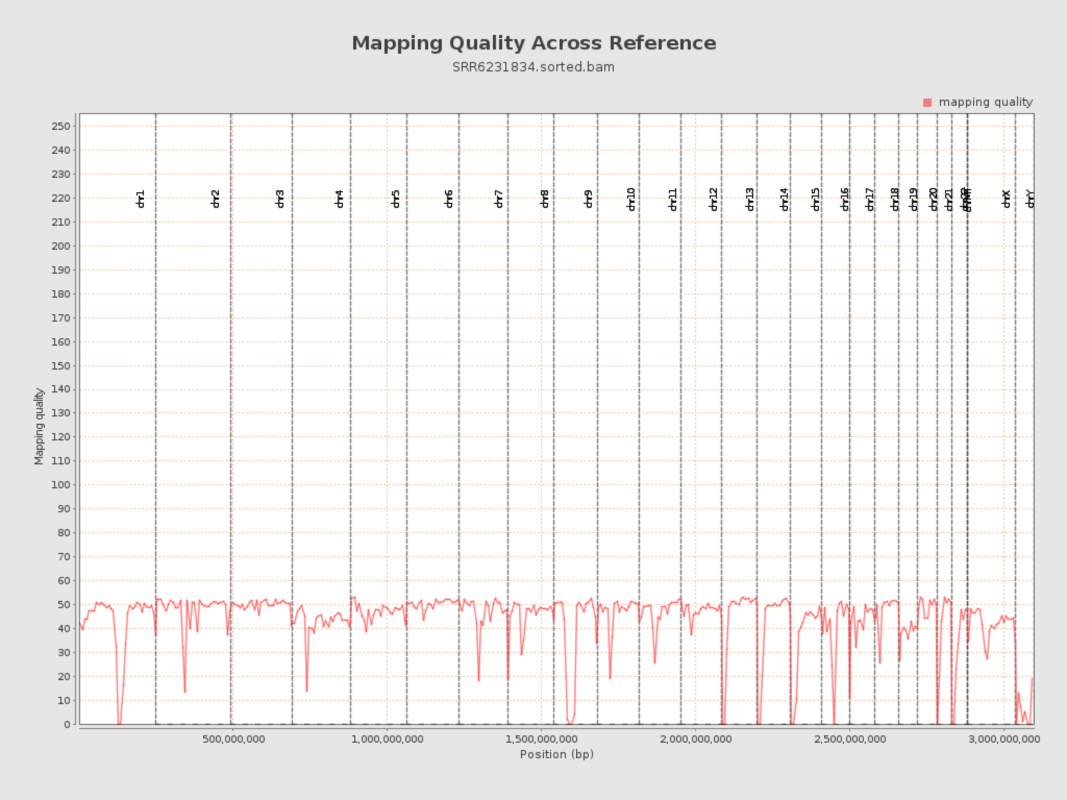
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram