Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:37:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231824.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_SRR6231824 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231824.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:37:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231824.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,393,981
Mapped reads	242,503 / 17.4%
Unmapped reads	1,151,478 / 82.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,554 / 0.18%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	27,729 / 1.99%
Duplication rate	8.86%
Clipped reads	157,920 / 11.33%

2.2. ACGT Content

Number/percentage of A's	3,816,790 / 26.29%
Number/percentage of C's	2,876,115 / 19.81%
Number/percentage of T's	4,409,602 / 30.37%
Number/percentage of G's	3,415,721 / 23.52%
Number/percentage of N's	2,430 / 0.02%
GC Percentage	43.33%

2.3. Coverage

Mean	0.0047

Standard Deviation	0.1163

2.4. Mapping Quality

Mean Mapping Quality	39.29

2.5. Mismatches and indels

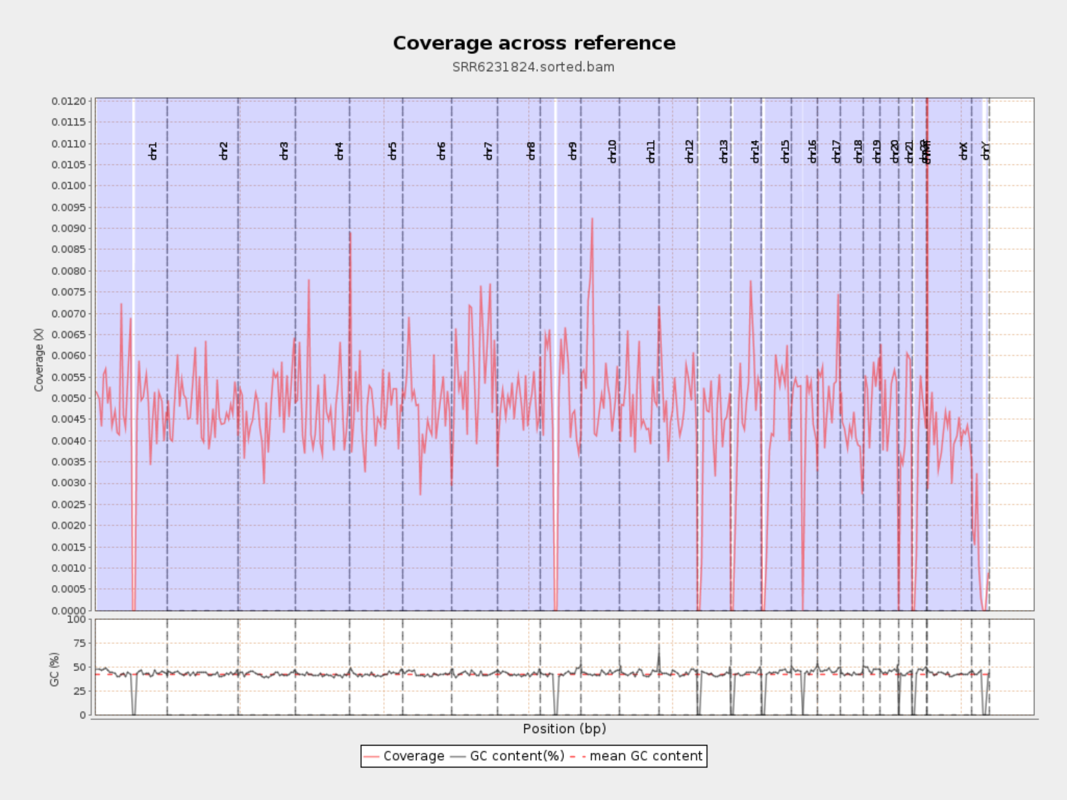
General error rate	1.01%
Mismatches	141,310
Insertions	2,230
Mapped reads with at least one insertion	0.9%
Deletions	4,403
Mapped reads with at least one deletion	1.79%
Homopolymer indels	37.58%

2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1153979	0.0046	0.1144
chr2	243199373	1168672	0.0048	0.1203
chr3	198022430	945476	0.0048	0.1062
chr4	191154276	914629	0.0048	0.1094
chr5	180915260	862216	0.0048	0.113
chr6	171115067	811706	0.0047	0.1114
chr7	159138663	901118	0.0057	0.1236

chr8	146364022	710398	0.0049	0.1113
chr9	141213431	656318	0.0046	0.1036
chr10	135534747	750602	0.0055	0.1217
chr11	135006516	656370	0.0049	0.1184
chr12	133851895	664697	0.005	0.1126
chr13	115169878	448556	0.0039	0.132
chr14	107349540	472560	0.0044	0.1202
chr15	102531392	411118	0.004	0.1007
chr16	90354753	403470	0.0045	0.1209
chr17	81195210	429071	0.0053	0.1185
chr18	78077248	322141	0.0041	0.1073
chr19	59128983	303365	0.0051	0.1109
chr20	63025520	306705	0.0049	0.1135
chr21	48129895	200969	0.0042	0.0989
chr22	51304566	170663	0.0033	0.0865
chrMT	16571	159950	9.6524	8.0165
chrX	155270560	639688	0.0041	0.105
chrY	59373566	63894	0.0011	0.048

3. Results : Coverage across reference



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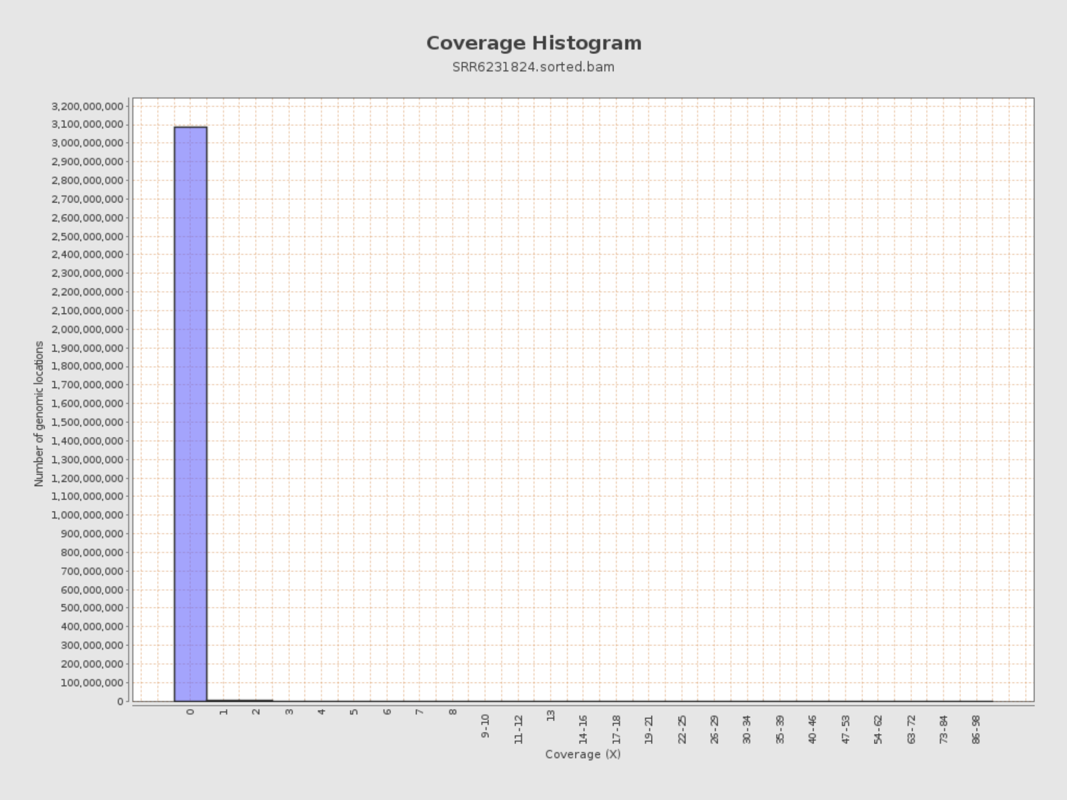
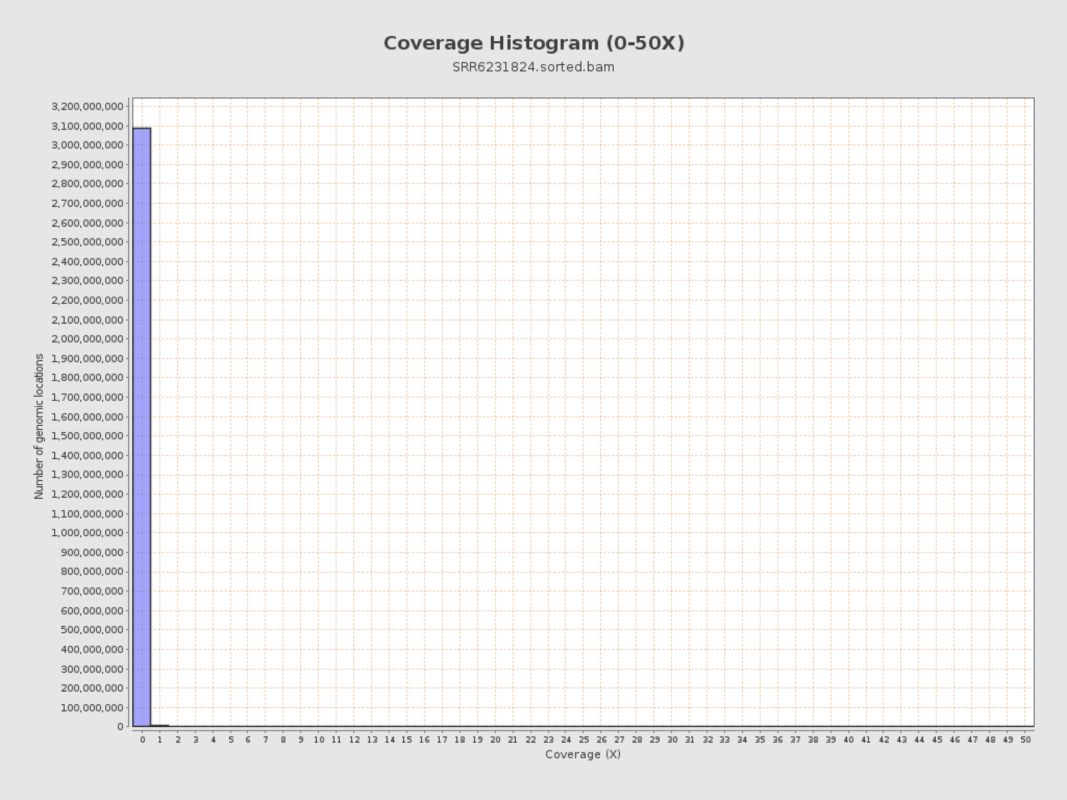
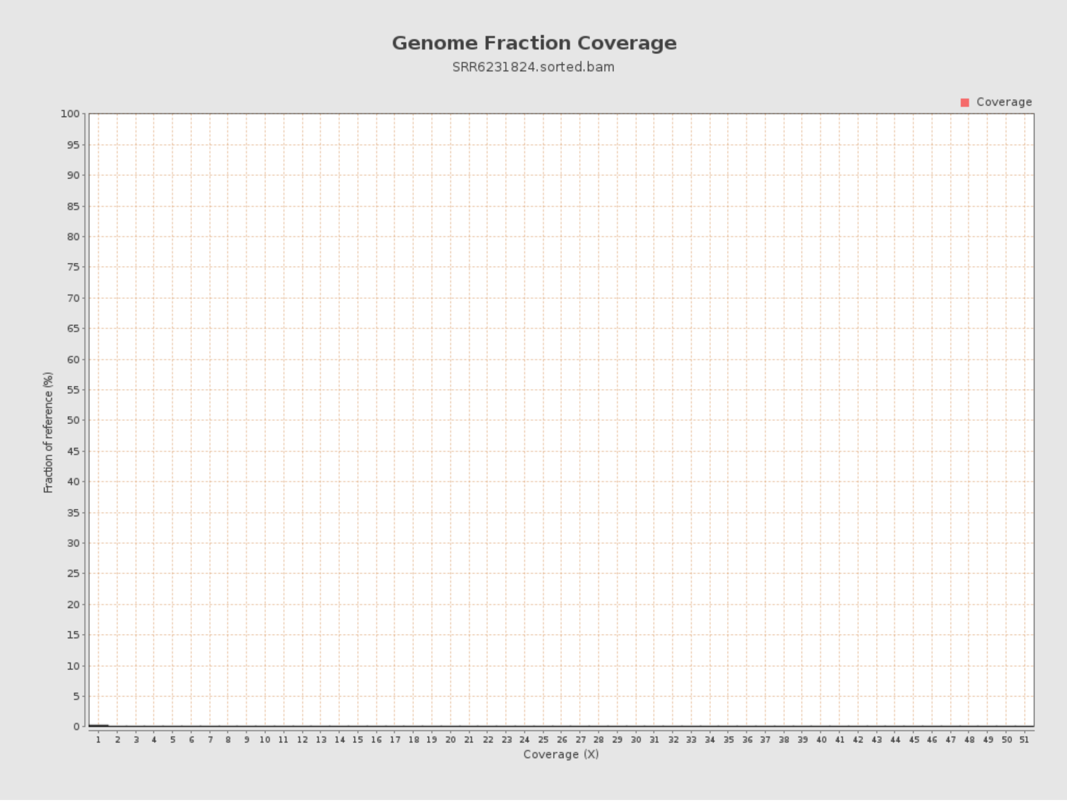
4. Results : Coverage Histogram



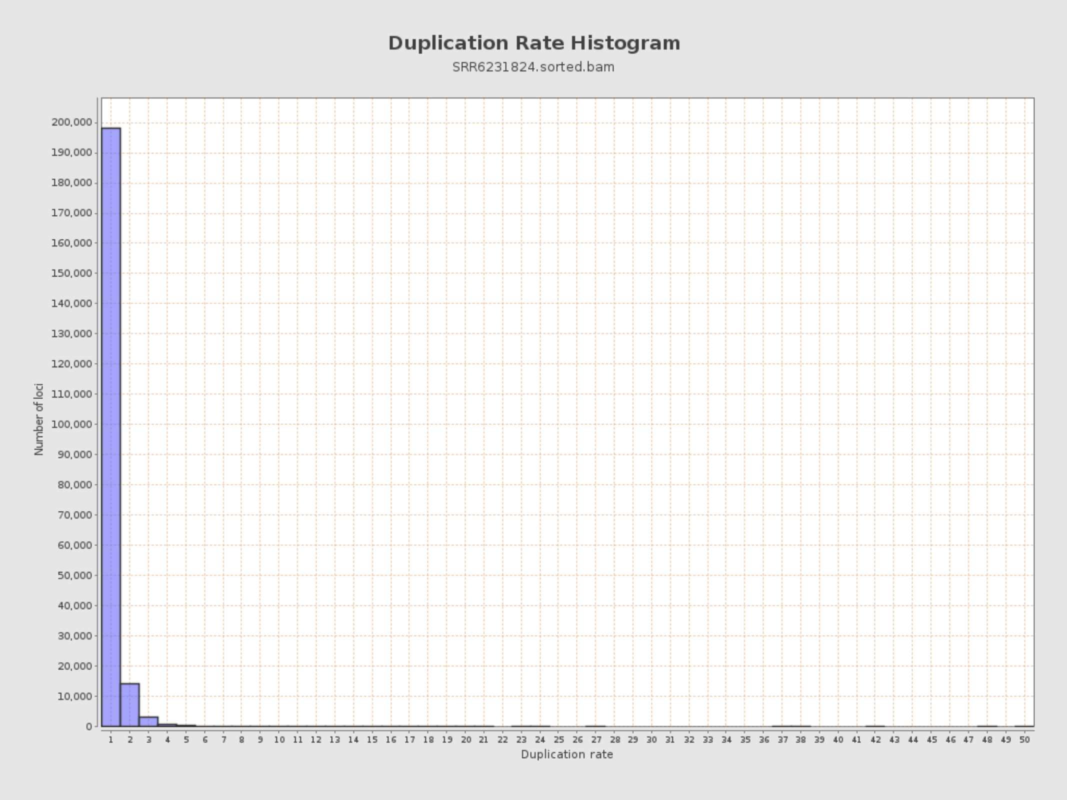
5. Results : Coverage Histogram (0-50X)



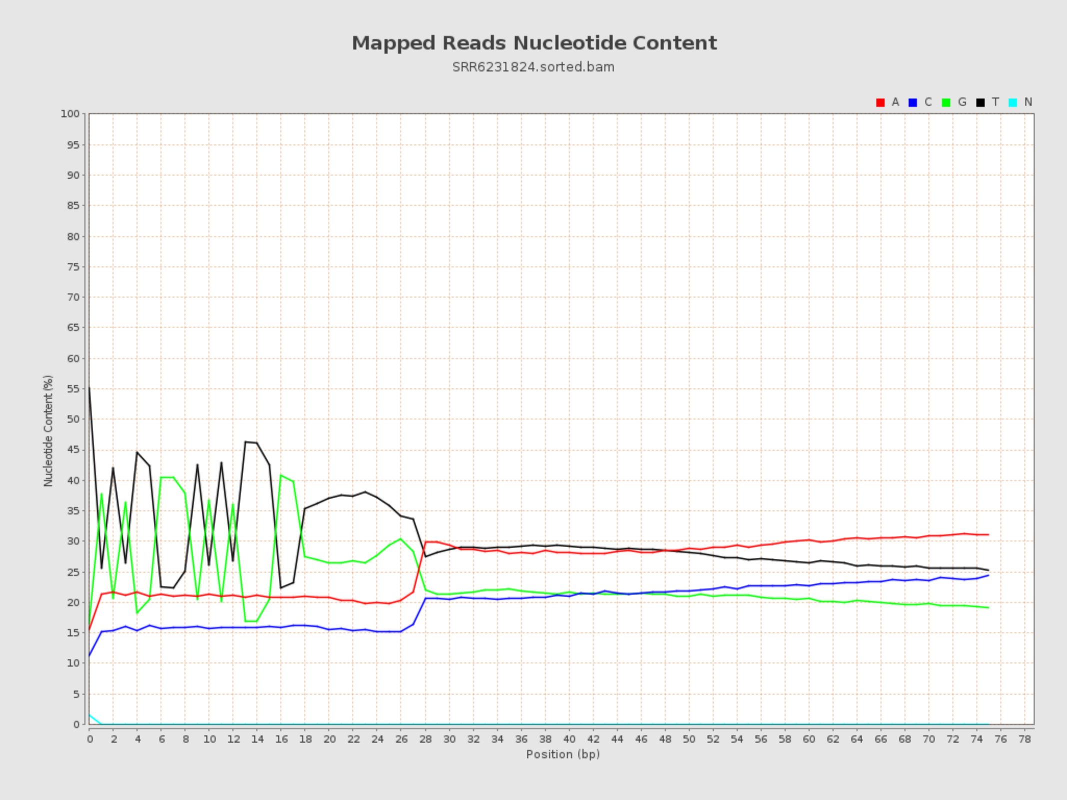
6. Results : Genome Fraction Coverage



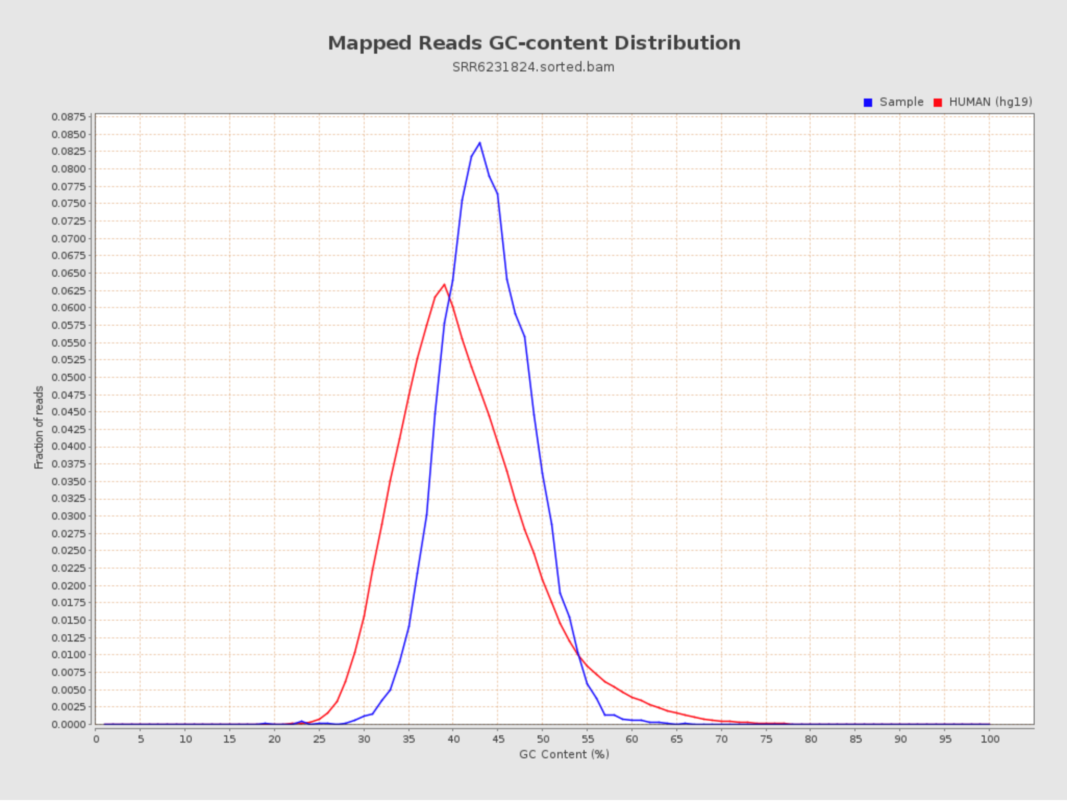
7. Results : Duplication Rate Histogram



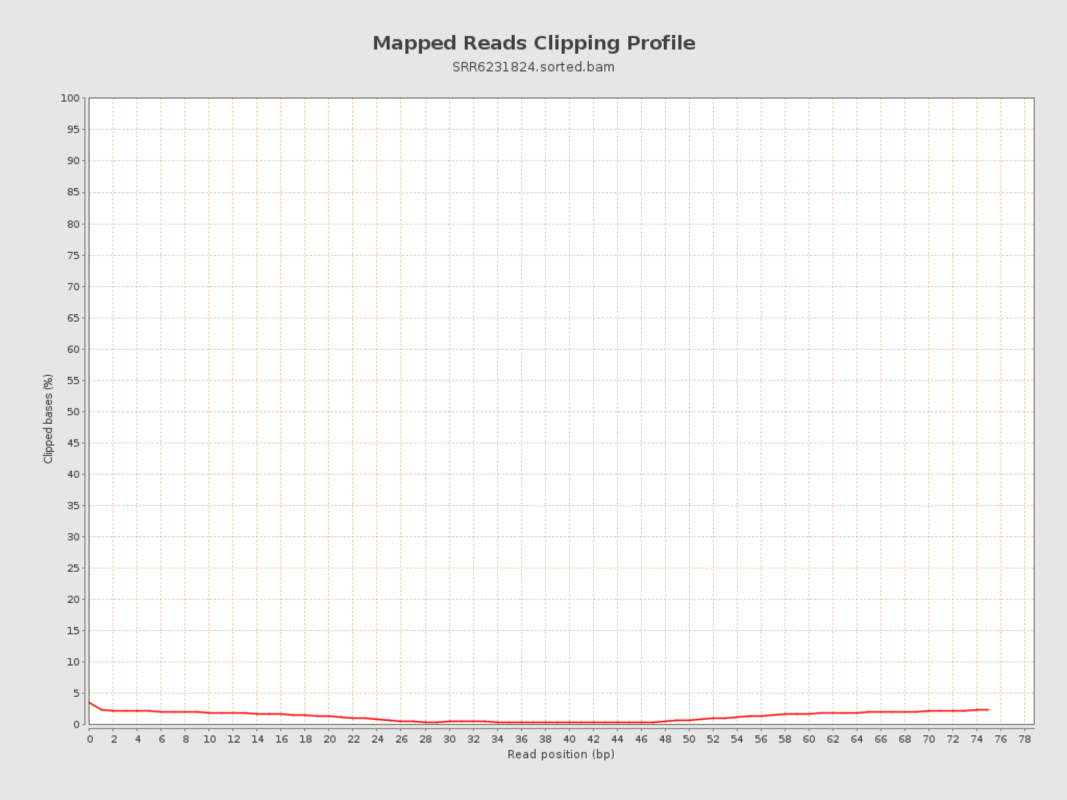
8. Results : Mapped Reads Nucleotide Content



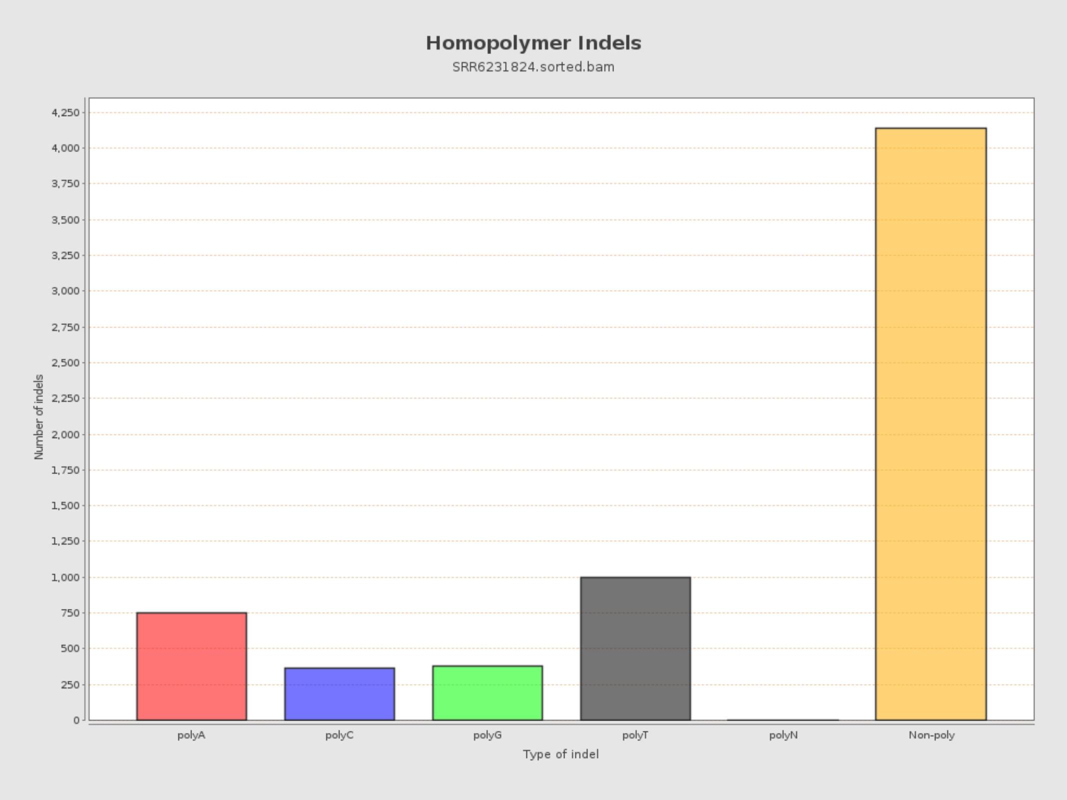
9. Results : Mapped Reads GC-content Distribution



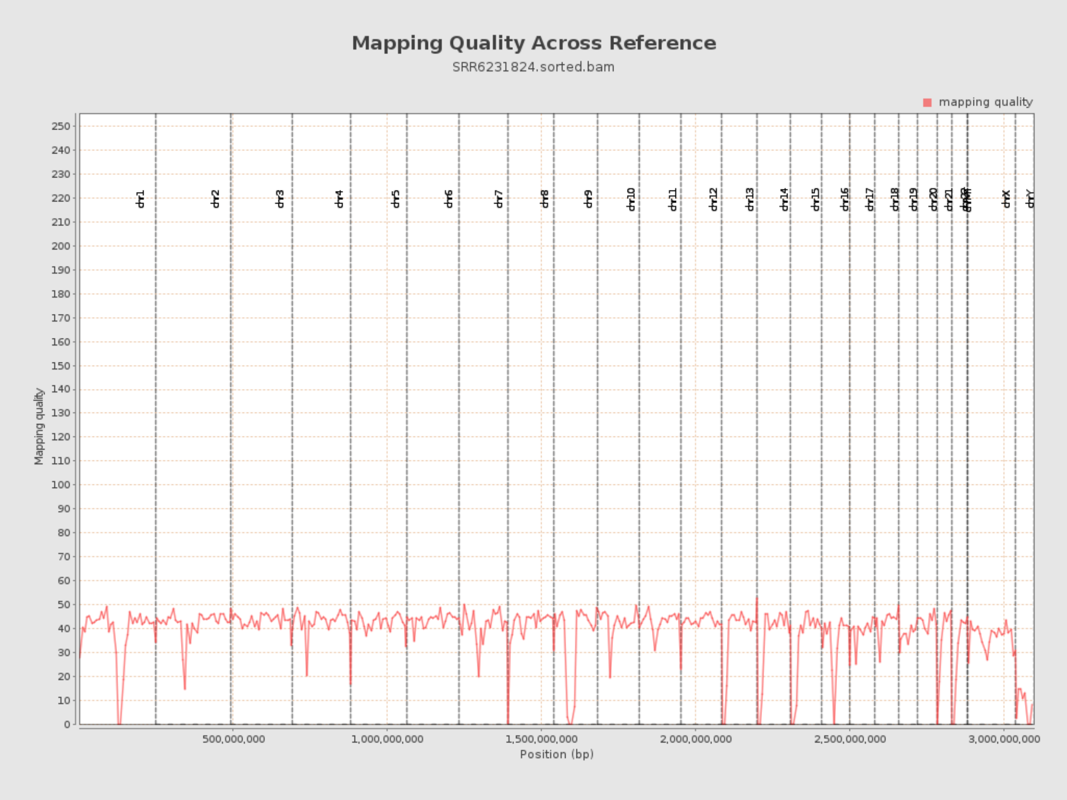
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram