Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 08:06:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231853.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_SRR6231853 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231853.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 08:05:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231853.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,164,891
Mapped reads	4,841,057 / 93.73%
Unmapped reads	323,834 / 6.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,923 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	472,038 / 9.14%
Duplication rate	7.91%
Clipped reads	2,680,565 / 51.9%

2.2. ACGT Content

Number/percentage of A's	79,661,550 / 25.91%
Number/percentage of C's	54,783,649 / 17.82%
Number/percentage of T's	100,021,197 / 32.53%
Number/percentage of G's	72,922,671 / 23.71%
Number/percentage of N's	116,018 / 0.04%
GC Percentage	41.53%

2.3. Coverage

Mean	0.0994

Standard Deviation	0.9866

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

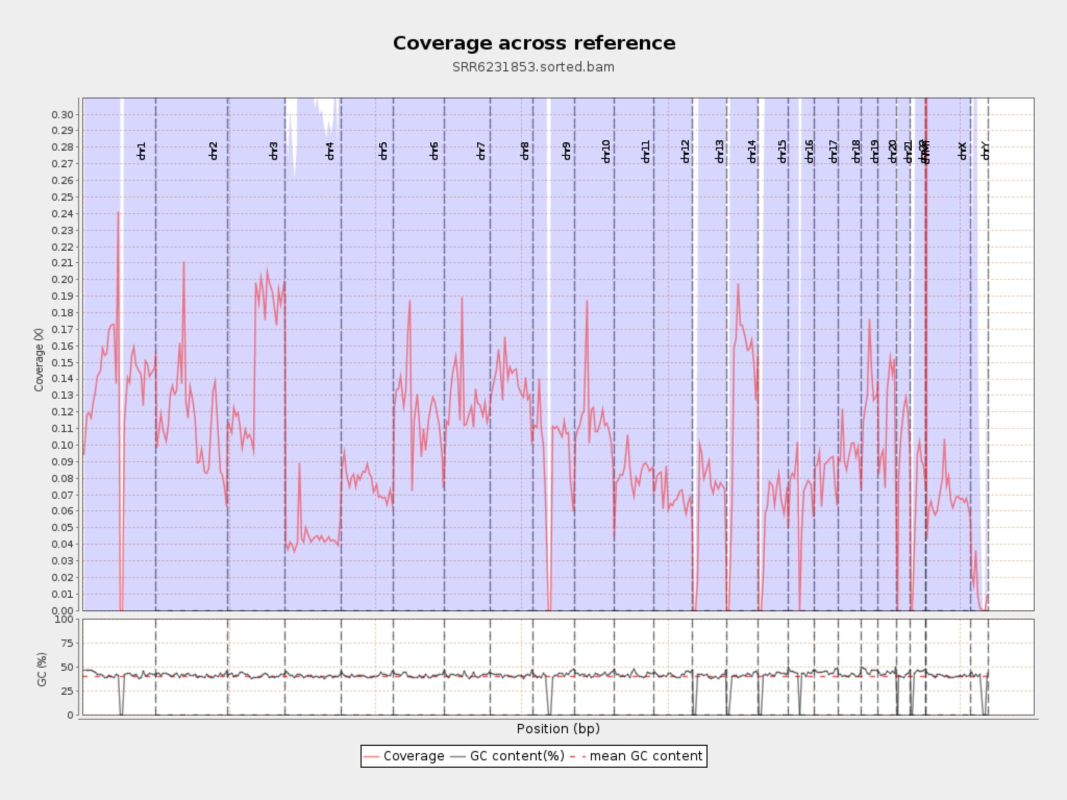
General error rate	0.6%
Mismatches	1,805,954
Insertions	18,311
Mapped reads with at least one insertion	0.37%
Deletions	60,988
Mapped reads with at least one deletion	1.25%
Homopolymer indels	44.43%

2.6. Chromosome stats

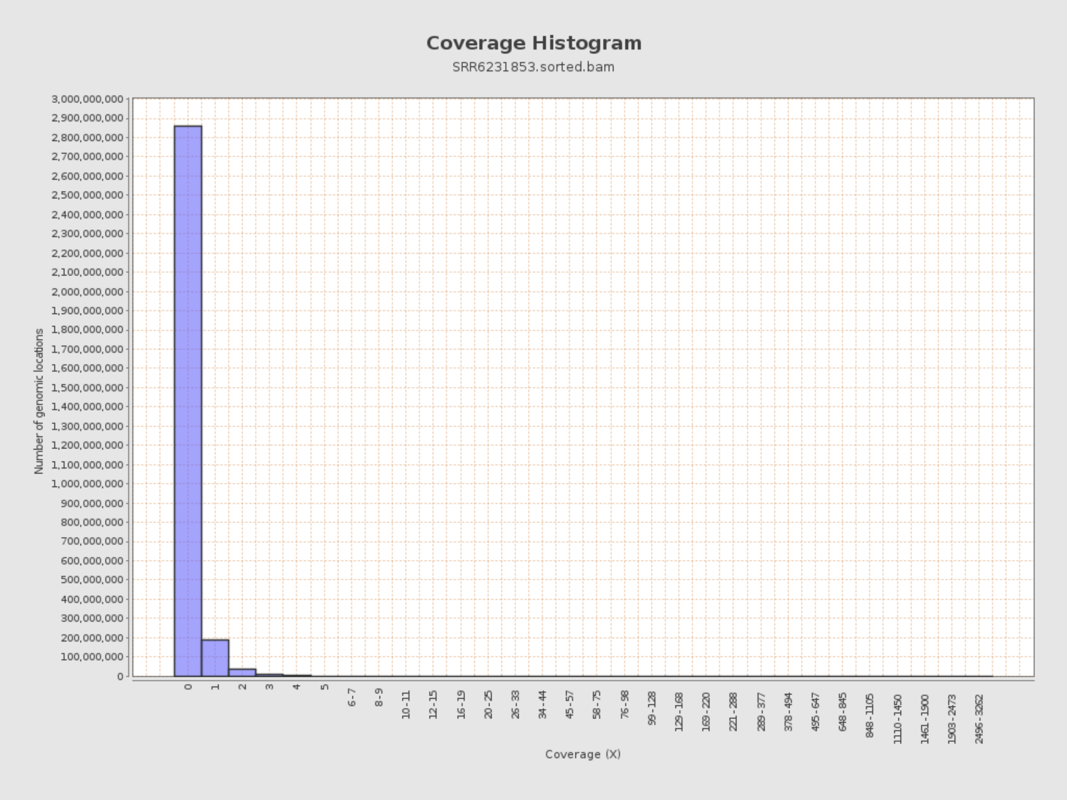
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33946405	0.1362	2.4182
chr2	243199373	27729292	0.114	1
chr3	198022430	29992185	0.1515	0.4954
chr4	191154276	8543926	0.0447	0.3122
chr5	180915260	13993156	0.0773	0.3623
chr6	171115067	20796947	0.1215	0.694
chr7	159138663	20017891	0.1258	1.3742

chr8	146364022	20282146	0.1386	0.8876
chr9	141213431	13005343	0.0921	0.7066
chr10	135534747	15695007	0.1158	0.8869
chr11	135006516	11182682	0.0828	0.73
chr12	133851895	9351380	0.0699	0.3582
chr13	115169878	7789146	0.0676	0.3241
chr14	107349540	14476826	0.1349	0.5115
chr15	102531392	5727065	0.0559	0.3405
chr16	90354753	6088935	0.0674	0.4261
chr17	81195210	6918469	0.0852	0.4356
chr18	78077248	7492202	0.096	1.6119
chr19	59128983	7826826	0.1324	1.2753
chr20	63025520	7278459	0.1155	0.464
chr21	48129895	4753595	0.0988	0.4279
chr22	51304566	3329480	0.0649	0.3123
chrMT	16571	206321	12.4507	7.8095
chrX	155270560	10515424	0.0677	0.4855
chrY	59373566	673491	0.0113	0.2191

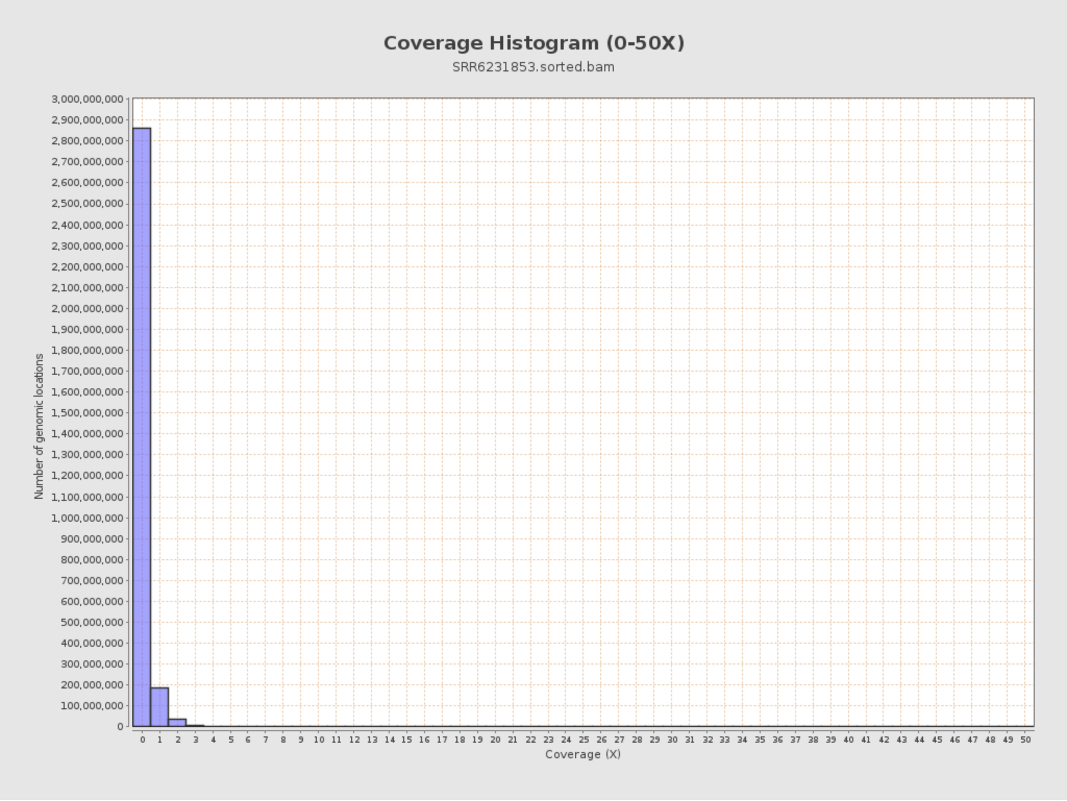
3. Results : Coverage across reference



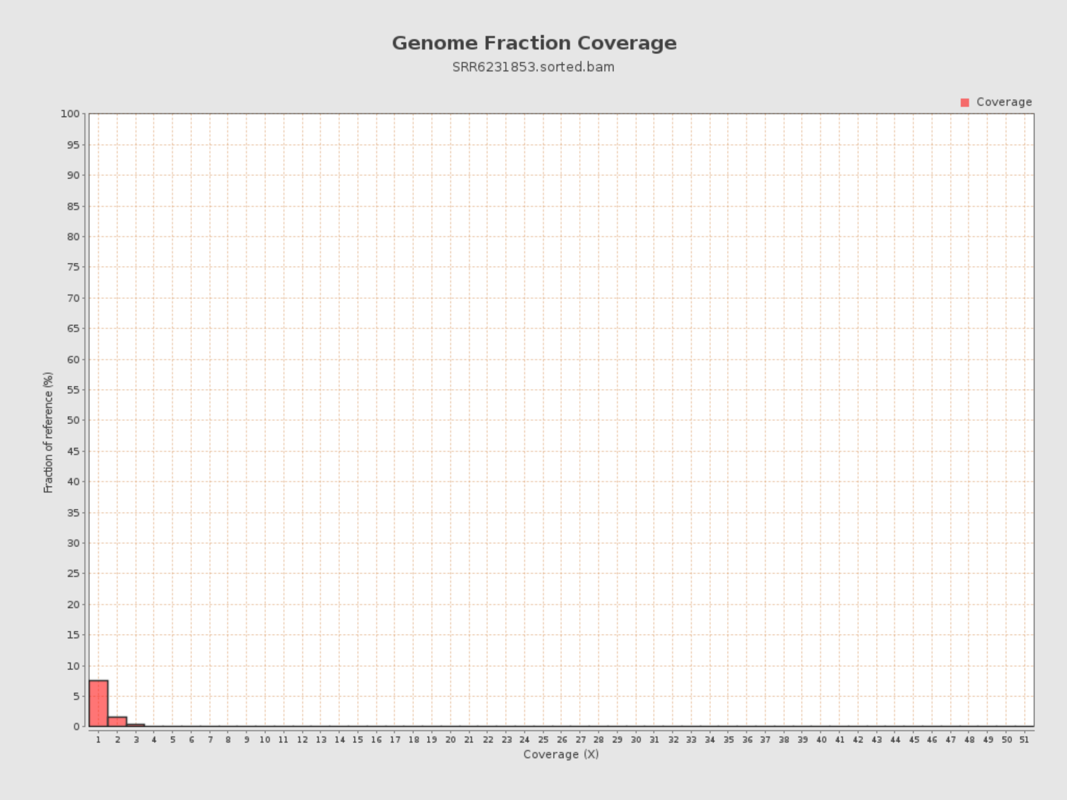
4. Results : Coverage Histogram



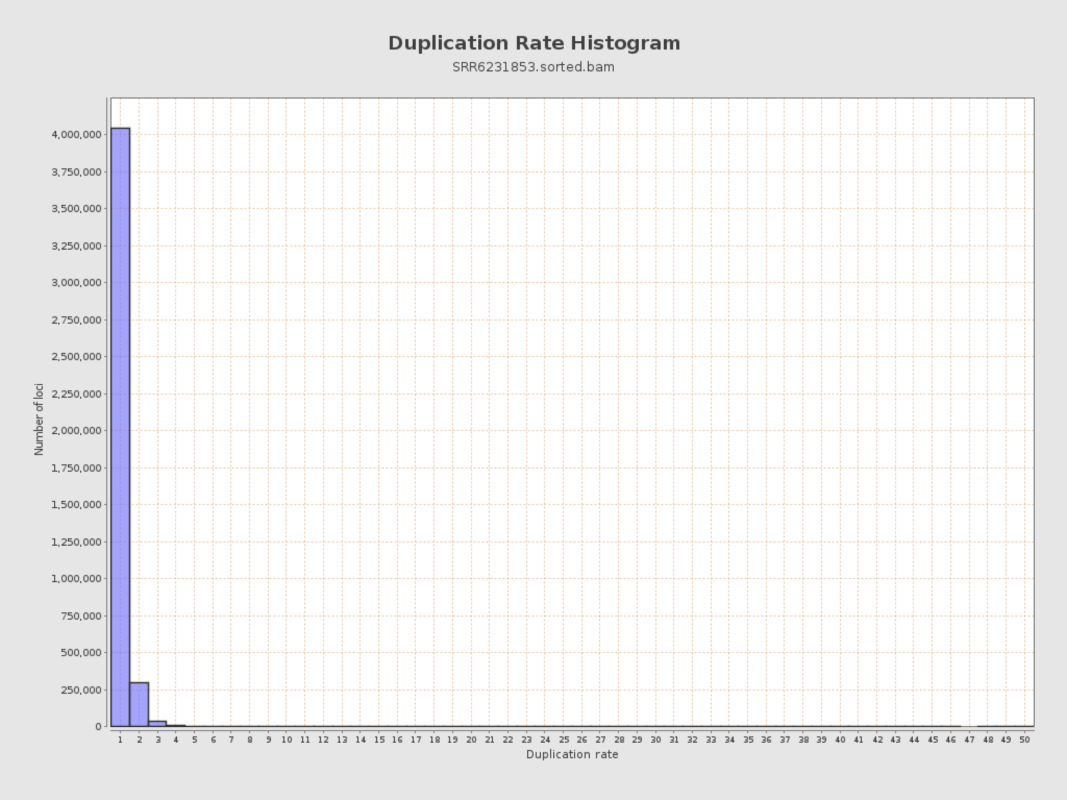
5. Results : Coverage Histogram (0-50X)



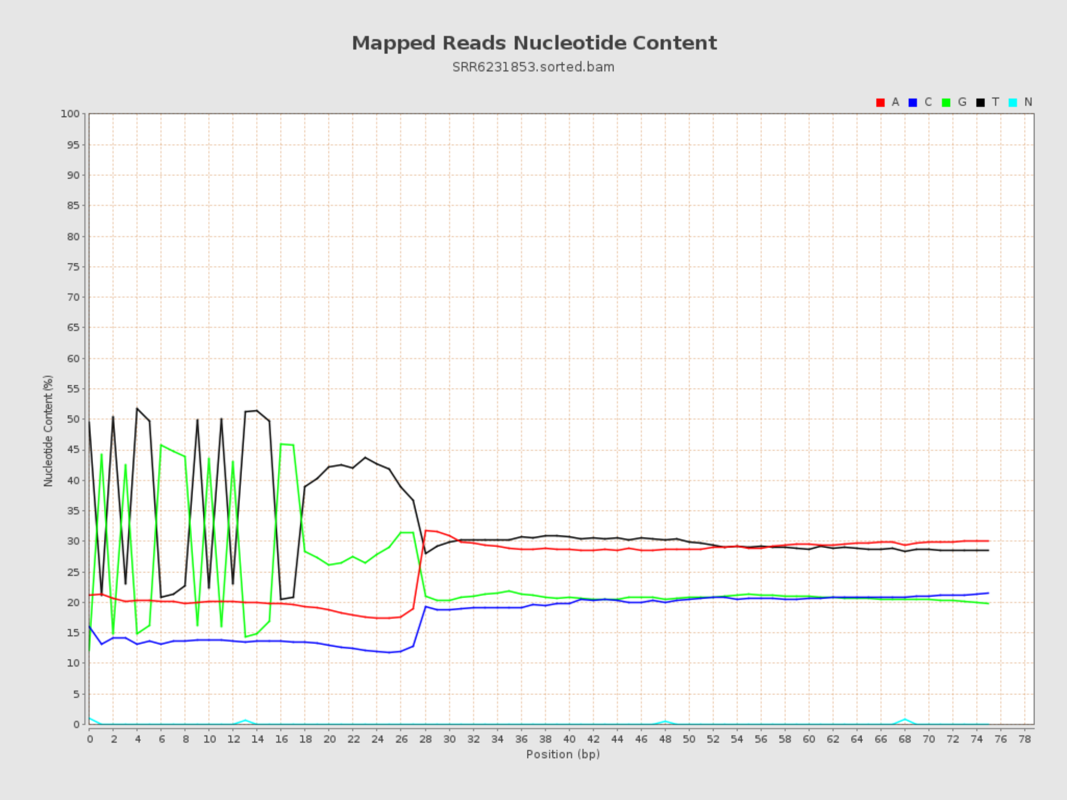
6. Results : Genome Fraction Coverage



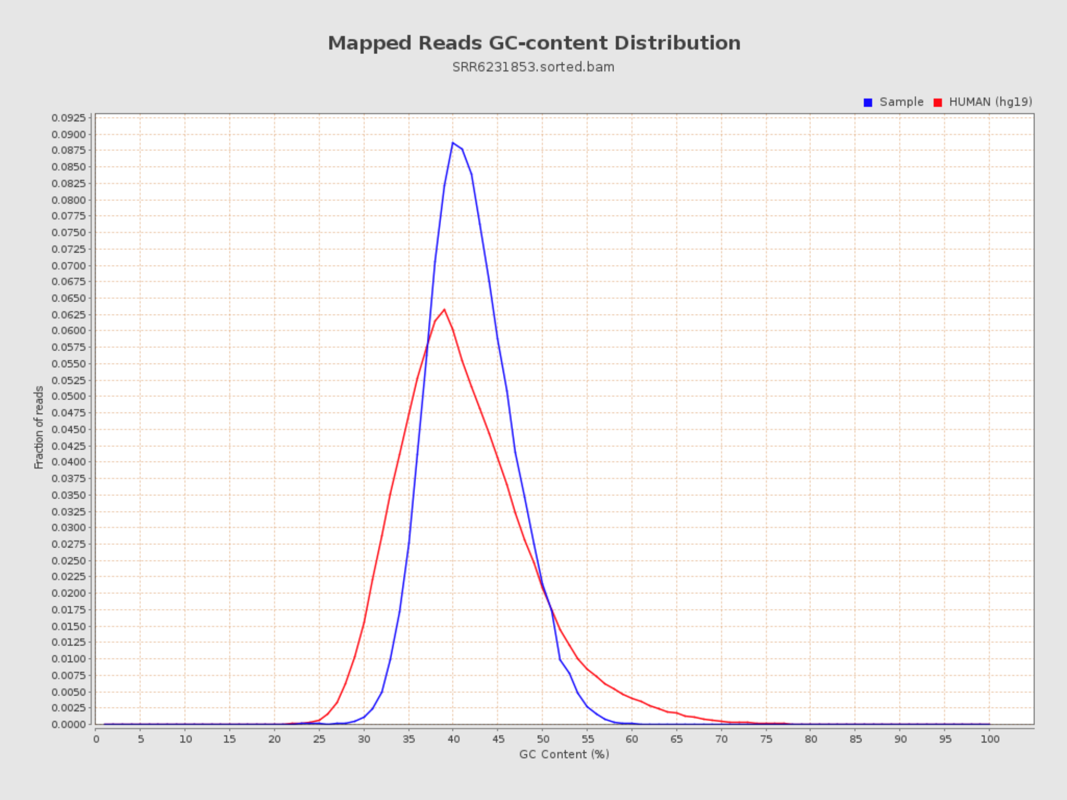
7. Results : Duplication Rate Histogram



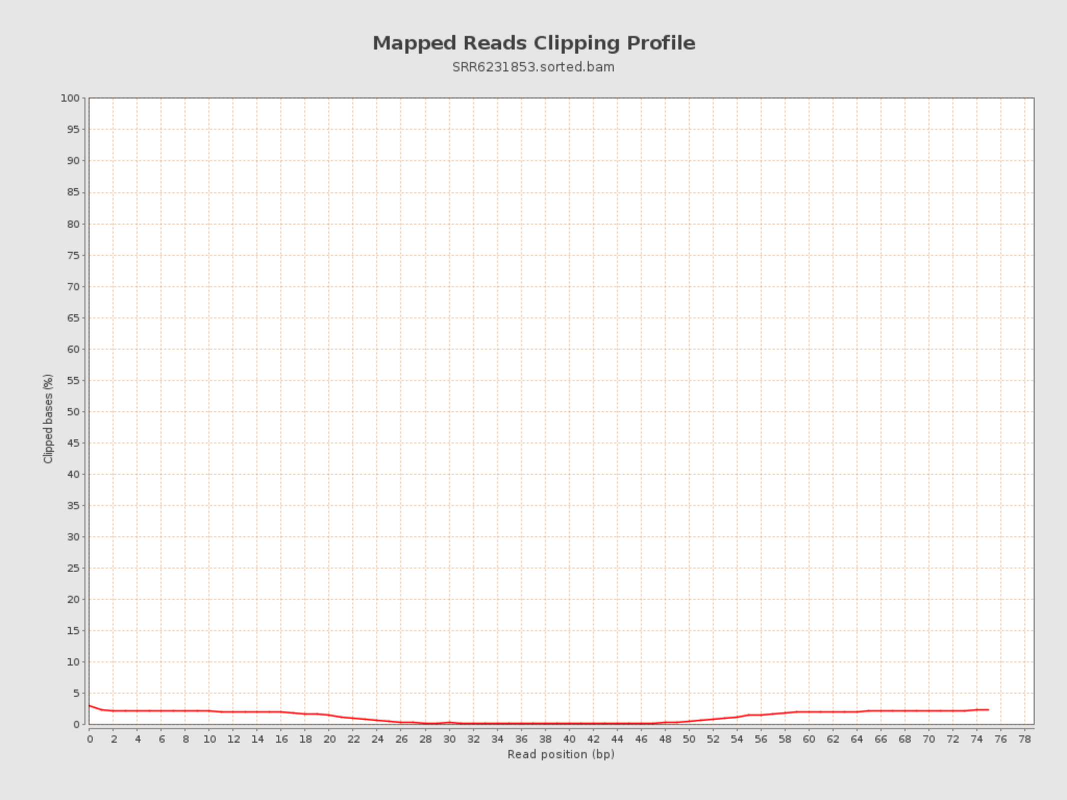
8. Results : Mapped Reads Nucleotide Content



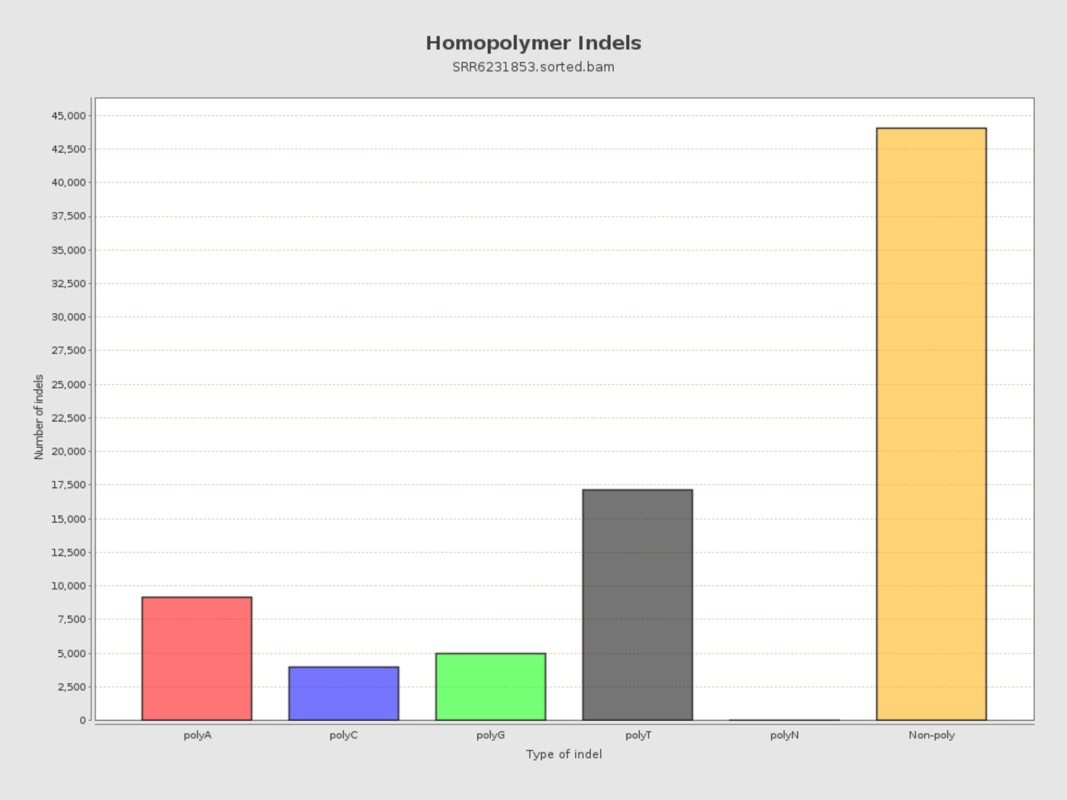
9. Results : Mapped Reads GC-content Distribution



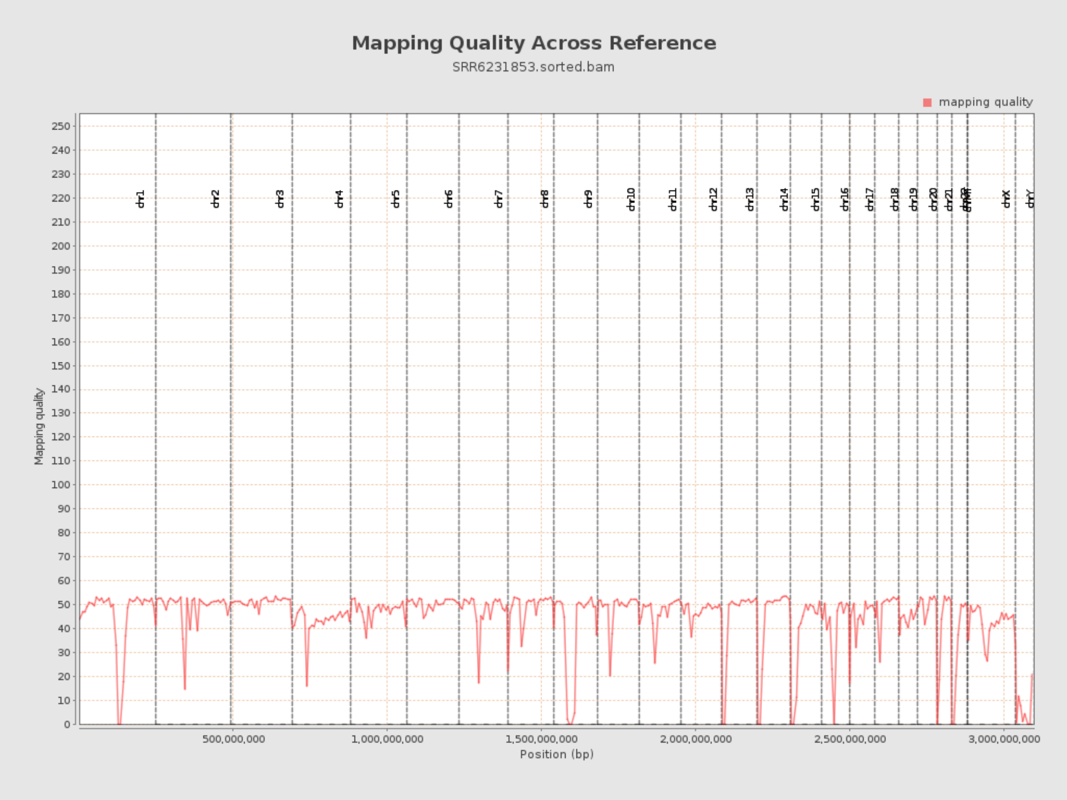
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram