Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 03:45:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231801.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_SRR6231801 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231801.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 03:45:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231801.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,494,920
Mapped reads	3,238,693 / 92.67%
Unmapped reads	256,227 / 7.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,274 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	198,644 / 5.68%
Duplication rate	4.07%
Clipped reads	1,666,833 / 47.69%

2.2. ACGT Content

Number/percentage of A's	63,564,475 / 29.79%
Number/percentage of C's	42,443,064 / 19.89%
Number/percentage of T's	61,864,601 / 29%
Number/percentage of G's	45,462,404 / 21.31%
Number/percentage of N's	17,084 / 0.01%
GC Percentage	41.2%

2.3. Coverage

Mean	0.0689

Standard Deviation	3.2805

2.4. Mapping Quality

Mean Mapping Quality	46.19

2.5. Mismatches and indels

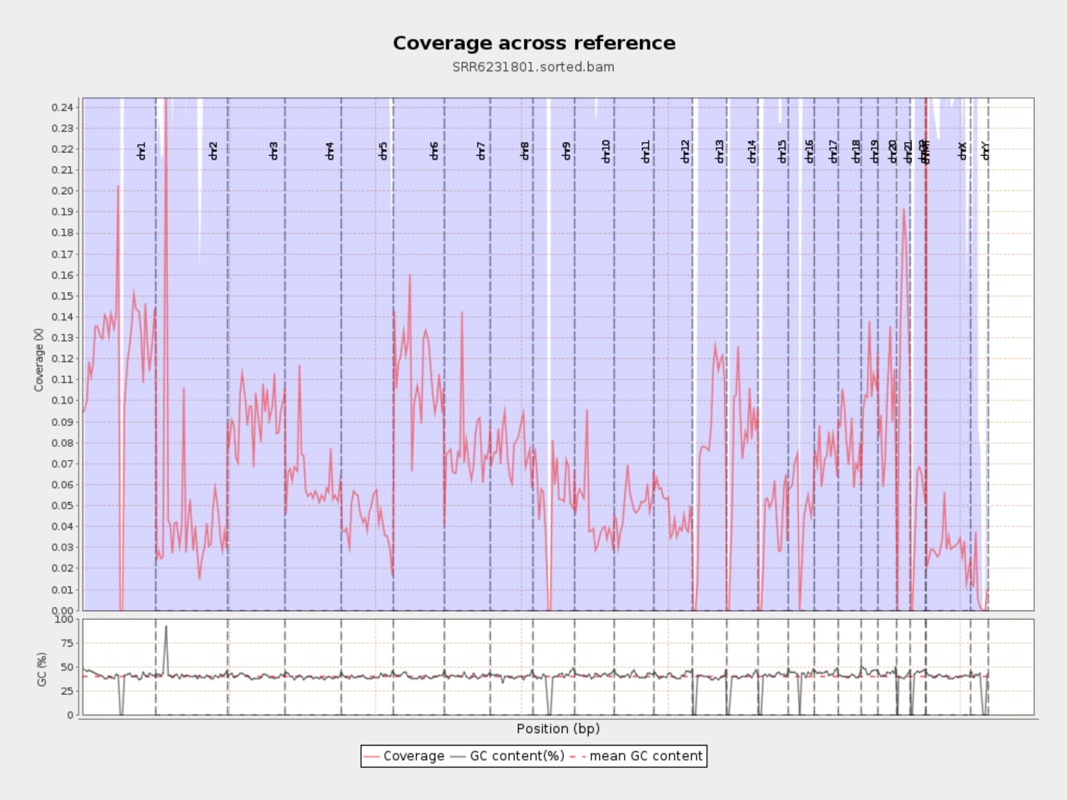
General error rate	0.6%
Mismatches	1,253,588
Insertions	15,532
Mapped reads with at least one insertion	0.48%
Deletions	48,242
Mapped reads with at least one deletion	1.47%
Homopolymer indels	45.67%

2.6. Chromosome stats

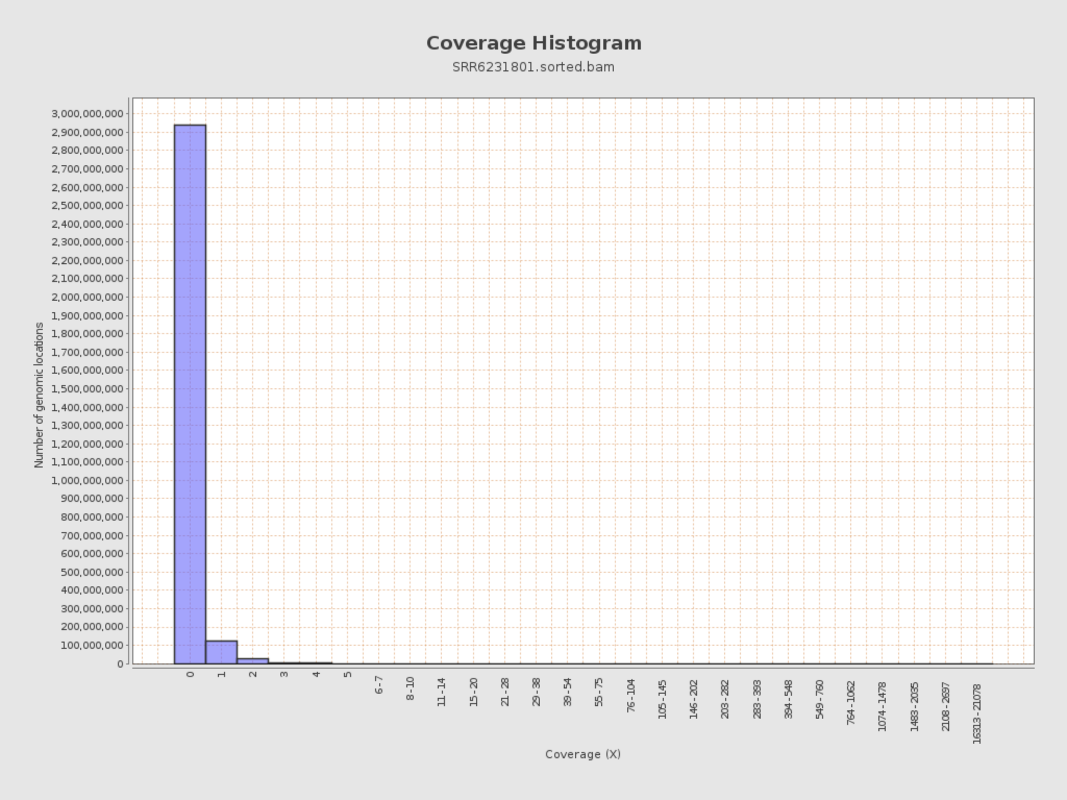
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30578827	0.1227	1.8353
chr2	243199373	10741856	0.0442	11.3983
chr3	198022430	18366871	0.0928	0.382
chr4	191154276	11859524	0.062	0.3539
chr5	180915260	7800406	0.0431	0.2692
chr6	171115067	19390846	0.1133	0.5537
chr7	159138663	12216422	0.0768	0.9085

chr8	146364022	11248011	0.0768	1.3644
chr9	141213431	7494356	0.0531	0.5058
chr10	135534747	6014406	0.0444	0.4483
chr11	135006516	6706073	0.0497	0.4403
chr12	133851895	6245247	0.0467	0.2862
chr13	115169878	9392514	0.0816	0.3592
chr14	107349540	8439185	0.0786	0.3919
chr15	102531392	4084371	0.0398	0.2473
chr16	90354753	4415579	0.0489	0.3469
chr17	81195210	6089783	0.075	0.3934
chr18	78077248	6351129	0.0813	1.0989
chr19	59128983	6303550	0.1066	0.9666
chr20	63025520	5877712	0.0933	0.4082
chr21	48129895	6218497	0.1292	0.4902
chr22	51304566	2294827	0.0447	0.2616
chrMT	16571	135120	8.154	5.3309
chrX	155270560	4590597	0.0296	0.2823
chrY	59373566	577795	0.0097	0.256

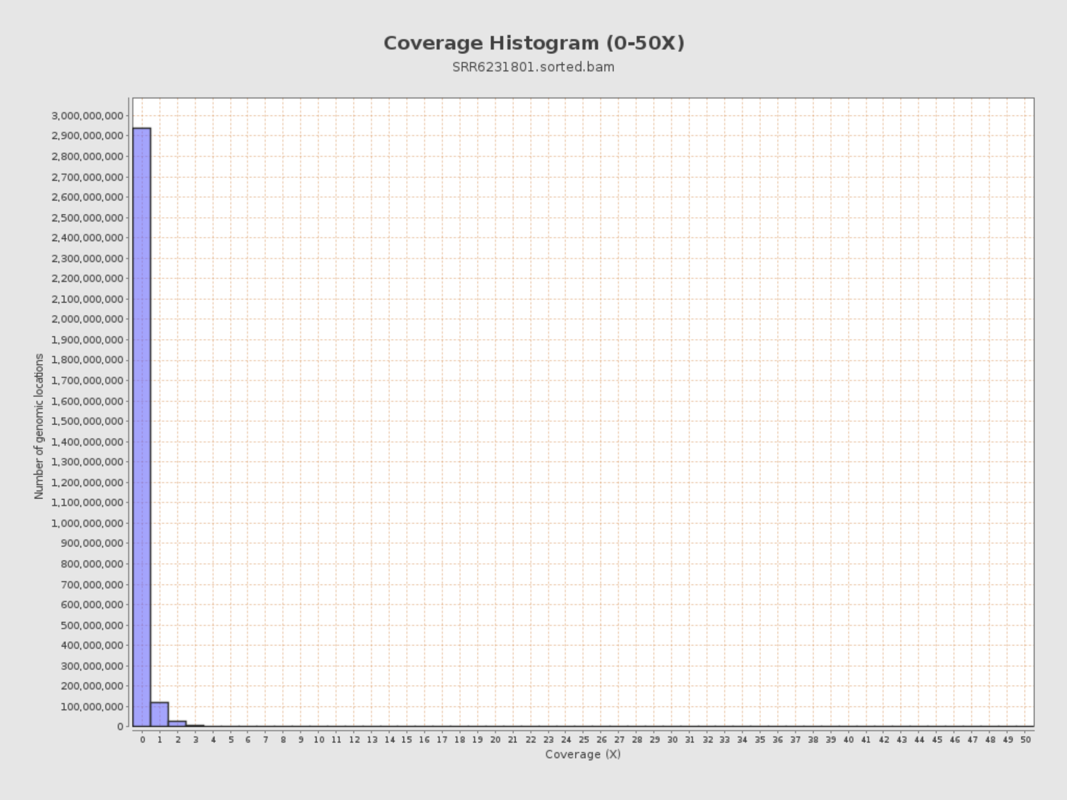
3. Results : Coverage across reference



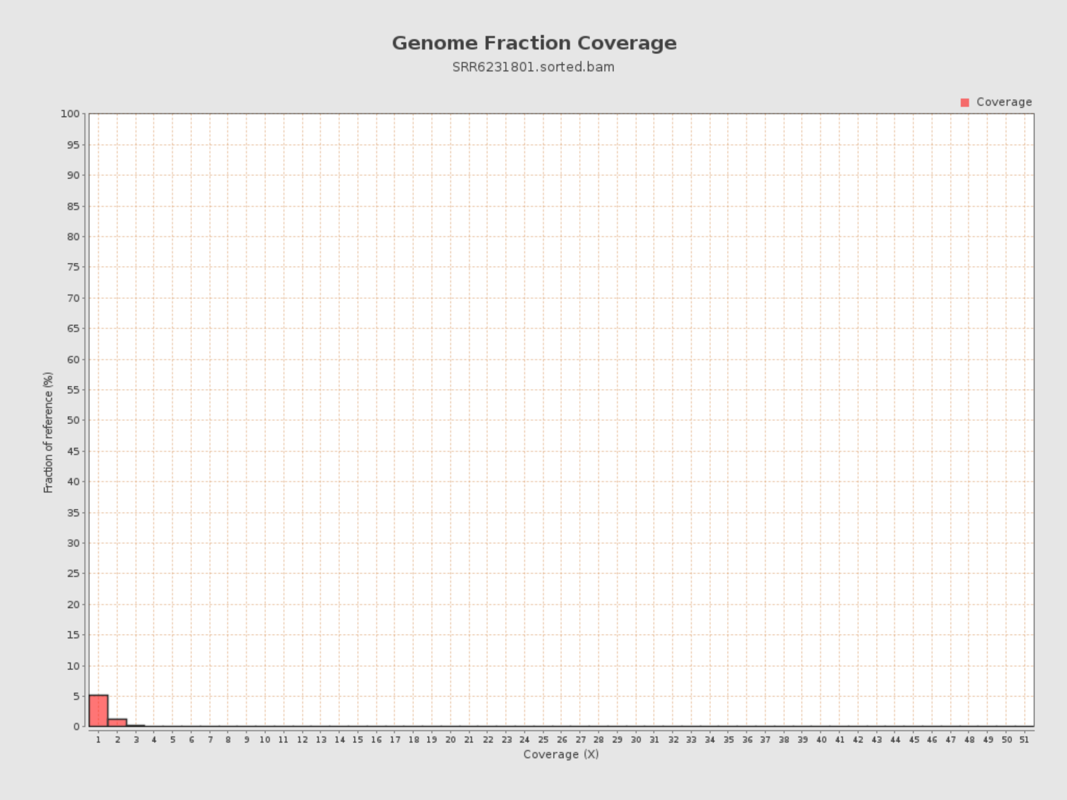
4. Results : Coverage Histogram



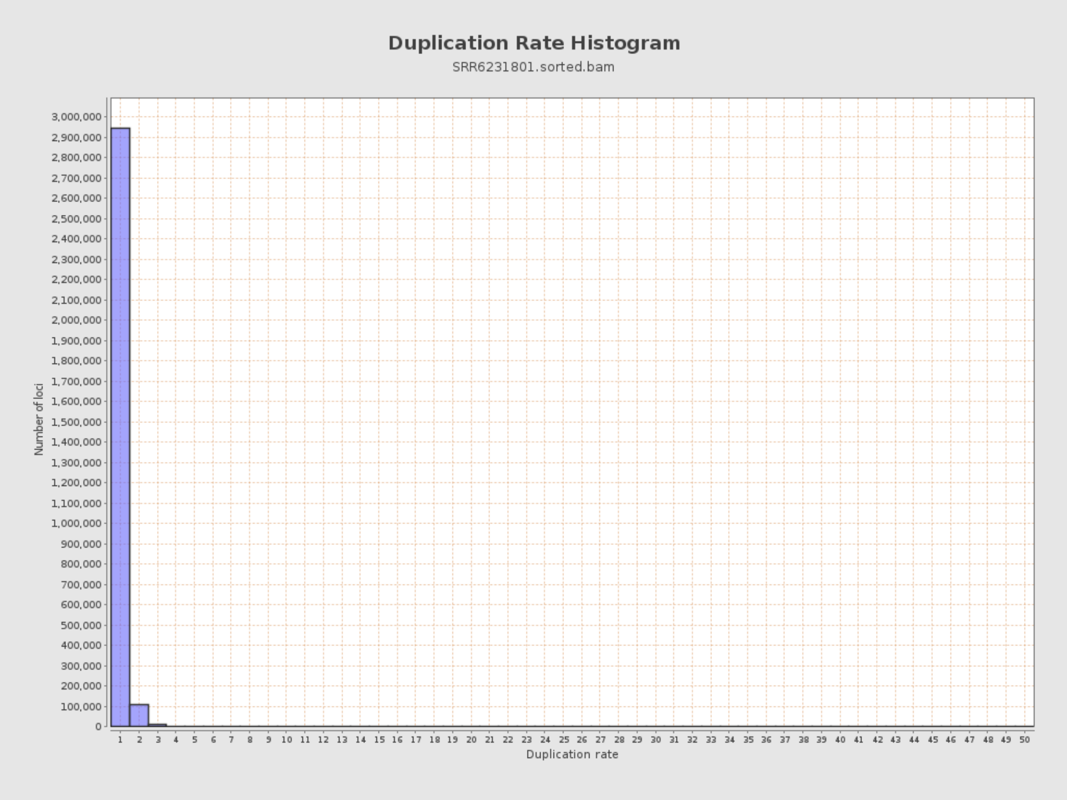
5. Results : Coverage Histogram (0-50X)



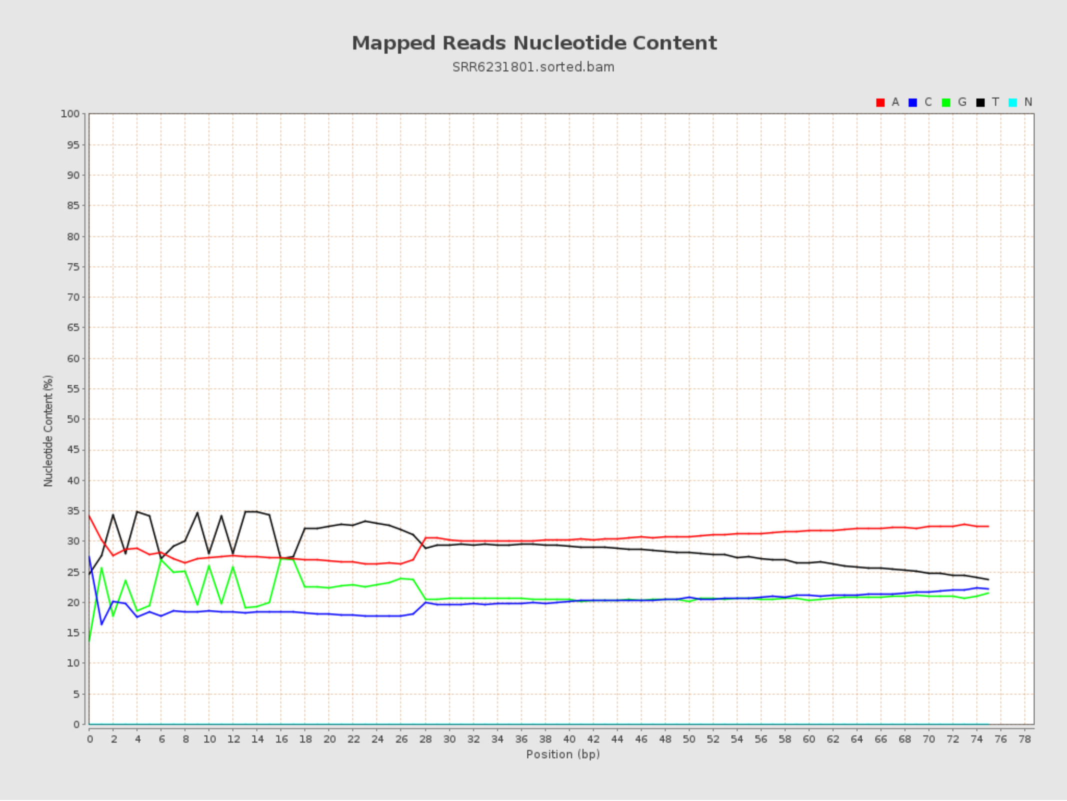
6. Results : Genome Fraction Coverage



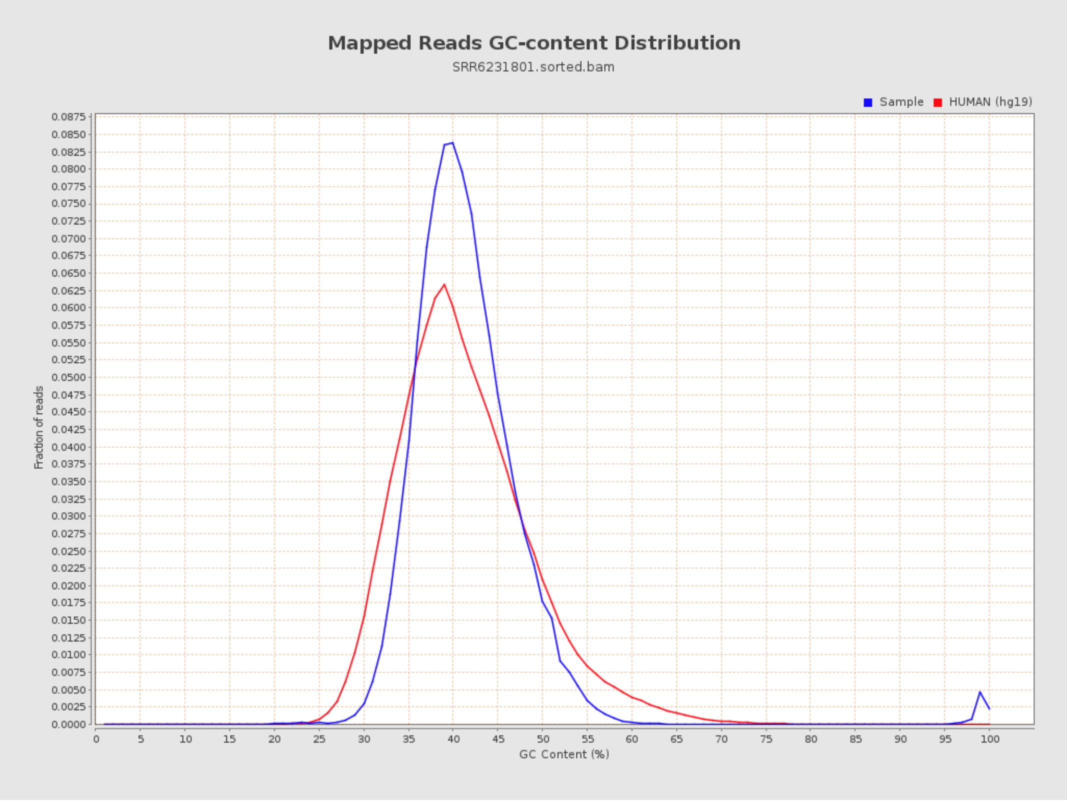
7. Results : Duplication Rate Histogram



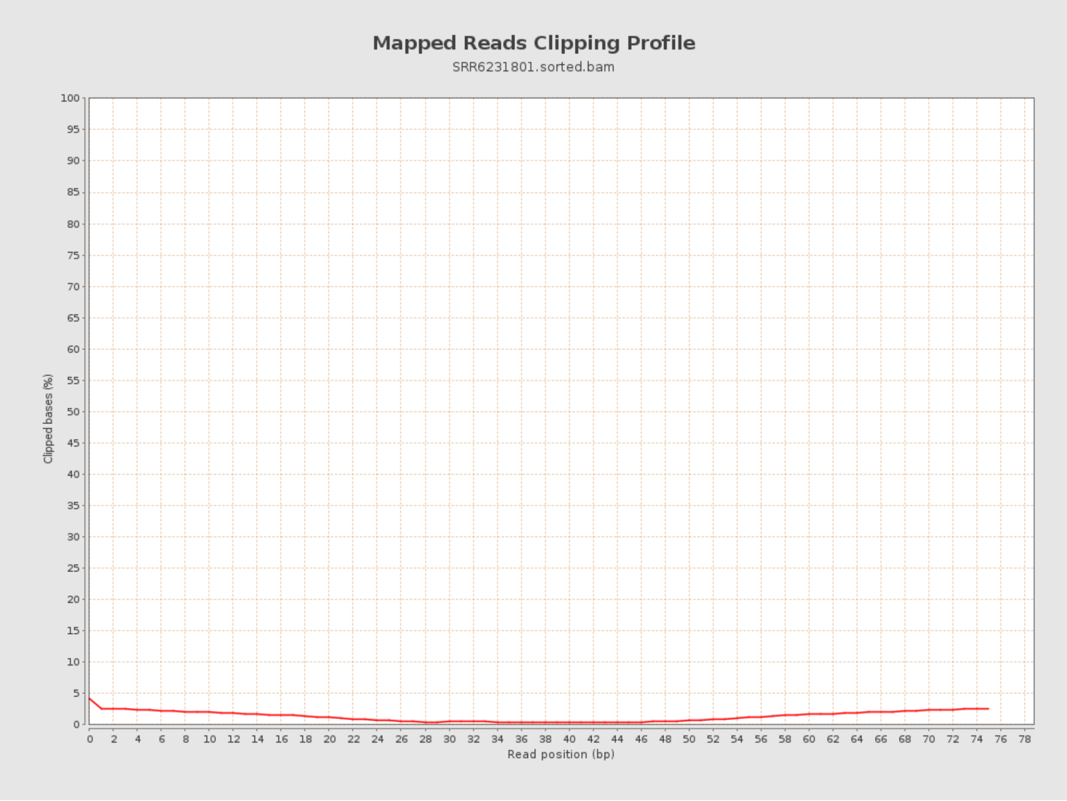
8. Results : Mapped Reads Nucleotide Content



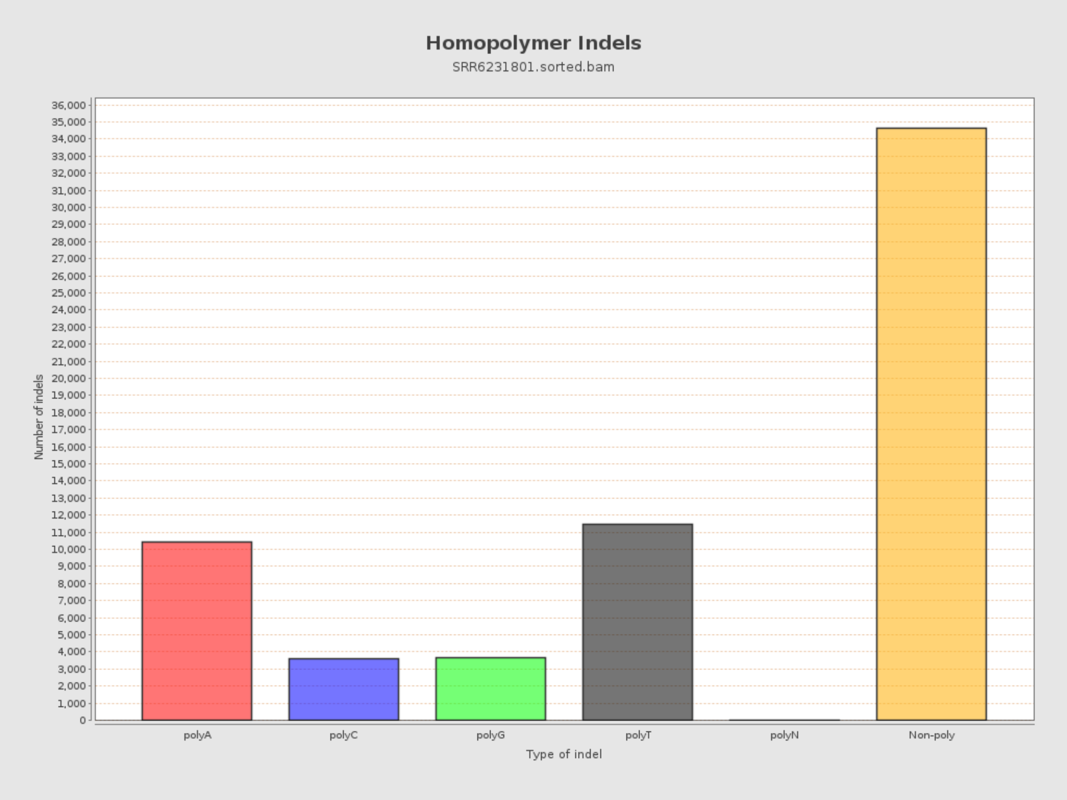
9. Results : Mapped Reads GC-content Distribution



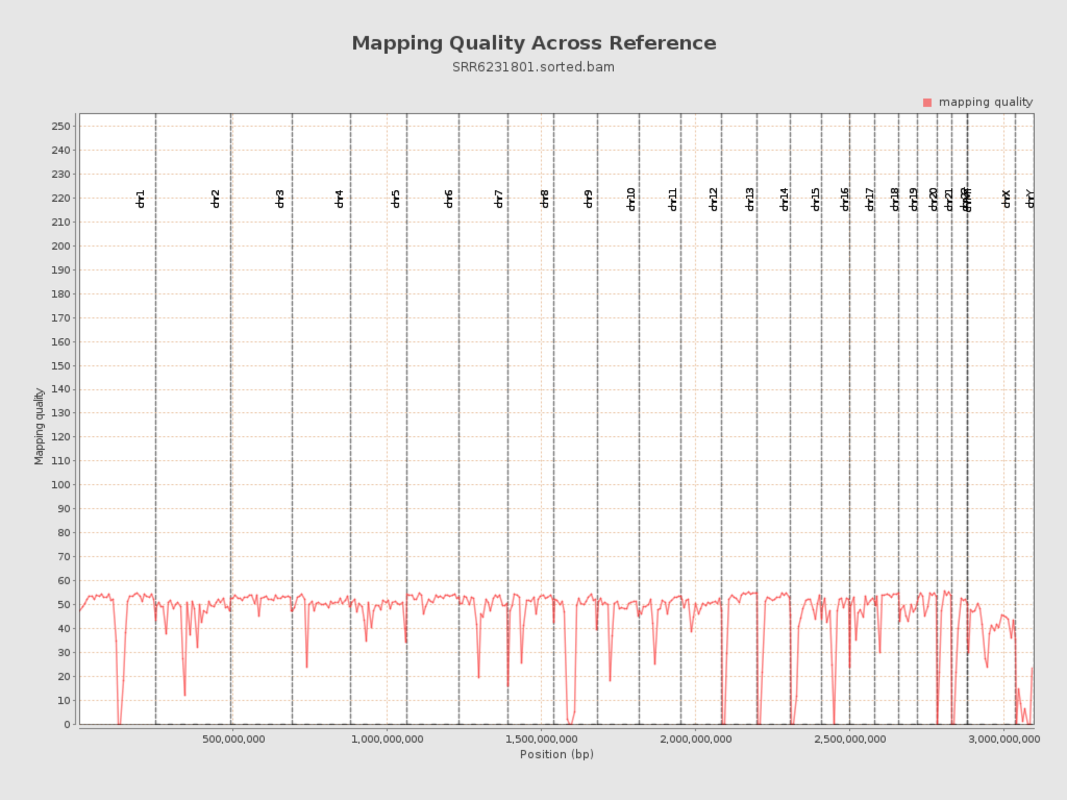
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram