Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:30:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231770.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_SRR6231770 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231770.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:30:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231770.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,400,287
Mapped reads	341,377 / 24.38%
Unmapped reads	1,058,910 / 75.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,647 / 0.19%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	21,056 / 1.5%
Duplication rate	5.28%
Clipped reads	204,042 / 14.57%

2.2. ACGT Content

Number/percentage of A's	5,587,720 / 26.05%
Number/percentage of C's	4,076,692 / 19.01%
Number/percentage of T's	6,676,779 / 31.13%
Number/percentage of G's	5,101,009 / 23.78%
Number/percentage of N's	5,068 / 0.02%
GC Percentage	42.79%

2.3. Coverage

Mean	0.0069

Standard Deviation	0.1153

2.4. Mapping Quality

Mean Mapping Quality	44.21

2.5. Mismatches and indels

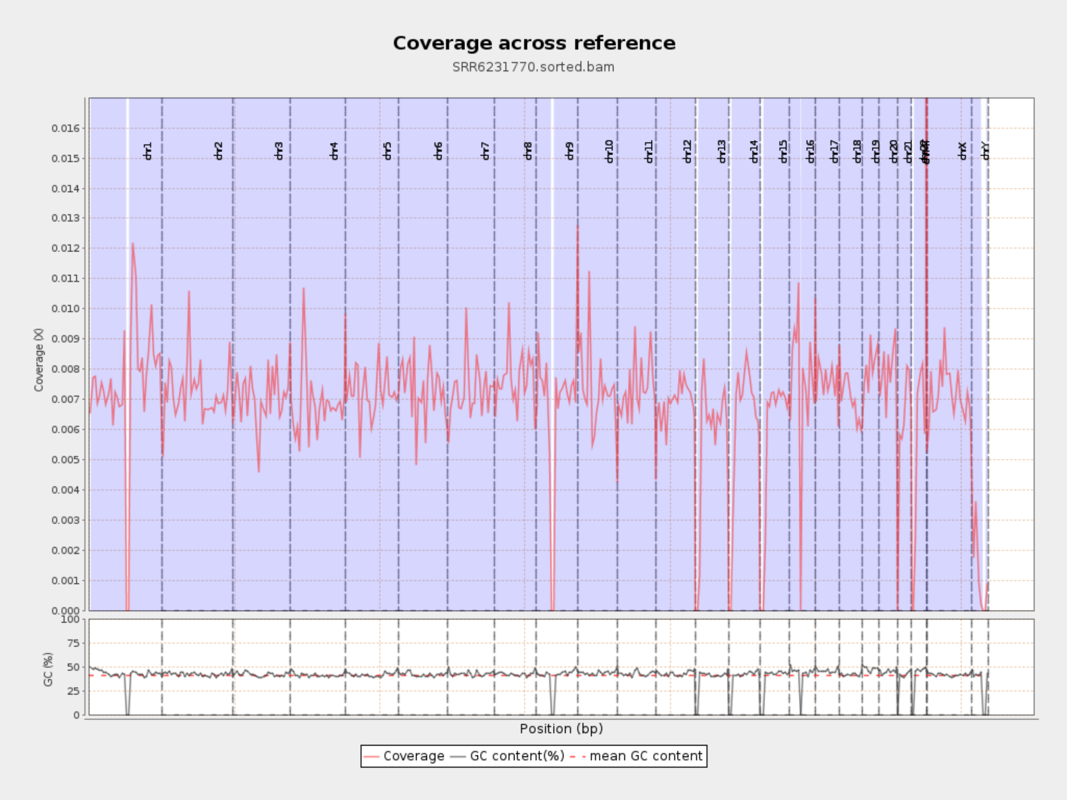
General error rate	0.96%
Mismatches	202,495
Insertions	1,784
Mapped reads with at least one insertion	0.52%
Deletions	6,989
Mapped reads with at least one deletion	2.02%
Homopolymer indels	45.33%

2.6. Chromosome stats

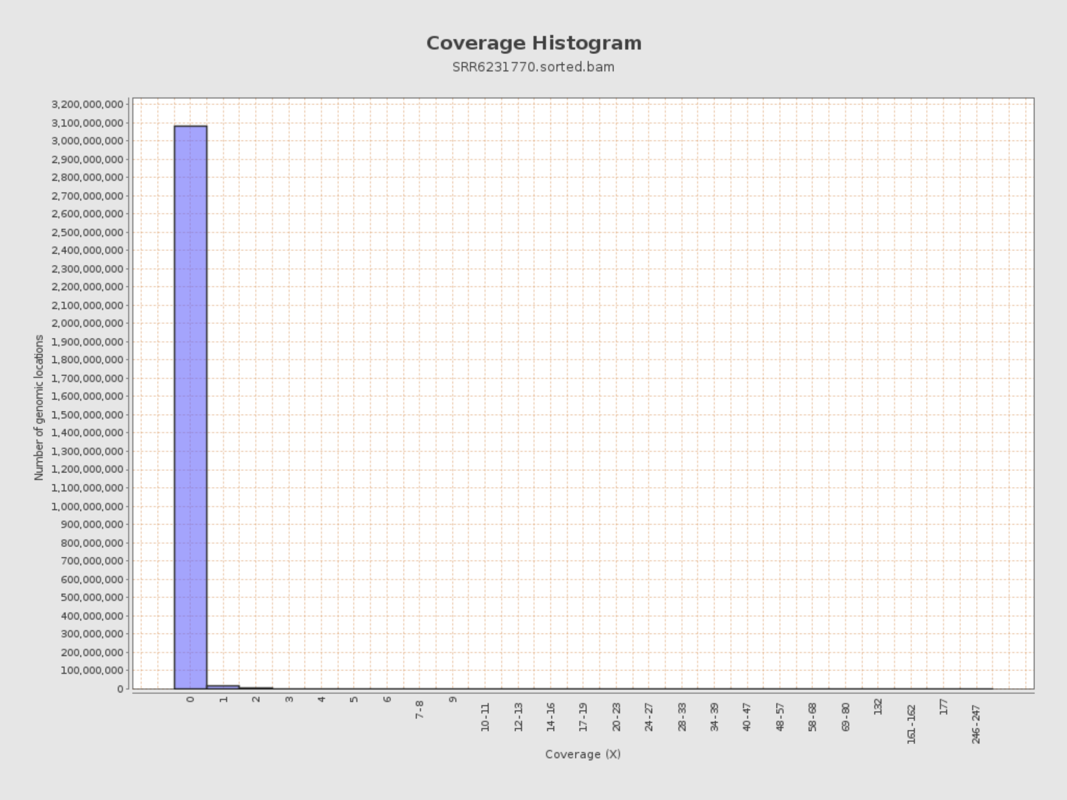
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1860485	0.0075	0.1295
chr2	243199373	1766884	0.0073	0.1505
chr3	198022430	1392357	0.007	0.1079
chr4	191154276	1302293	0.0068	0.1062
chr5	180915260	1306773	0.0072	0.1086
chr6	171115067	1257764	0.0074	0.1197
chr7	159138663	1162421	0.0073	0.1224

chr8	146364022	1120867	0.0077	0.1186
chr9	141213431	930340	0.0066	0.1074
chr10	135534747	1001066	0.0074	0.116
chr11	135006516	985722	0.0073	0.1127
chr12	133851895	931055	0.007	0.1064
chr13	115169878	637563	0.0055	0.097
chr14	107349540	651826	0.0061	0.1009
chr15	102531392	582729	0.0057	0.0973
chr16	90354753	675317	0.0075	0.1137
chr17	81195210	614635	0.0076	0.1125
chr18	78077248	549988	0.007	0.1298
chr19	59128983	475181	0.008	0.1227
chr20	63025520	500230	0.0079	0.1152
chr21	48129895	293978	0.0061	0.0994
chr22	51304566	256659	0.005	0.0919
chrMT	16571	16498	0.9956	1.5413
chrX	155270560	1112392	0.0072	0.1089
chrY	59373566	73483	0.0012	0.0453

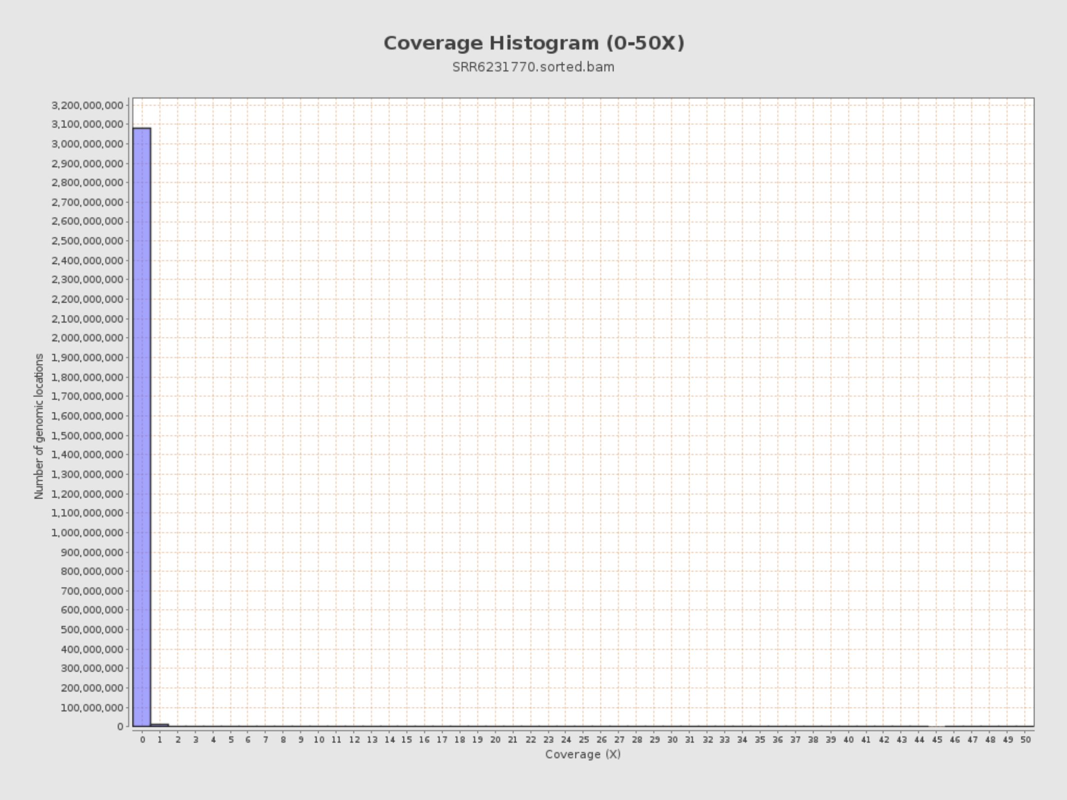
3. Results : Coverage across reference



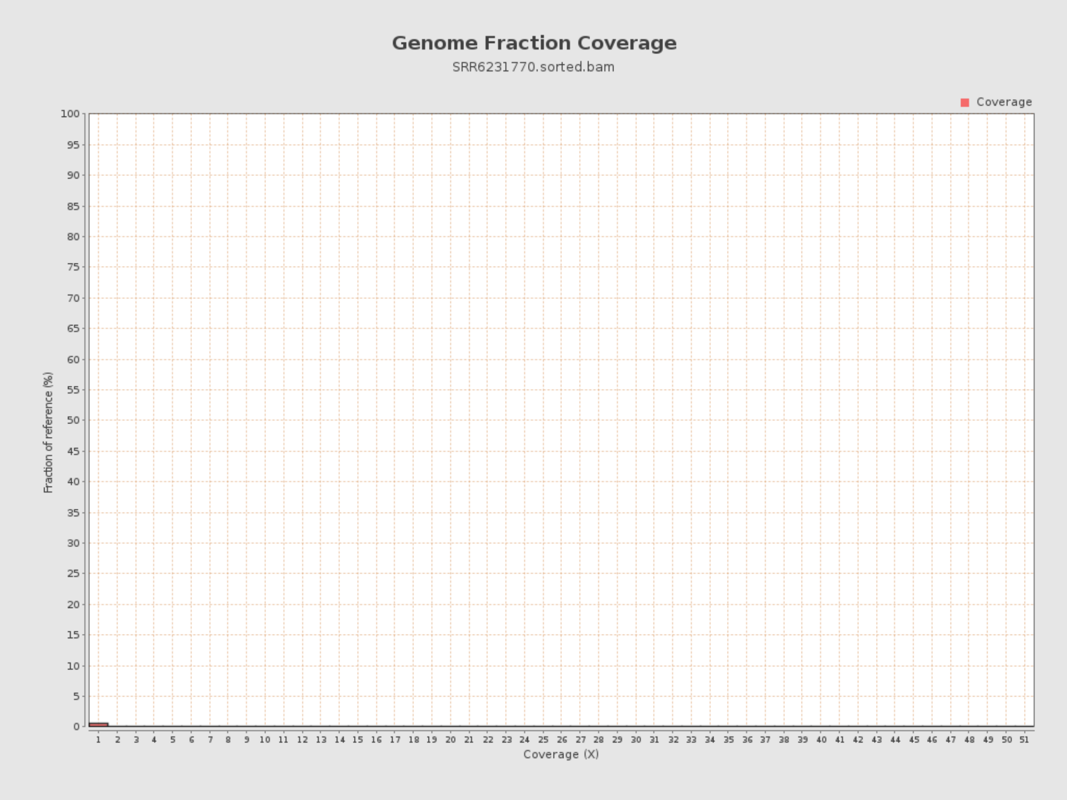
4. Results : Coverage Histogram



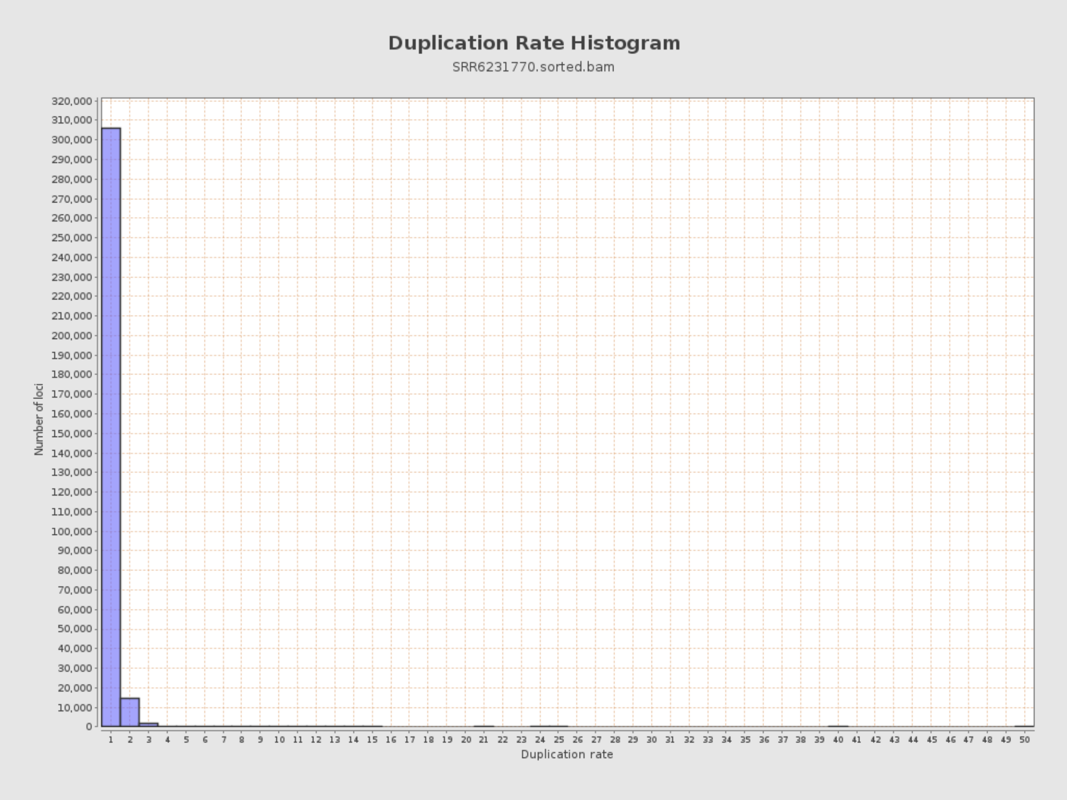
5. Results : Coverage Histogram (0-50X)



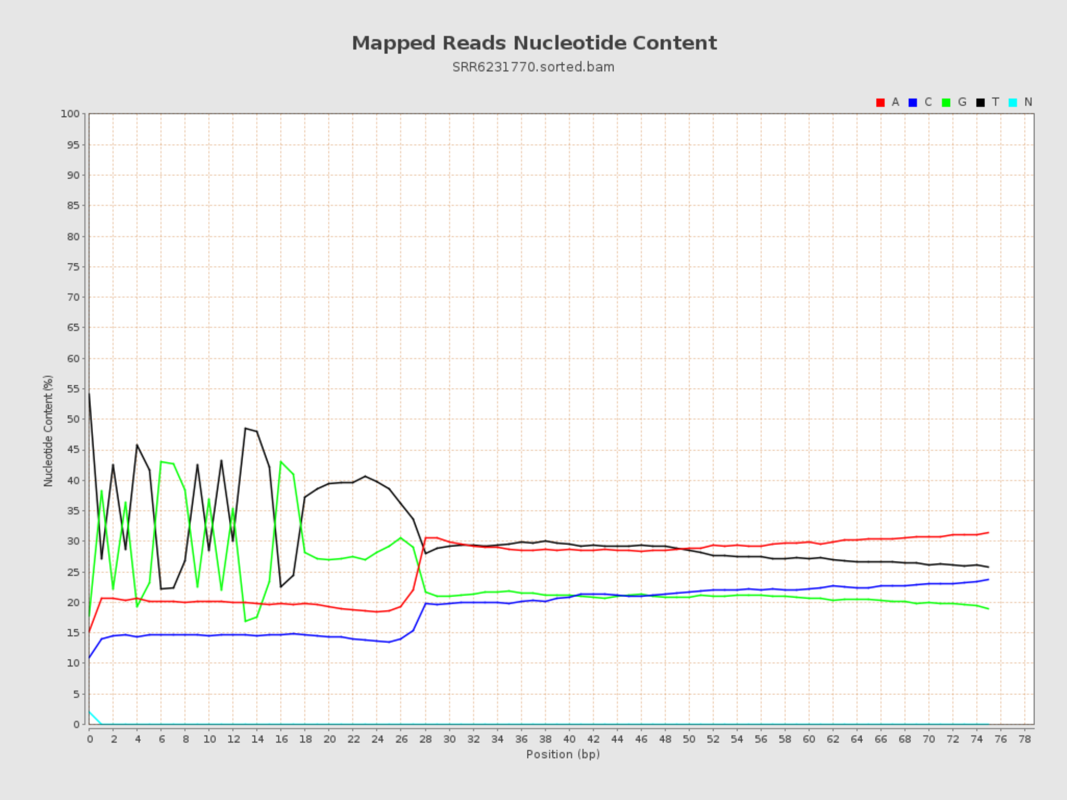
6. Results : Genome Fraction Coverage



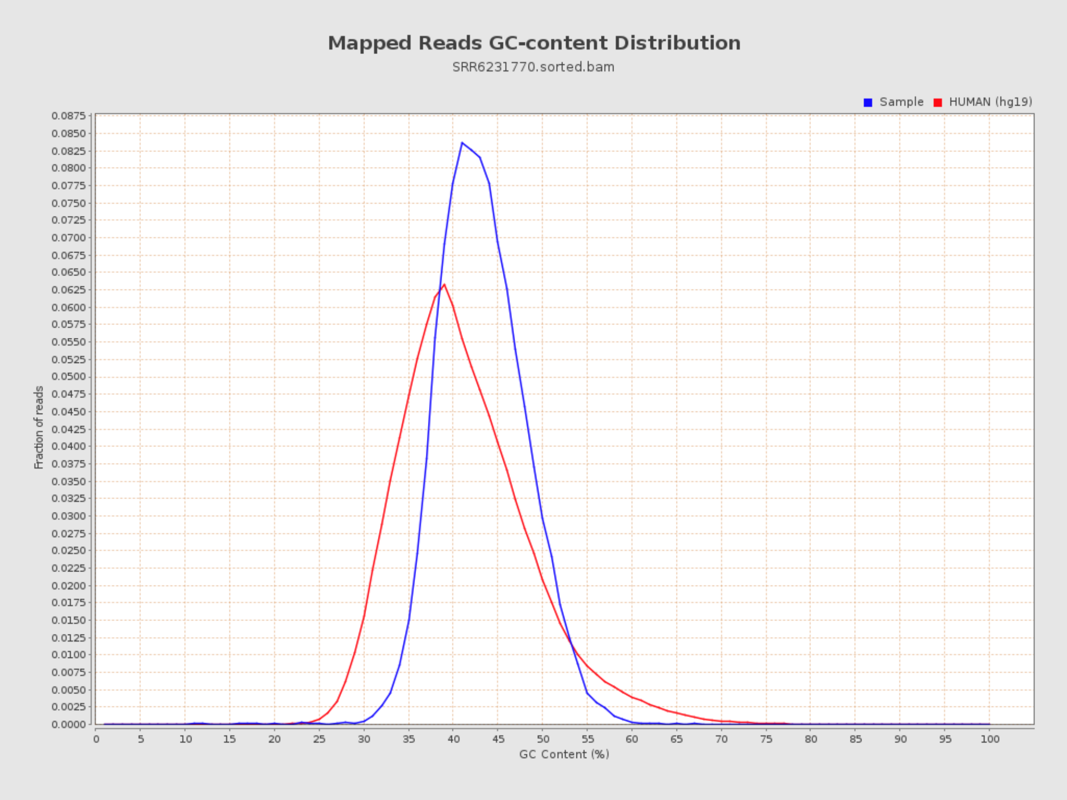
7. Results : Duplication Rate Histogram



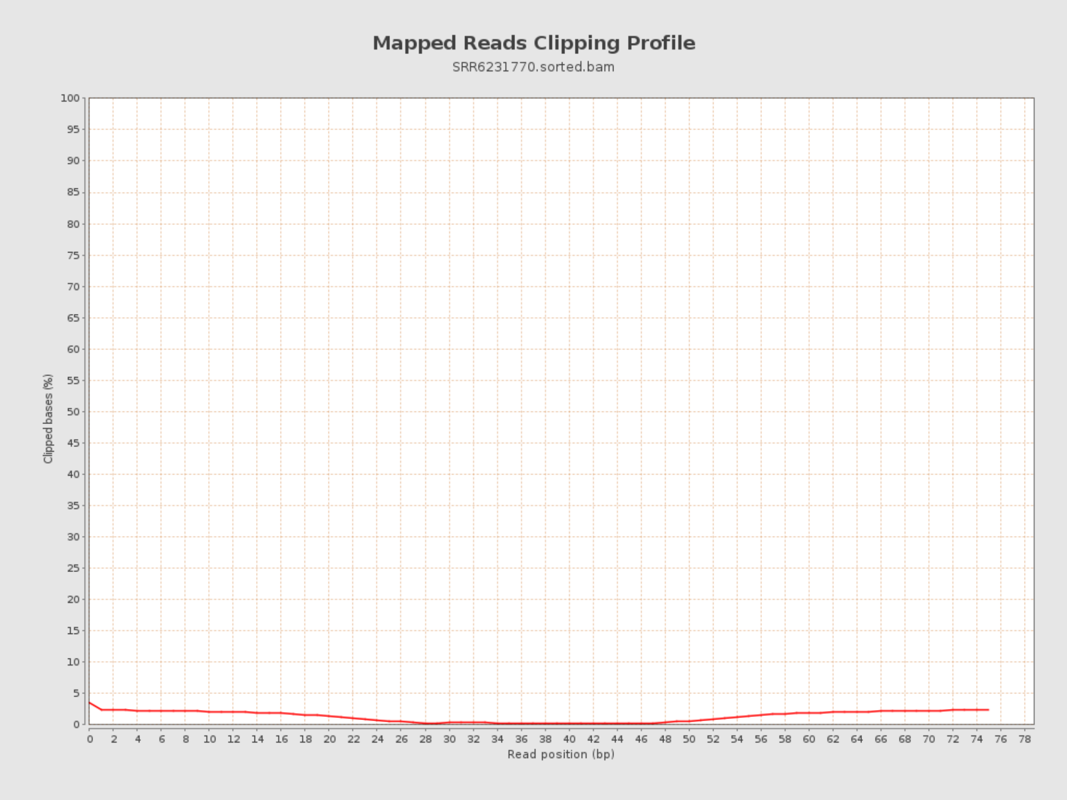
8. Results : Mapped Reads Nucleotide Content



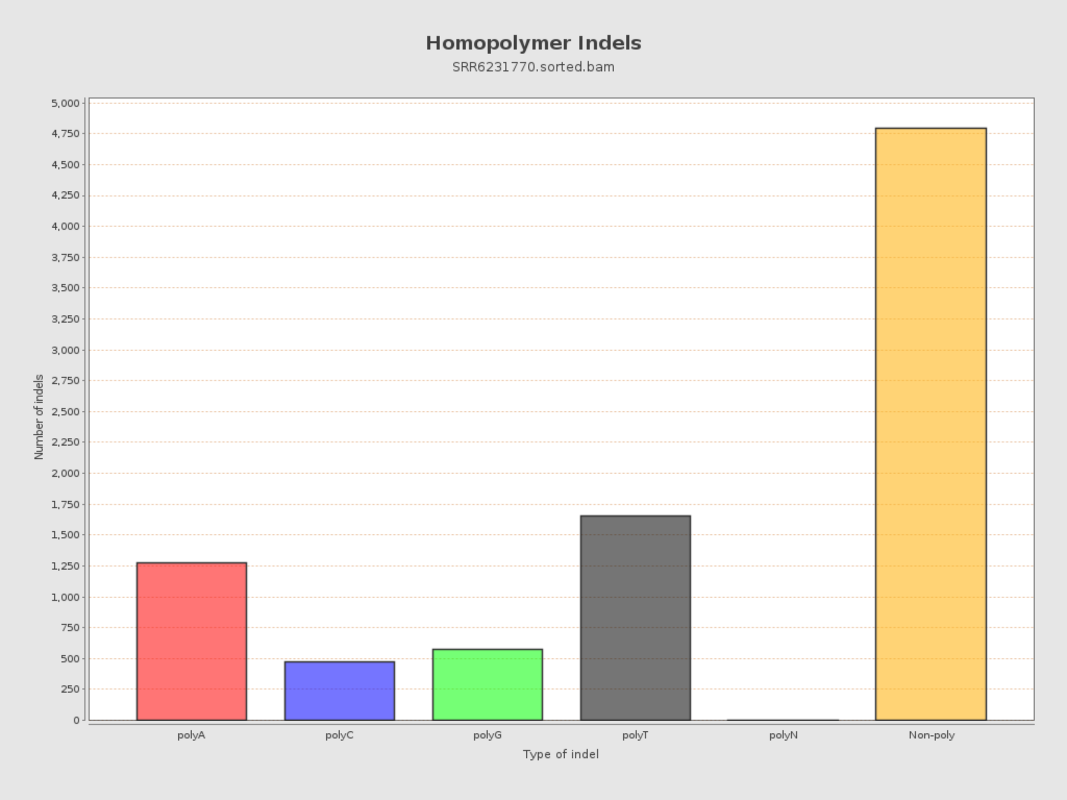
9. Results : Mapped Reads GC-content Distribution



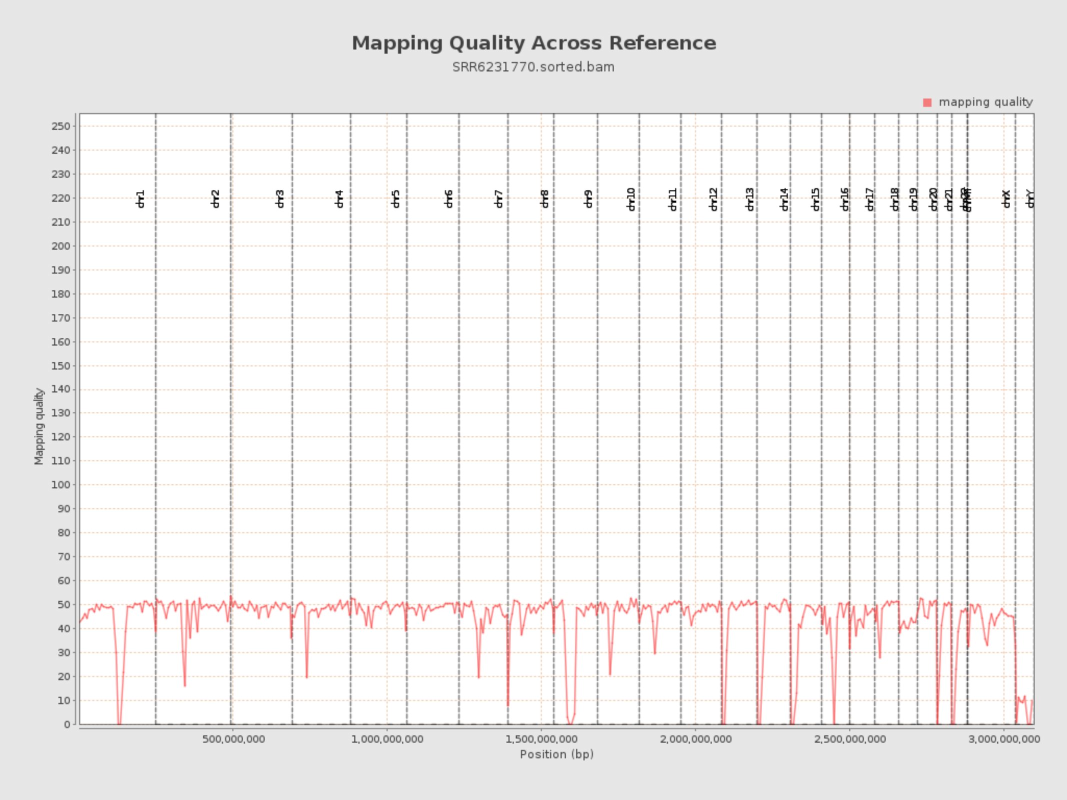
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram