Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 00:21:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231754.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_SRR6231754 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231754.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 00:21:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231754.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,748,558
Mapped reads	4,472,564 / 94.19%
Unmapped reads	275,994 / 5.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,789 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	339,117 / 7.14%
Duplication rate	3.31%
Clipped reads	1,864,061 / 39.26%

2.2. ACGT Content

Number/percentage of A's	78,821,649 / 26.14%
Number/percentage of C's	58,324,207 / 19.34%
Number/percentage of T's	86,284,127 / 28.62%
Number/percentage of G's	78,018,637 / 25.88%
Number/percentage of N's	64,809 / 0.02%
GC Percentage	45.22%

2.3. Coverage

Mean	0.0974

Standard Deviation	18.526

2.4. Mapping Quality

Mean Mapping Quality	43.09

2.5. Mismatches and indels

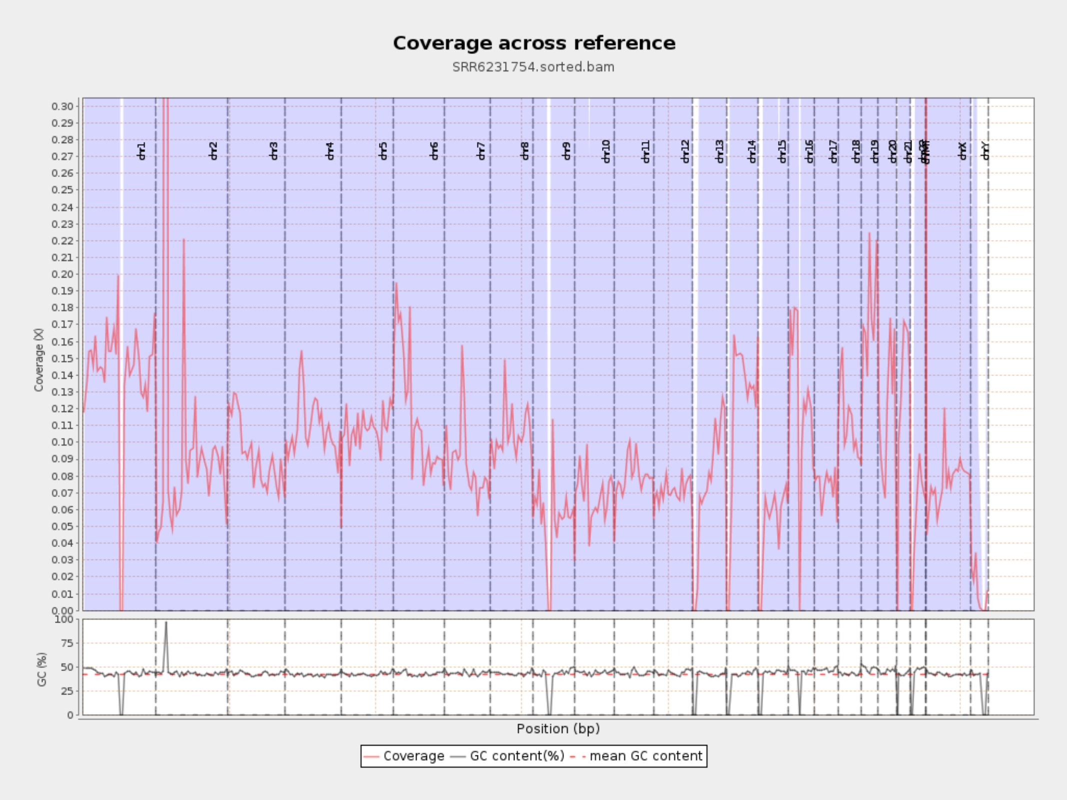
General error rate	0.69%
Mismatches	2,043,285
Insertions	21,597
Mapped reads with at least one insertion	0.48%
Deletions	66,613
Mapped reads with at least one deletion	1.47%
Homopolymer indels	46.16%

2.6. Chromosome stats

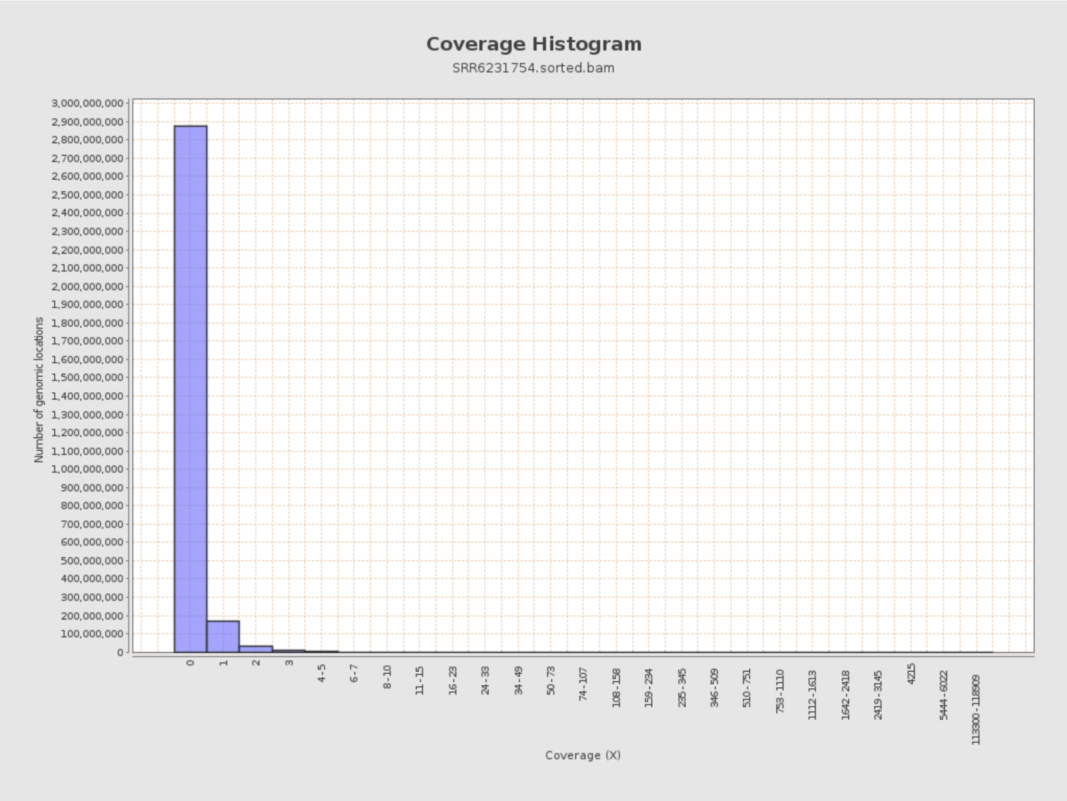
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34789800	0.1396	1.3925
chr2	243199373	29285321	0.1204	66.0399
chr3	198022430	18383453	0.0928	0.3875
chr4	191154276	20993767	0.1098	0.4719
chr5	180915260	19624943	0.1085	0.441
chr6	171115067	19929797	0.1165	0.6853
chr7	159138663	13883040	0.0872	1.2216

chr8	146364022	15377095	0.1051	0.7696
chr9	141213431	7749057	0.0549	0.8942
chr10	135534747	9321654	0.0688	0.5688
chr11	135006516	10773229	0.0798	0.9128
chr12	133851895	9578383	0.0716	0.3609
chr13	115169878	8717339	0.0757	0.3449
chr14	107349540	12793937	0.1192	0.6563
chr15	102531392	5230466	0.051	0.2903
chr16	90354753	10911126	0.1208	0.6091
chr17	81195210	6067698	0.0747	0.506
chr18	78077248	8787992	0.1126	1.8003
chr19	59128983	10343372	0.1749	1.1645
chr20	63025520	7362859	0.1168	0.474
chr21	48129895	6313073	0.1312	0.5684
chr22	51304566	2847688	0.0555	0.3011
chrMT	16571	7597	0.4585	1.1795
chrX	155270560	11860168	0.0764	0.5783
chrY	59373566	689886	0.0116	0.2201

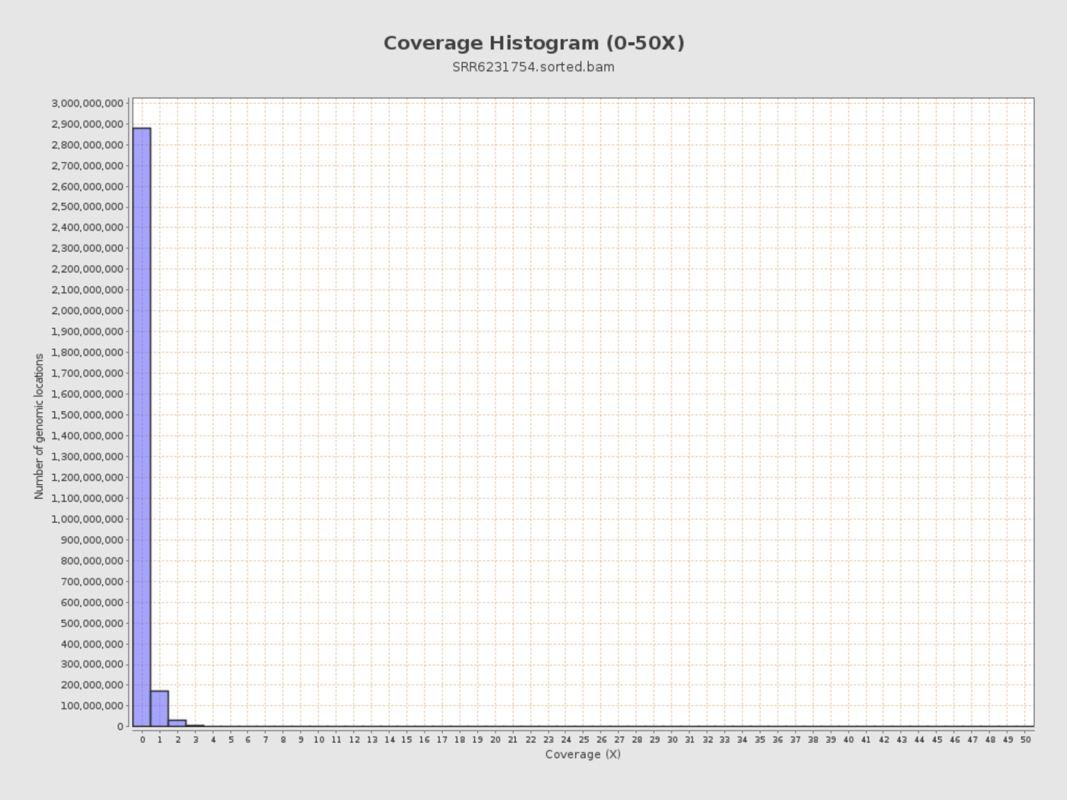
3. Results : Coverage across reference



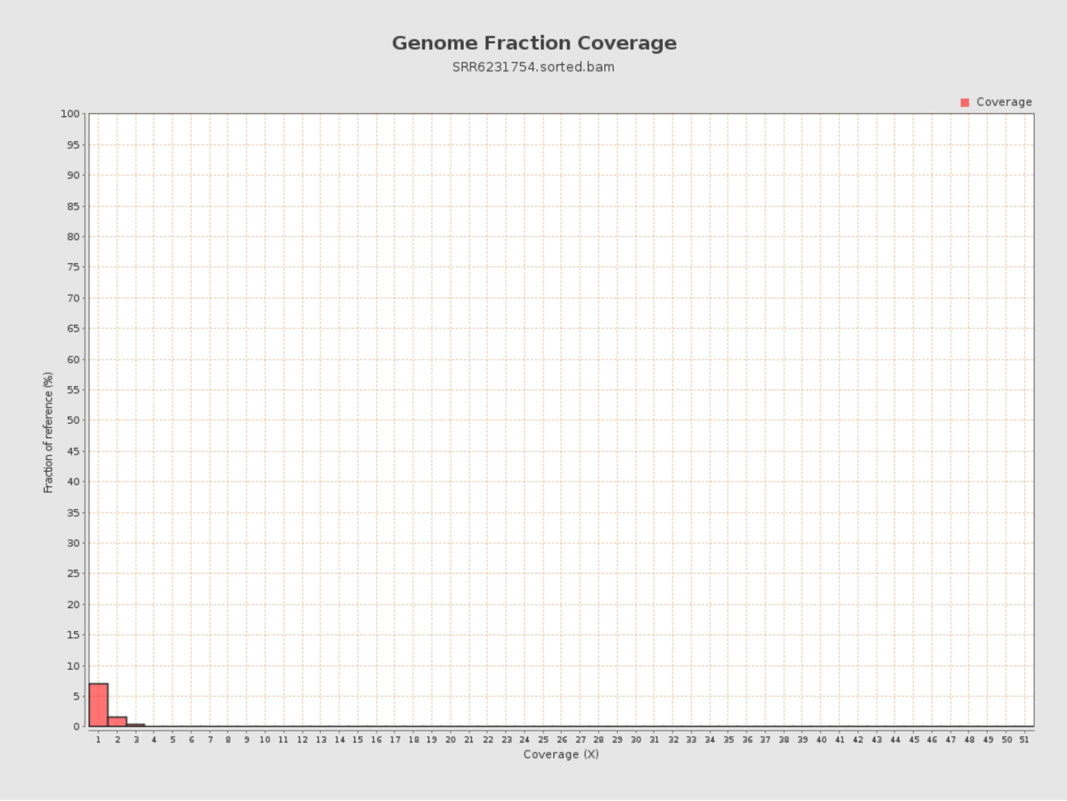
4. Results : Coverage Histogram



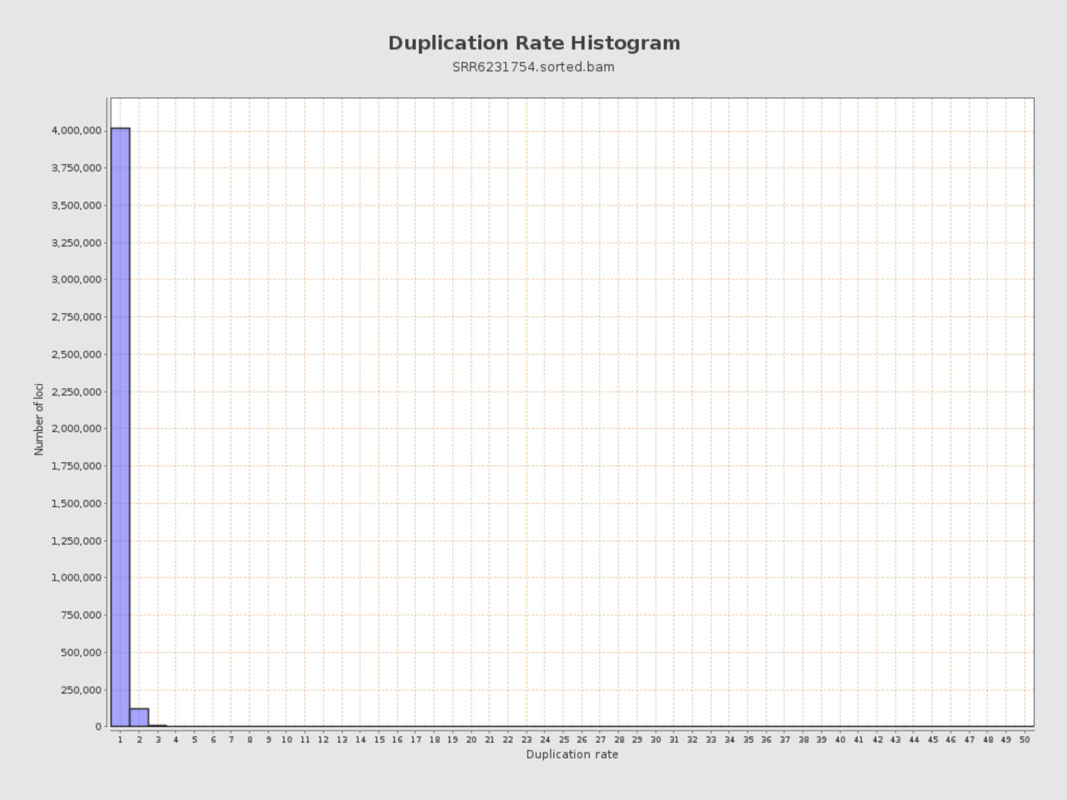
5. Results : Coverage Histogram (0-50X)



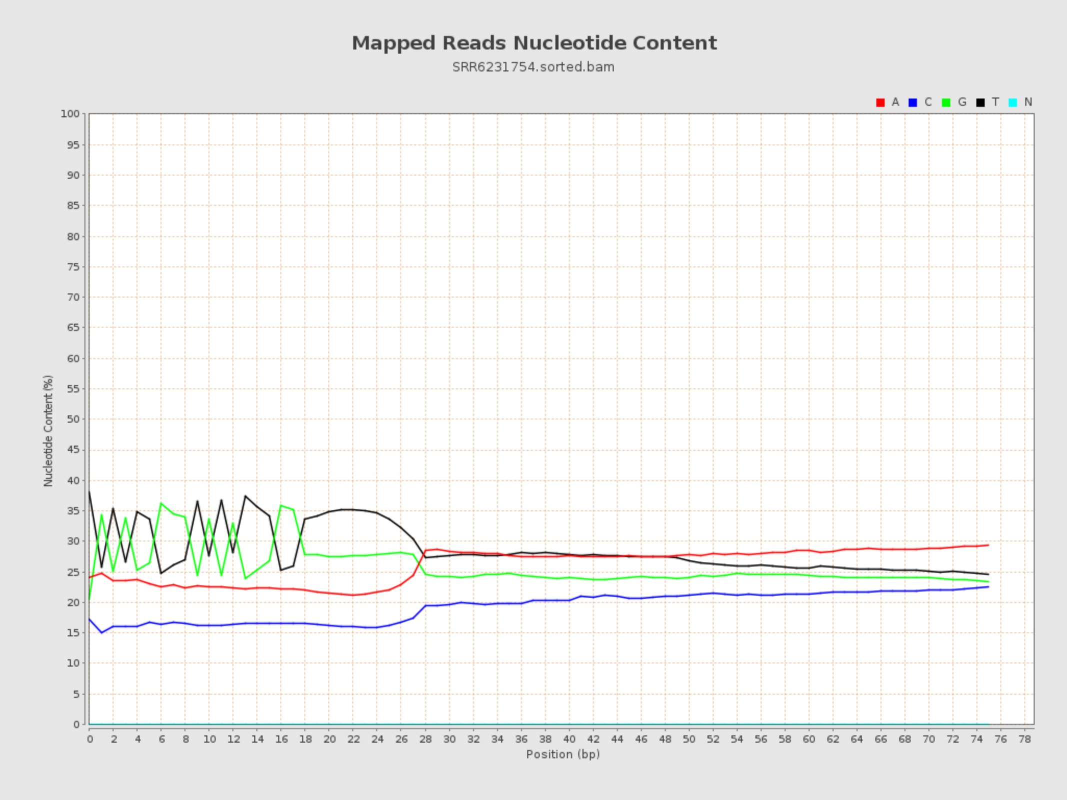
6. Results : Genome Fraction Coverage



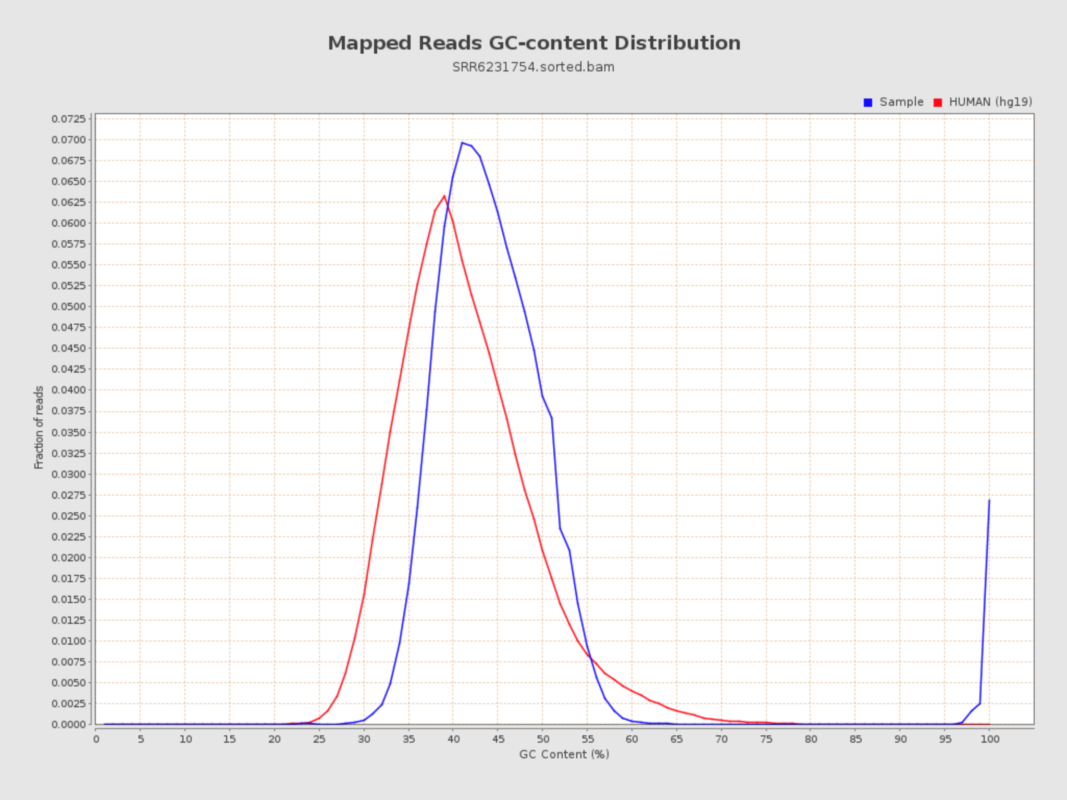
7. Results : Duplication Rate Histogram



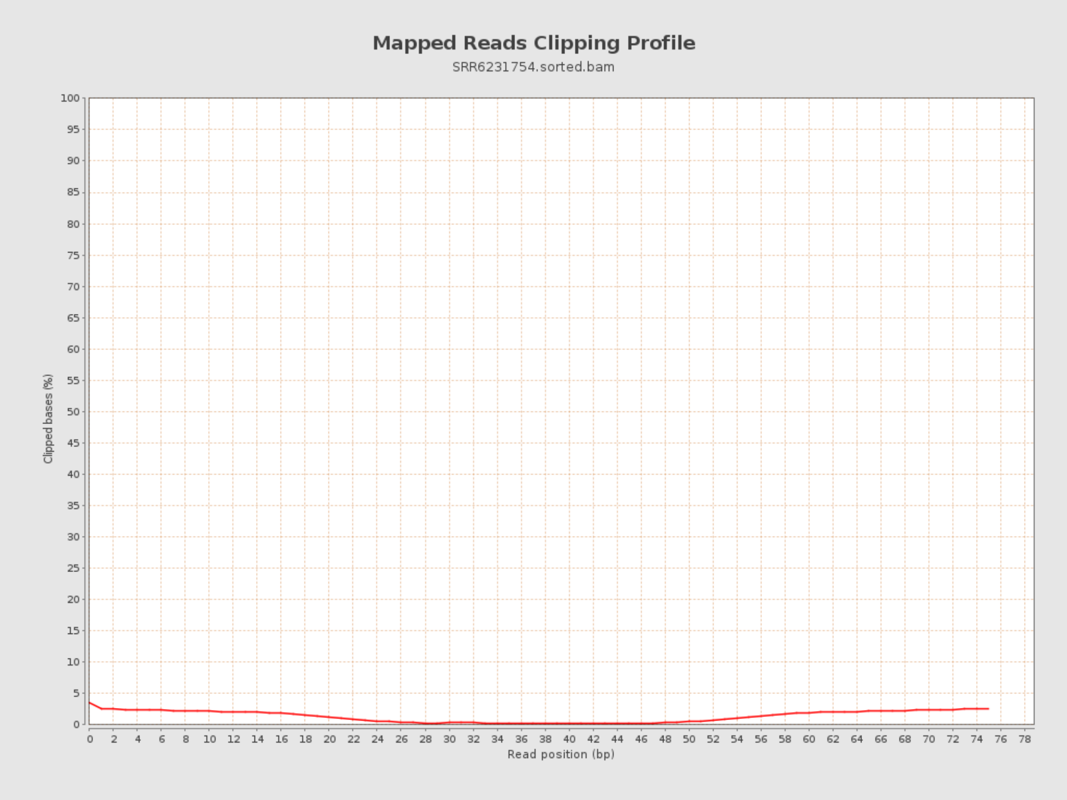
8. Results : Mapped Reads Nucleotide Content



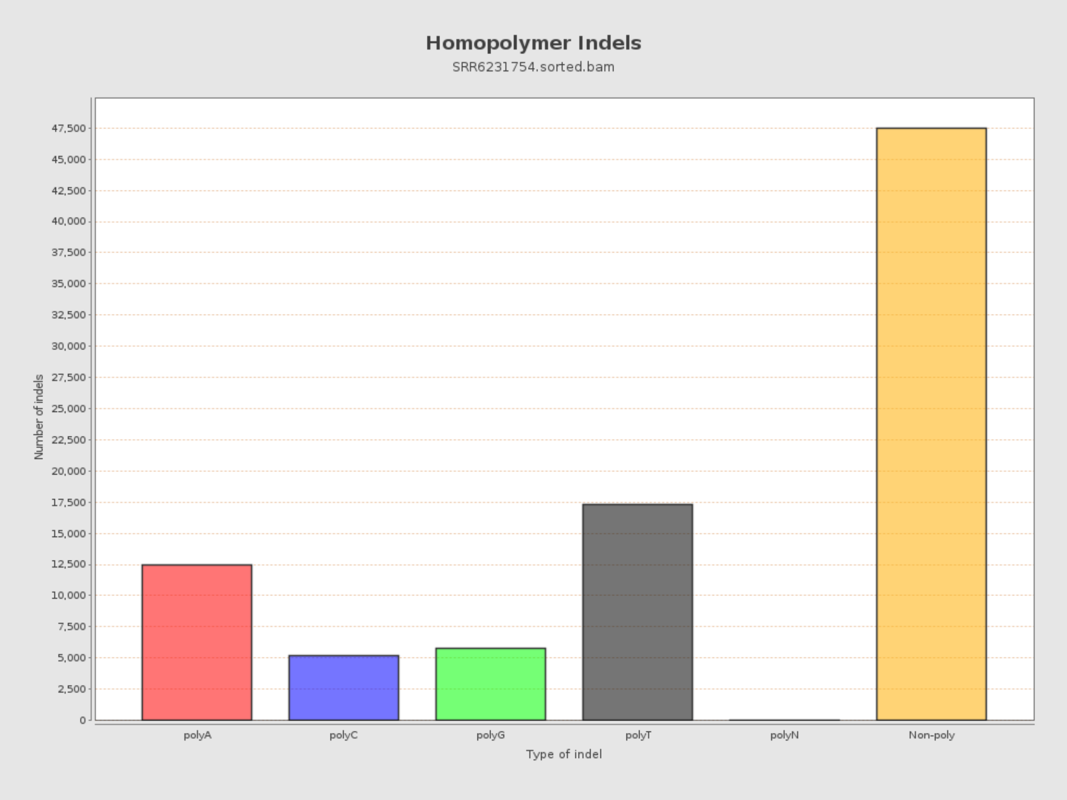
9. Results : Mapped Reads GC-content Distribution



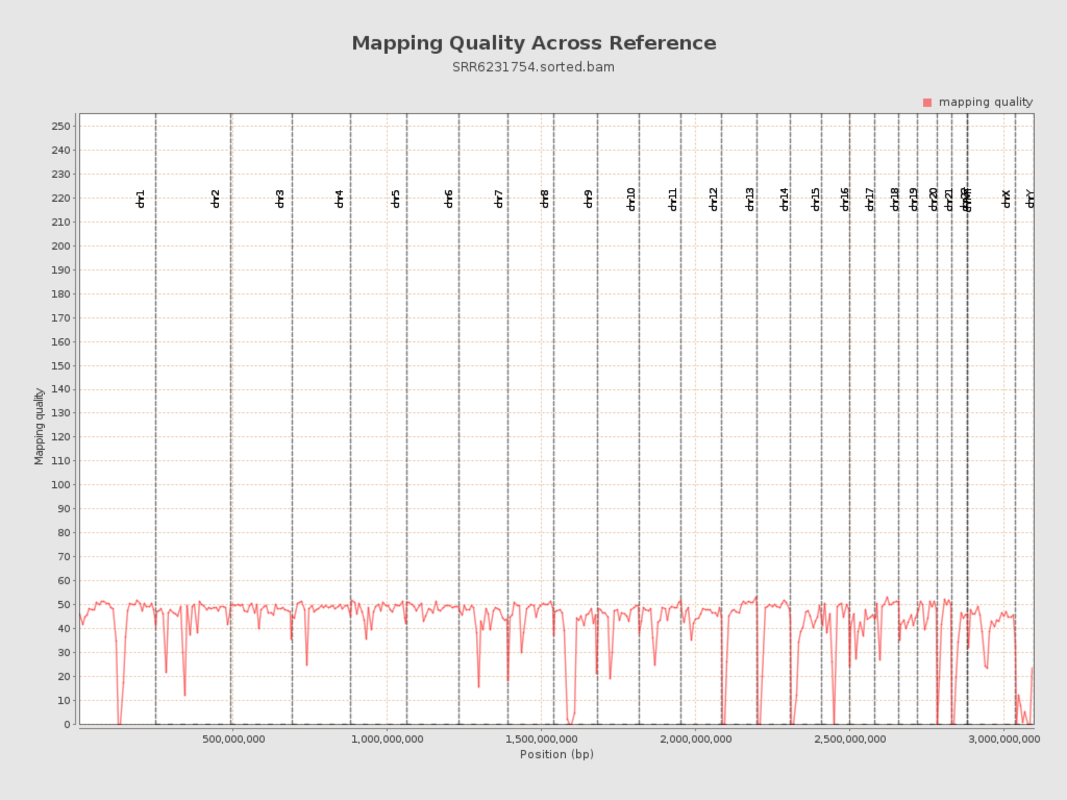
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram