Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 00:30:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231756.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_SRR6231756 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231756.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 00:30:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231756.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,459,544
Mapped reads	4,020,814 / 90.16%
Unmapped reads	438,730 / 9.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,784 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	874,958 / 19.62%
Duplication rate	10.02%
Clipped reads	1,435,796 / 32.2%

2.2. ACGT Content

Number/percentage of A's	69,518,394 / 25.17%
Number/percentage of C's	48,453,776 / 17.54%
Number/percentage of T's	75,019,795 / 27.16%
Number/percentage of G's	83,157,447 / 30.11%
Number/percentage of N's	59,454 / 0.02%
GC Percentage	47.65%

2.3. Coverage

Mean	0.0893

Standard Deviation	57.8297

2.4. Mapping Quality

Mean Mapping Quality	40.9

2.5. Mismatches and indels

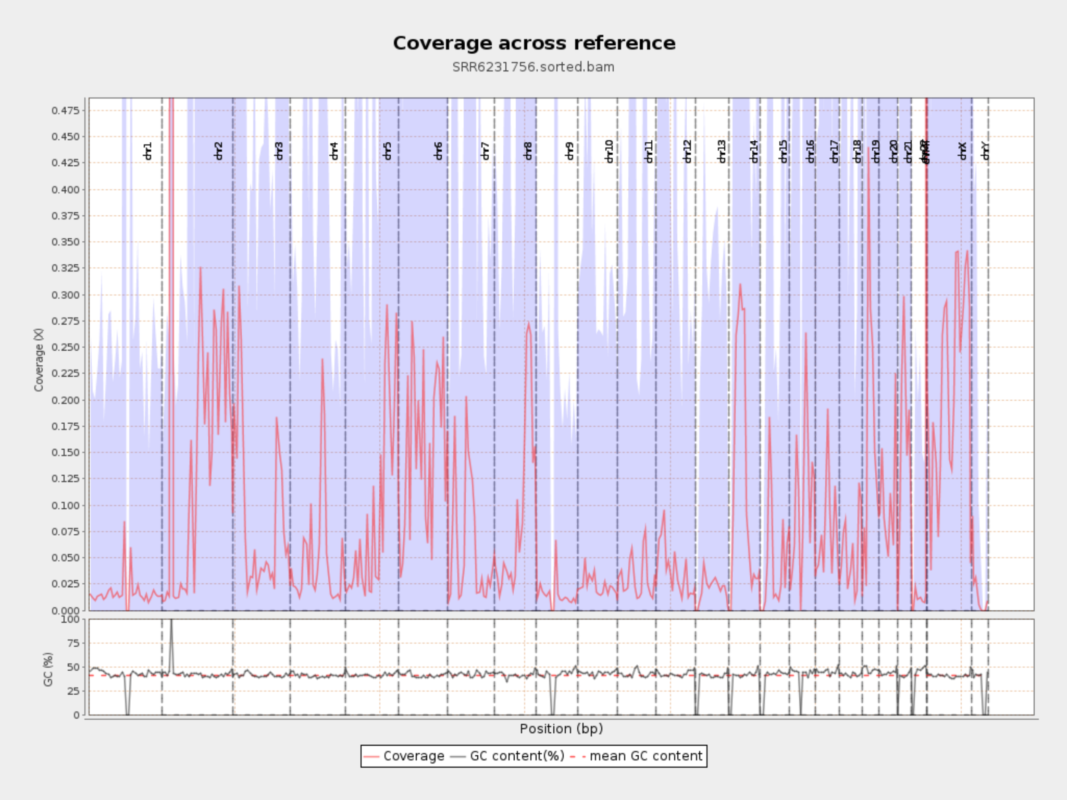
General error rate	0.62%
Mismatches	1,668,411
Insertions	17,518
Mapped reads with at least one insertion	0.43%
Deletions	52,369
Mapped reads with at least one deletion	1.29%
Homopolymer indels	47.18%

2.6. Chromosome stats

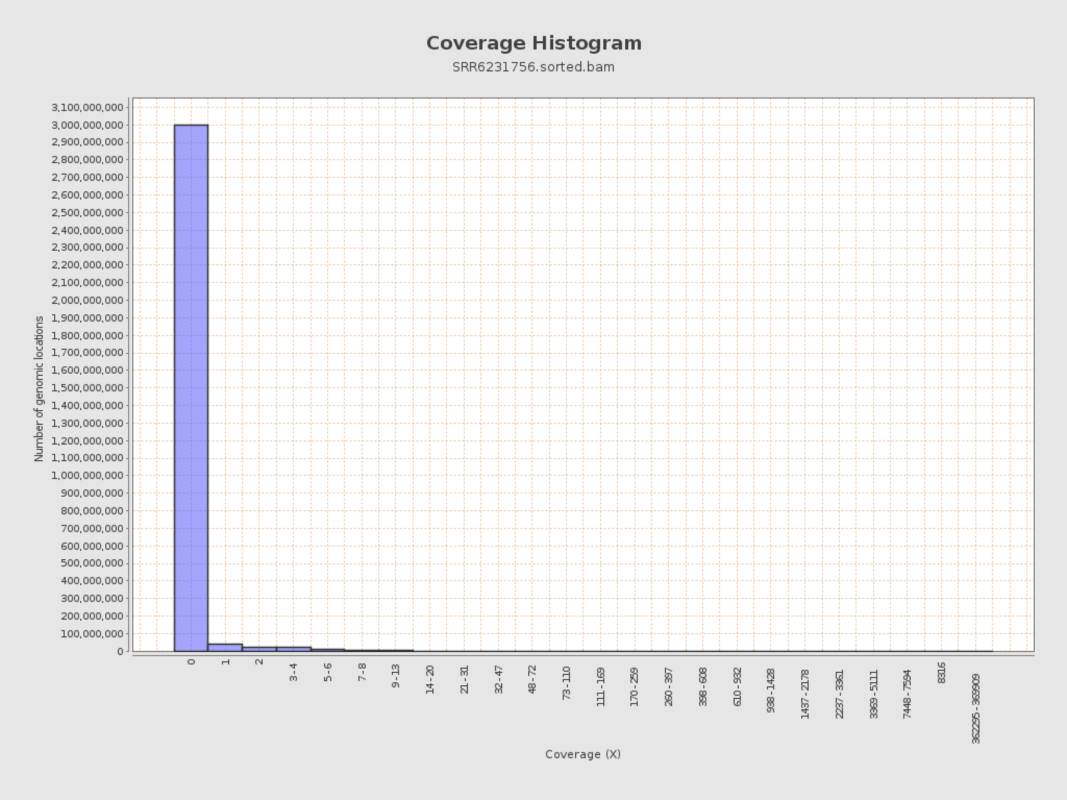
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4277641	0.0172	1.6178
chr2	243199373	61096781	0.2512	206.3028
chr3	198022430	17559554	0.0887	0.6375
chr4	191154276	9366129	0.049	0.463
chr5	180915260	17250833	0.0954	0.7149
chr6	171115067	26149919	0.1528	0.8982
chr7	159138663	10286377	0.0646	1.1908

chr8	146364022	13890597	0.0949	0.854
chr9	141213431	2107084	0.0149	0.4459
chr10	135534747	3245992	0.0239	0.337
chr11	135006516	4128524	0.0306	0.5489
chr12	133851895	5102196	0.0381	0.421
chr13	115169878	2390280	0.0208	0.2912
chr14	107349540	13726083	0.1279	0.8377
chr15	102531392	4844607	0.0472	0.4826
chr16	90354753	9499081	0.1051	0.7228
chr17	81195210	6362299	0.0784	0.6872
chr18	78077248	4280292	0.0548	0.9359
chr19	59128983	10554999	0.1785	1.1489
chr20	63025520	6777315	0.1075	0.7426
chr21	48129895	7727952	0.1606	0.8776
chr22	51304566	503892	0.0098	0.1739
chrMT	16571	183909	11.0982	12.4892
chrX	155270560	33956987	0.2187	1.0785
chrY	59373566	1024700	0.0173	0.2724

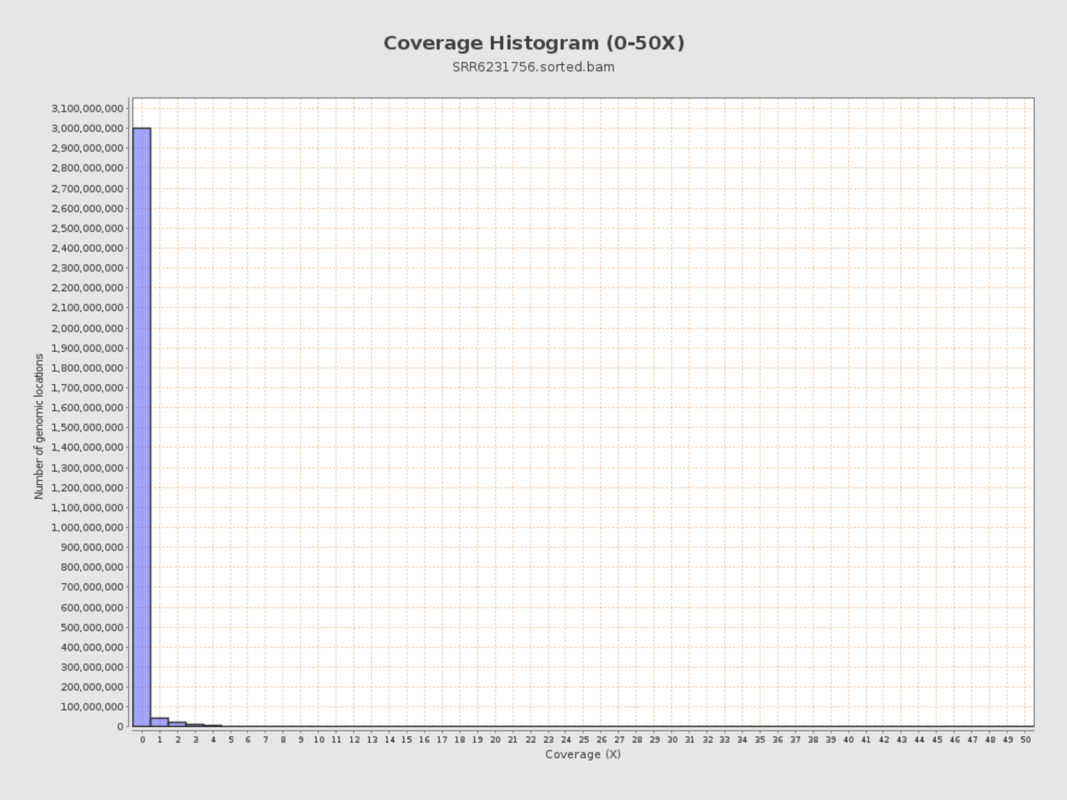
3. Results : Coverage across reference



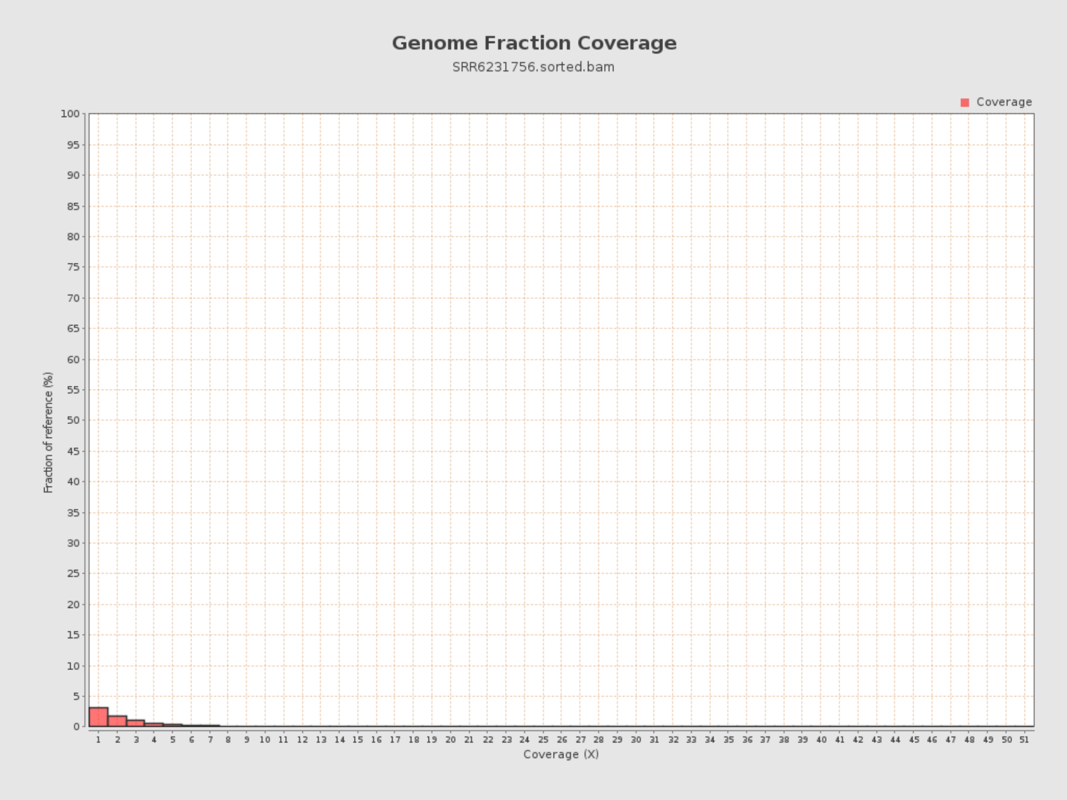
4. Results : Coverage Histogram



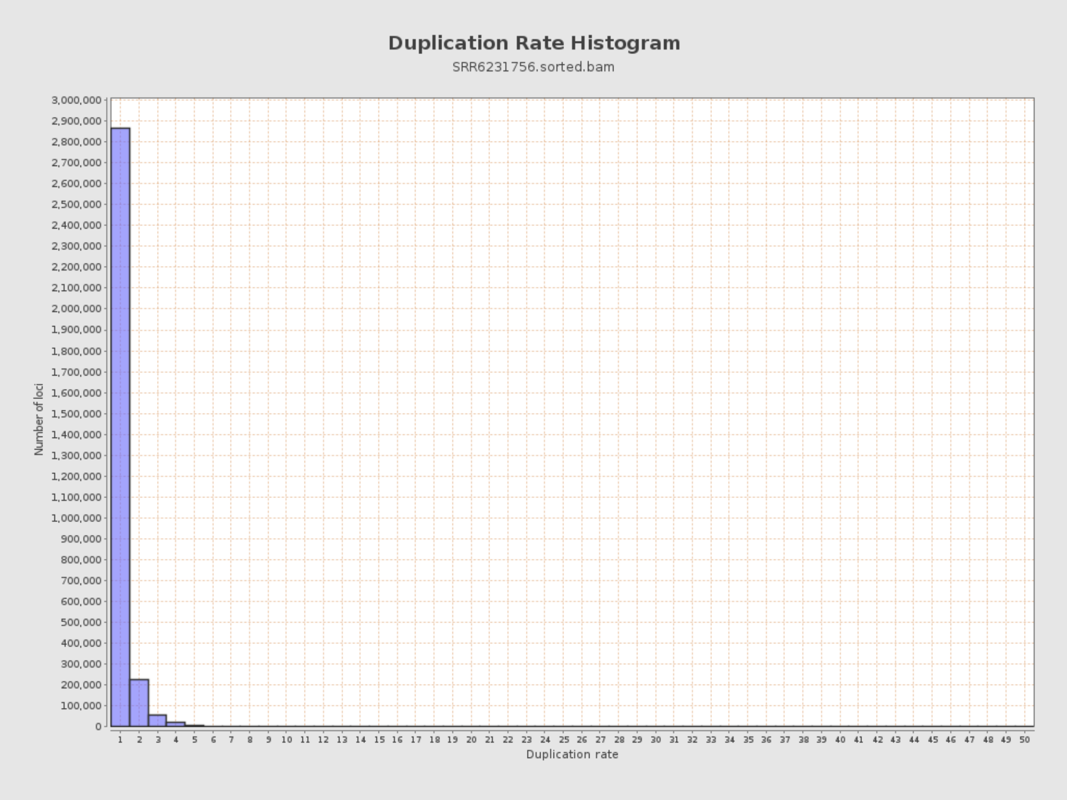
5. Results : Coverage Histogram (0-50X)



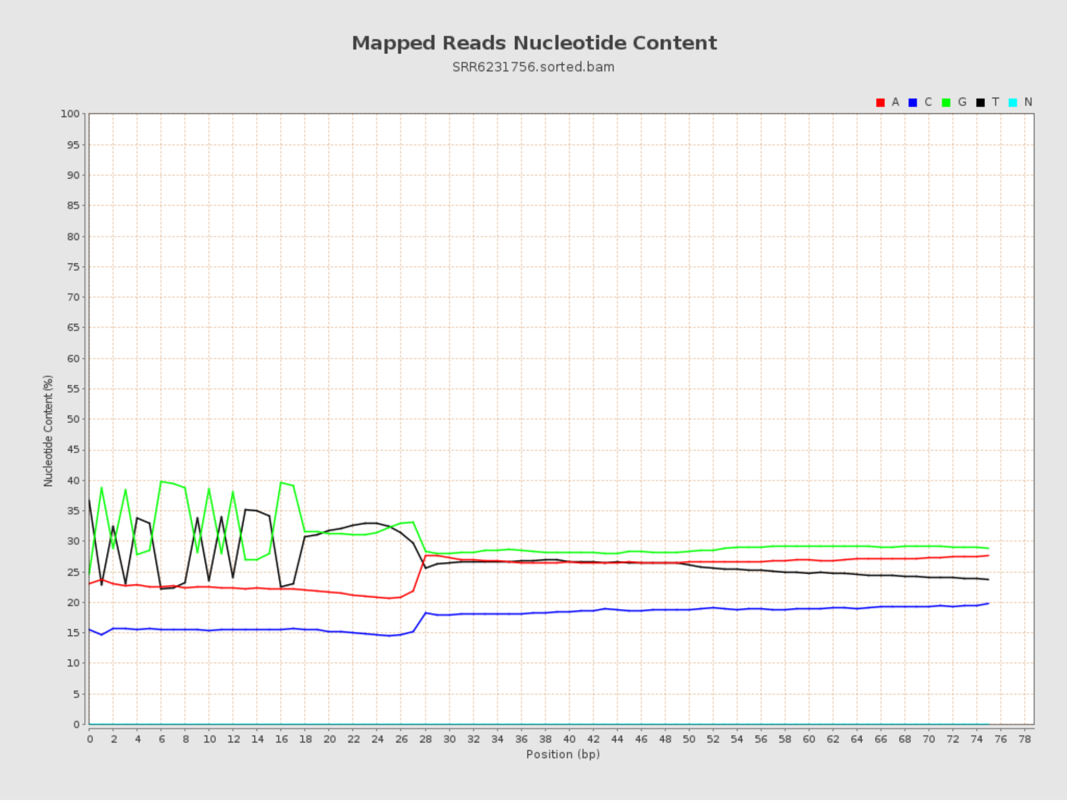
6. Results : Genome Fraction Coverage



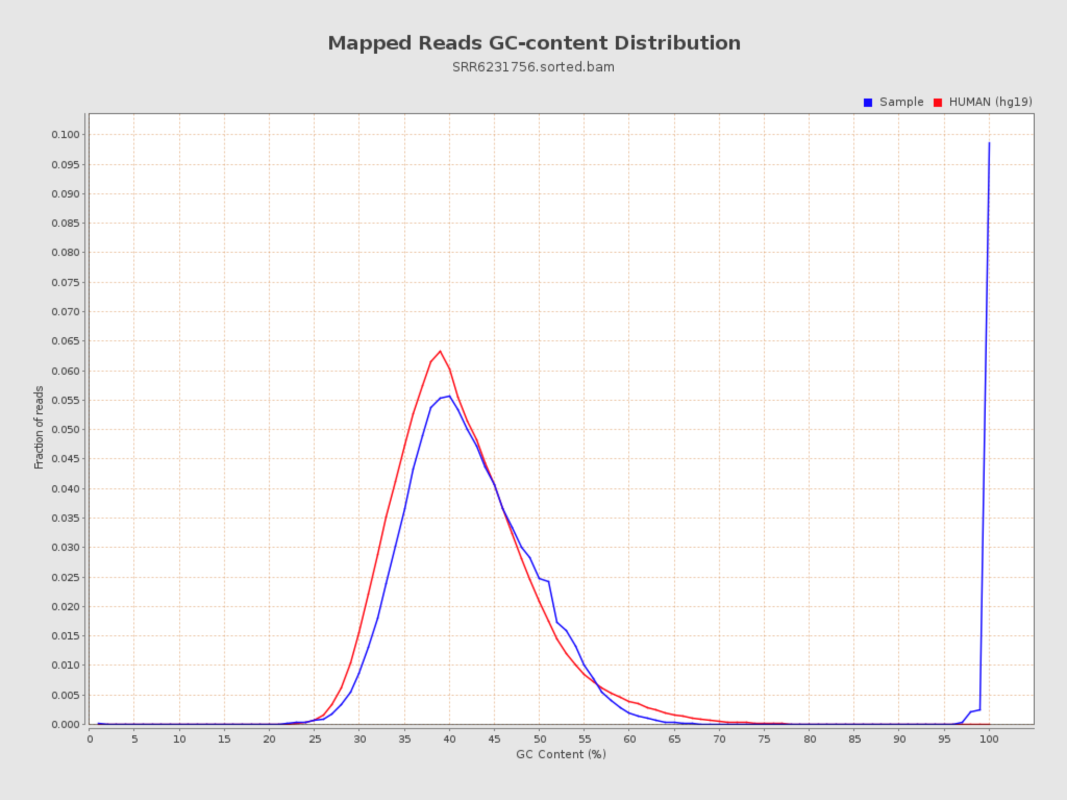
7. Results : Duplication Rate Histogram



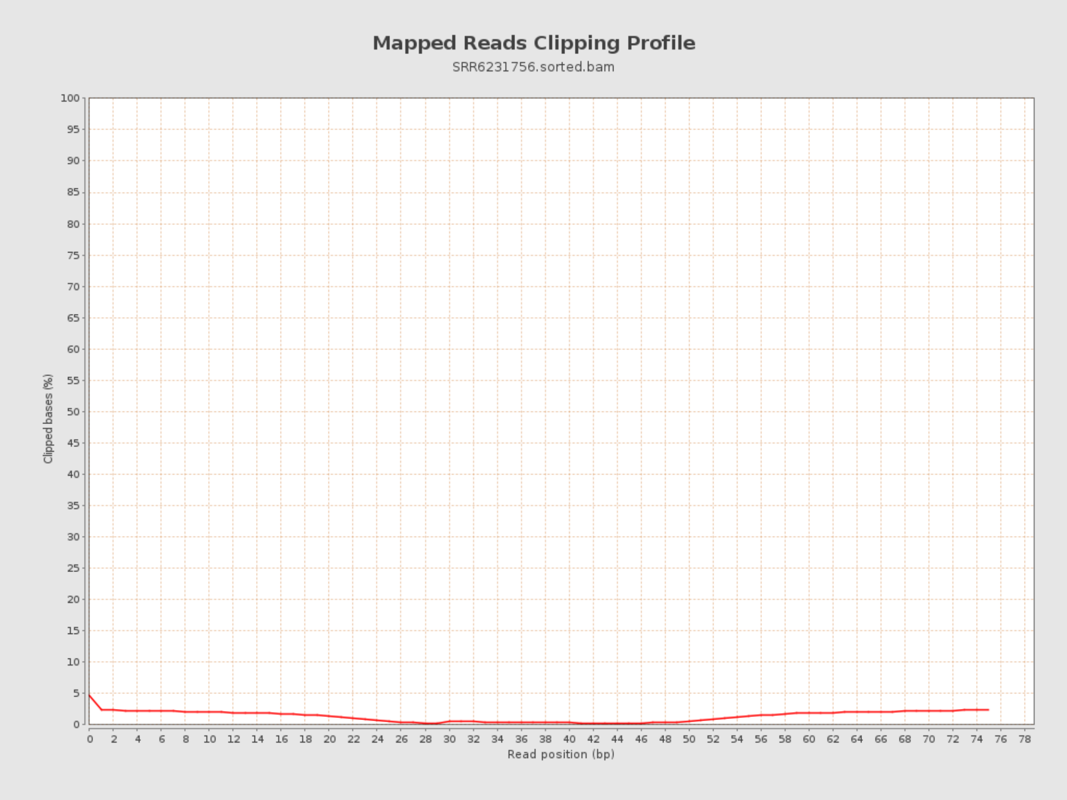
8. Results : Mapped Reads Nucleotide Content



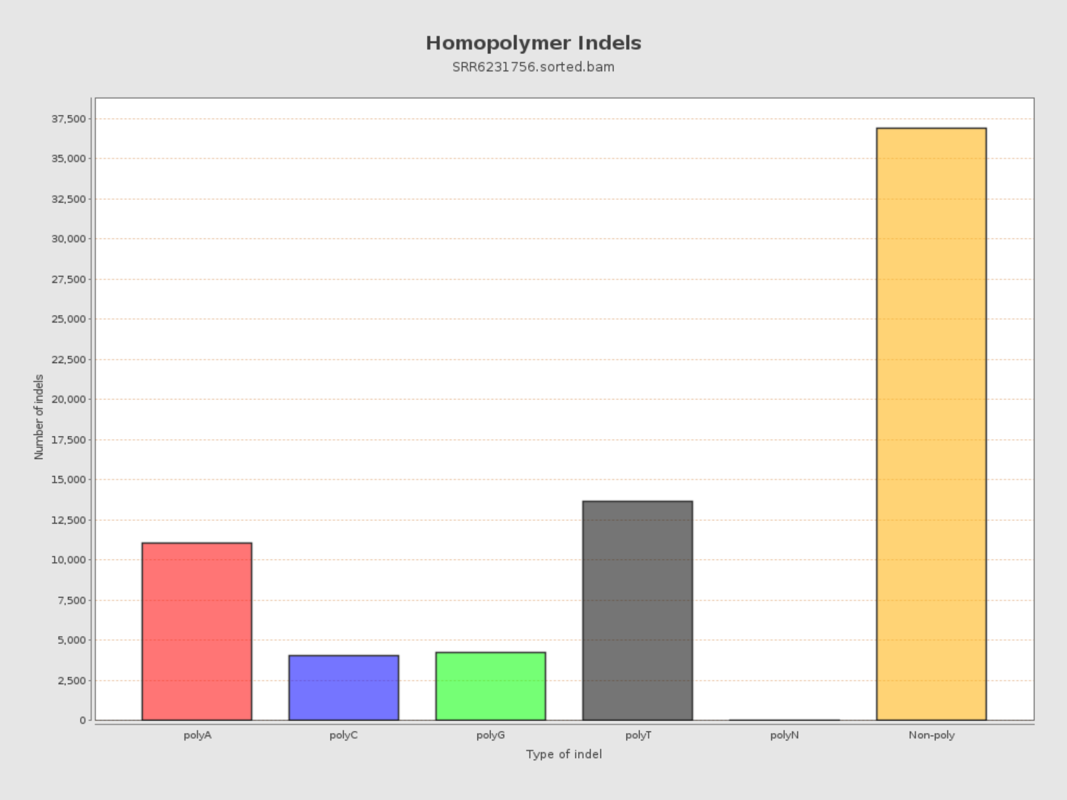
9. Results : Mapped Reads GC-content Distribution



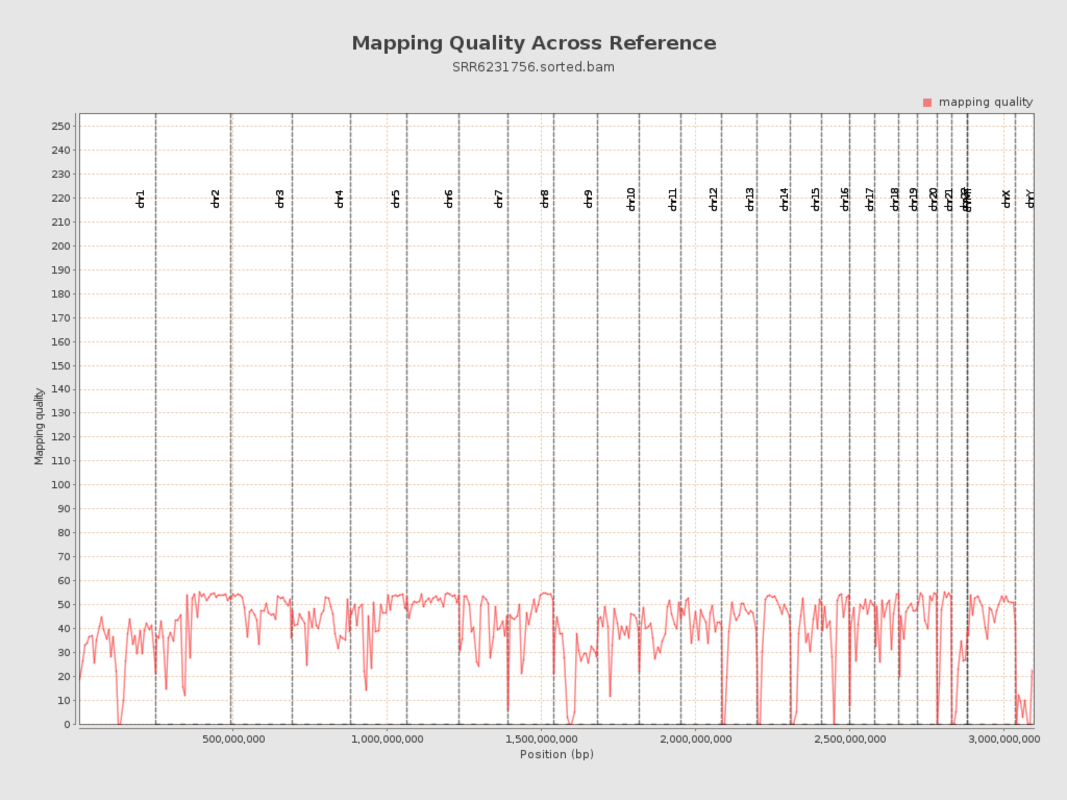
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram