Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 00:16:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231753.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_SRR6231753 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231753.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 00:16:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231753.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,862,224
Mapped reads	2,232,895 / 78.01%
Unmapped reads	629,329 / 21.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,371 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	926,320 / 32.36%
Duplication rate	14.99%
Clipped reads	737,866 / 25.78%

2.2. ACGT Content

Number/percentage of A's	32,443,315 / 21%
Number/percentage of C's	22,537,610 / 14.59%
Number/percentage of T's	35,015,897 / 22.67%
Number/percentage of G's	64,435,054 / 41.72%
Number/percentage of N's	29,499 / 0.02%
GC Percentage	56.31%

2.3. Coverage

Mean	0.0499

Standard Deviation	78.9643

2.4. Mapping Quality

Mean Mapping Quality	45.32

2.5. Mismatches and indels

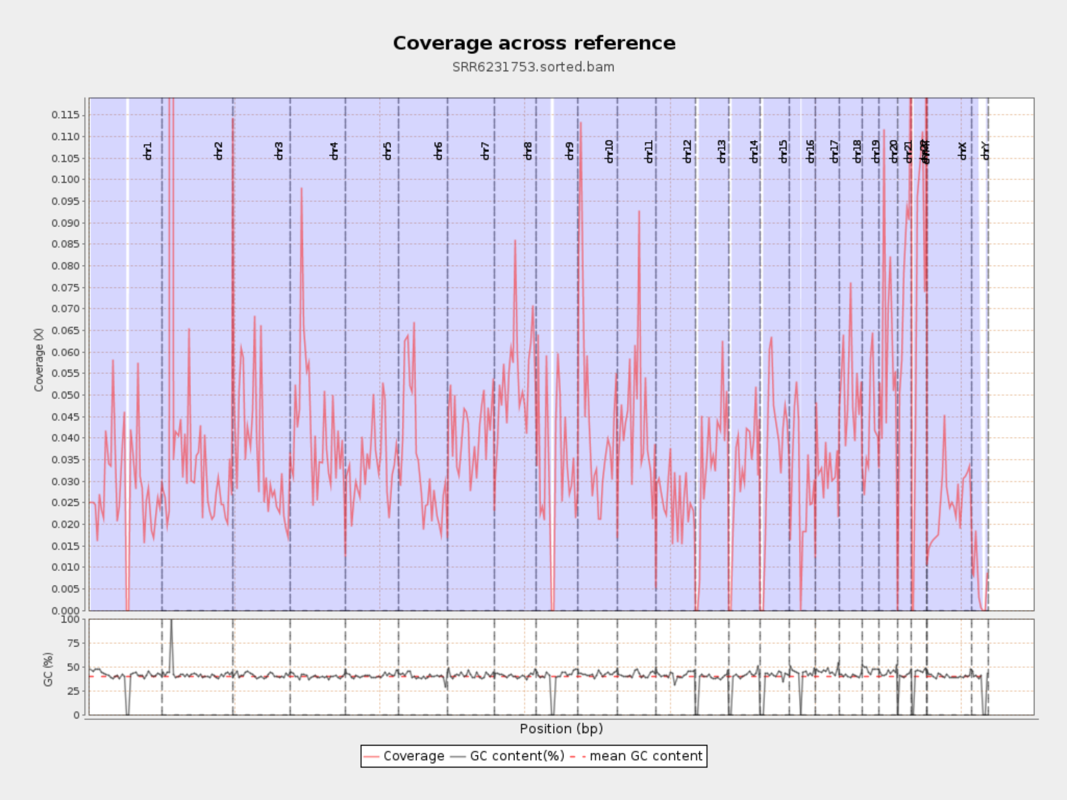
General error rate	0.58%
Mismatches	882,974
Insertions	9,541
Mapped reads with at least one insertion	0.42%
Deletions	26,688
Mapped reads with at least one deletion	1.18%
Homopolymer indels	46.62%

2.6. Chromosome stats

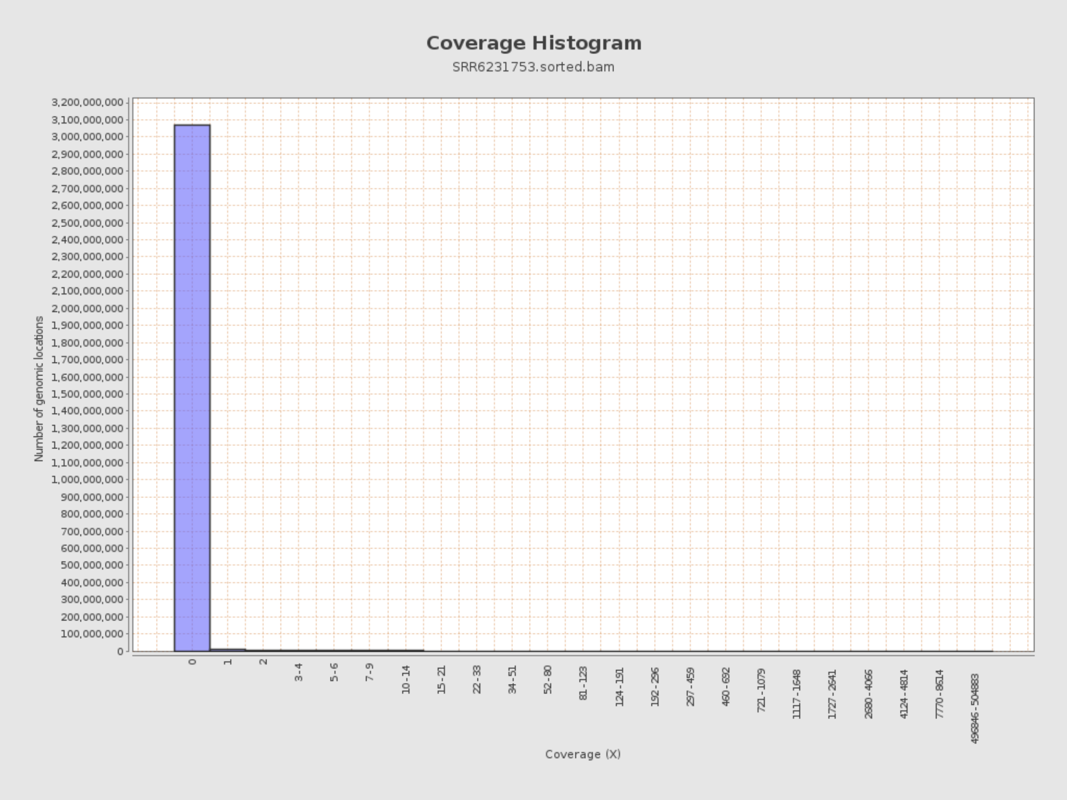
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7015115	0.0281	0.7018
chr2	243199373	46833812	0.1926	281.7159
chr3	198022430	7451271	0.0376	0.6588
chr4	191154276	8075960	0.0422	0.692
chr5	180915260	6158062	0.034	0.6088
chr6	171115067	5862589	0.0343	0.8734
chr7	159138663	6597574	0.0415	0.7115

chr8	146364022	7884780	0.0539	0.8306
chr9	141213431	4607270	0.0326	0.6127
chr10	135534747	6177177	0.0456	0.7018
chr11	135006516	5912447	0.0438	0.7707
chr12	133851895	3433618	0.0257	0.8477
chr13	115169878	3942477	0.0342	0.6375
chr14	107349540	3361649	0.0313	0.6357
chr15	102531392	3783749	0.0369	0.992
chr16	90354753	2654748	0.0294	0.5564
chr17	81195210	2715378	0.0334	0.6266
chr18	78077248	4032426	0.0516	0.9349
chr19	59128983	2489120	0.0421	0.7306
chr20	63025520	3920964	0.0622	0.8105
chr21	48129895	3581876	0.0744	0.9291
chr22	51304566	3447749	0.0672	0.8293
chrMT	16571	352808	21.2907	20.6893
chrX	155270560	3866898	0.0249	0.5486
chrY	59373566	346383	0.0058	0.2215

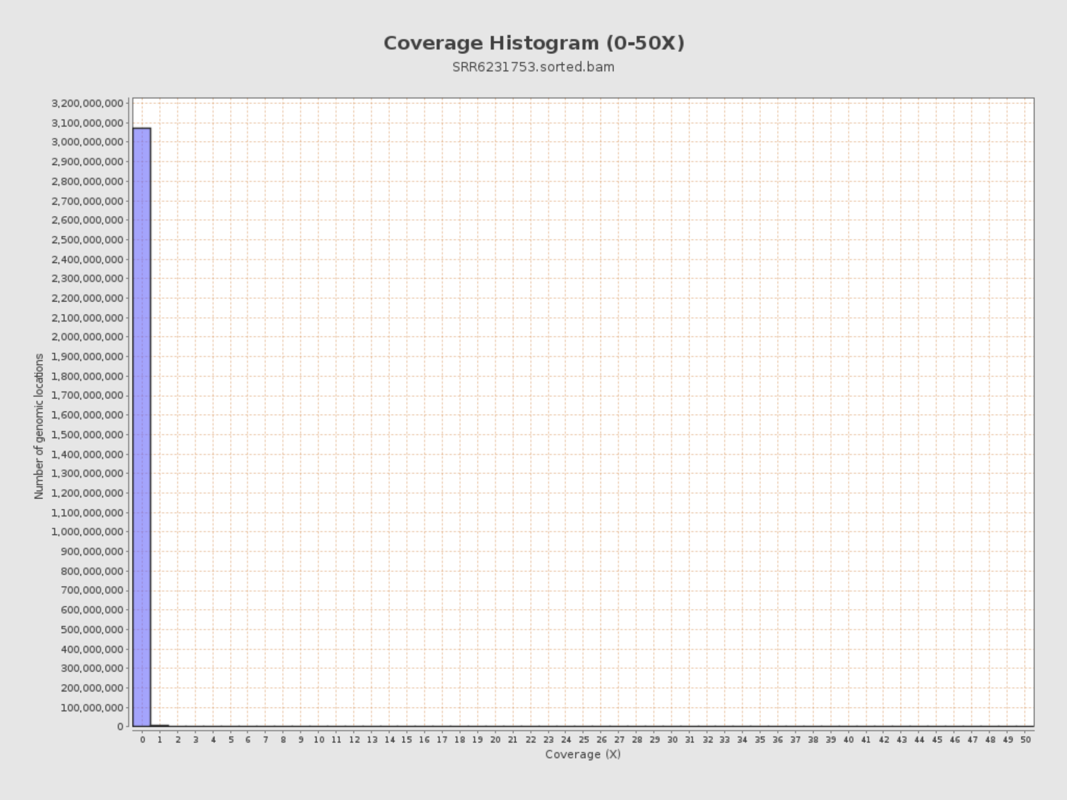
3. Results : Coverage across reference



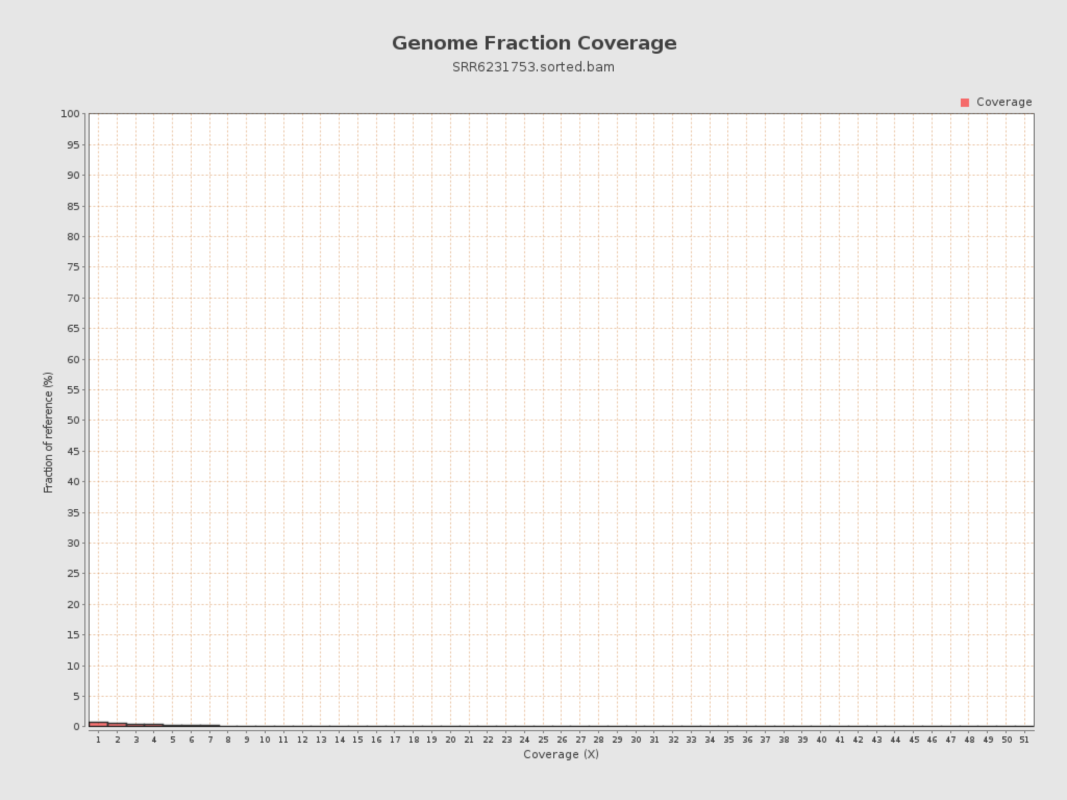
4. Results : Coverage Histogram



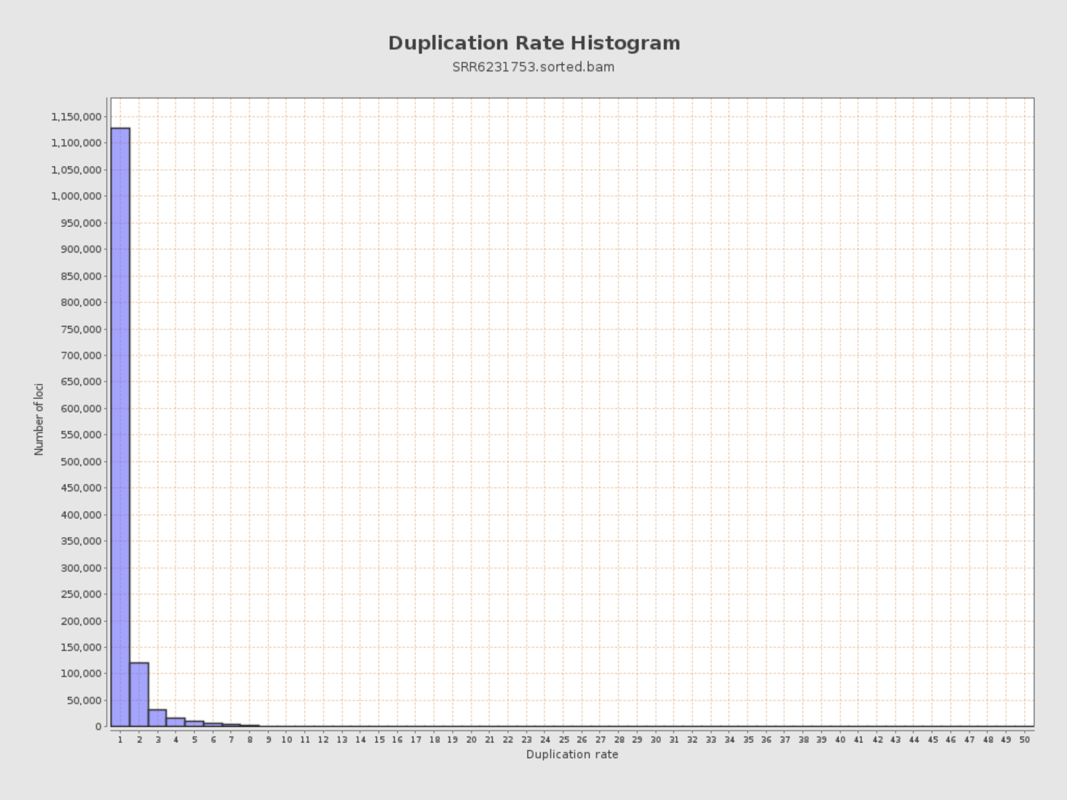
5. Results : Coverage Histogram (0-50X)



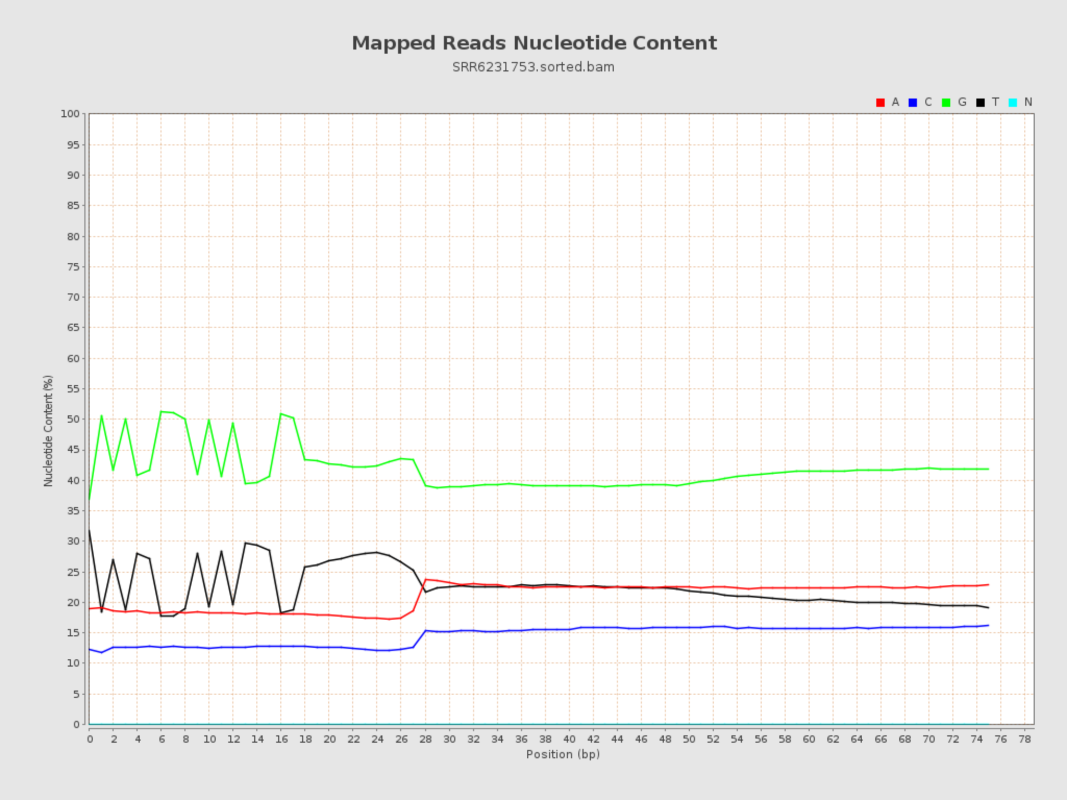
6. Results : Genome Fraction Coverage



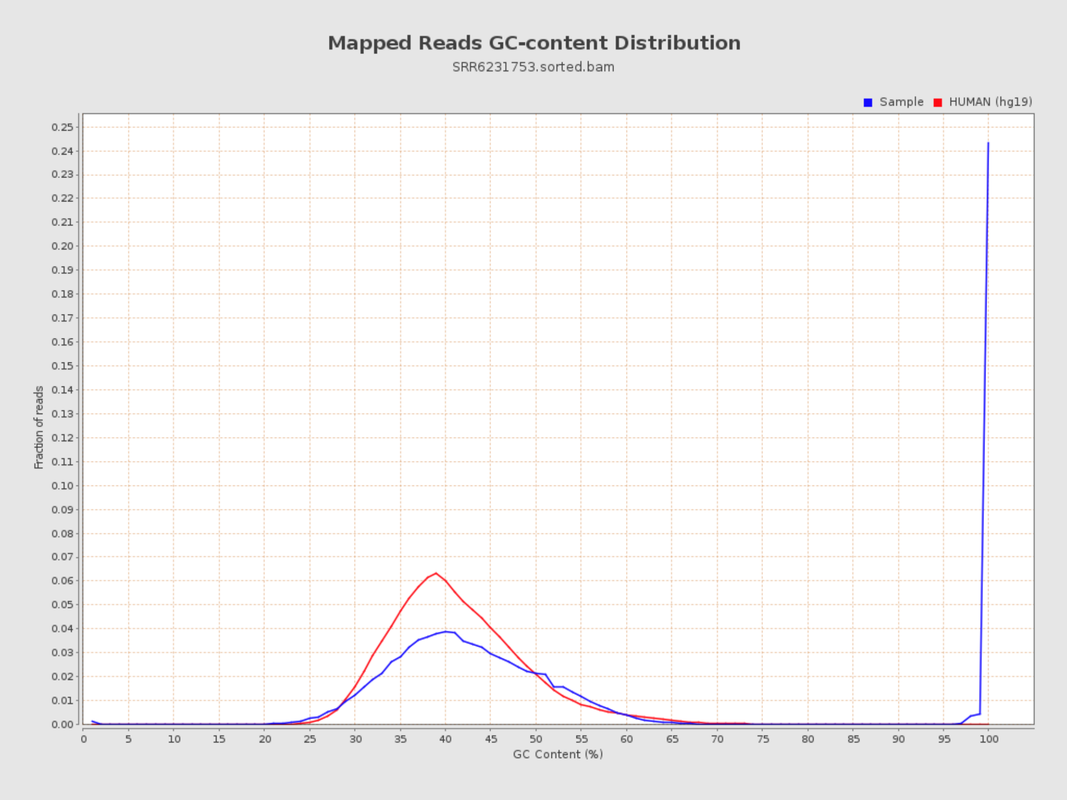
7. Results : Duplication Rate Histogram



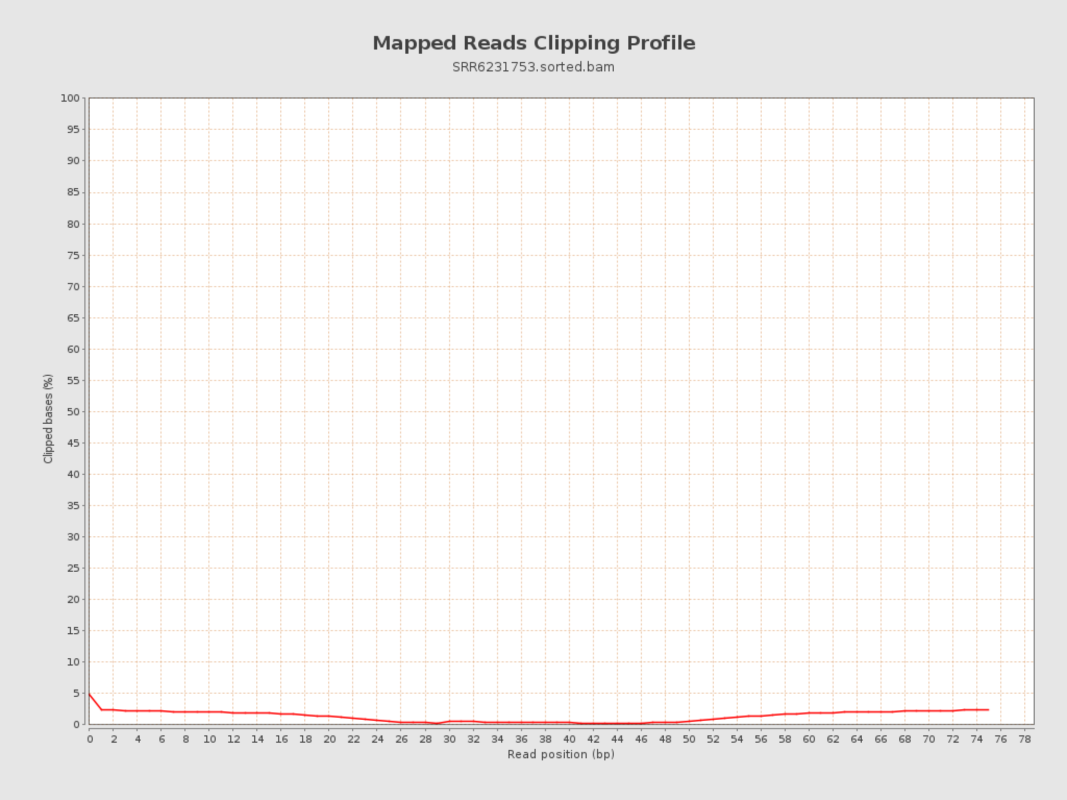
8. Results : Mapped Reads Nucleotide Content



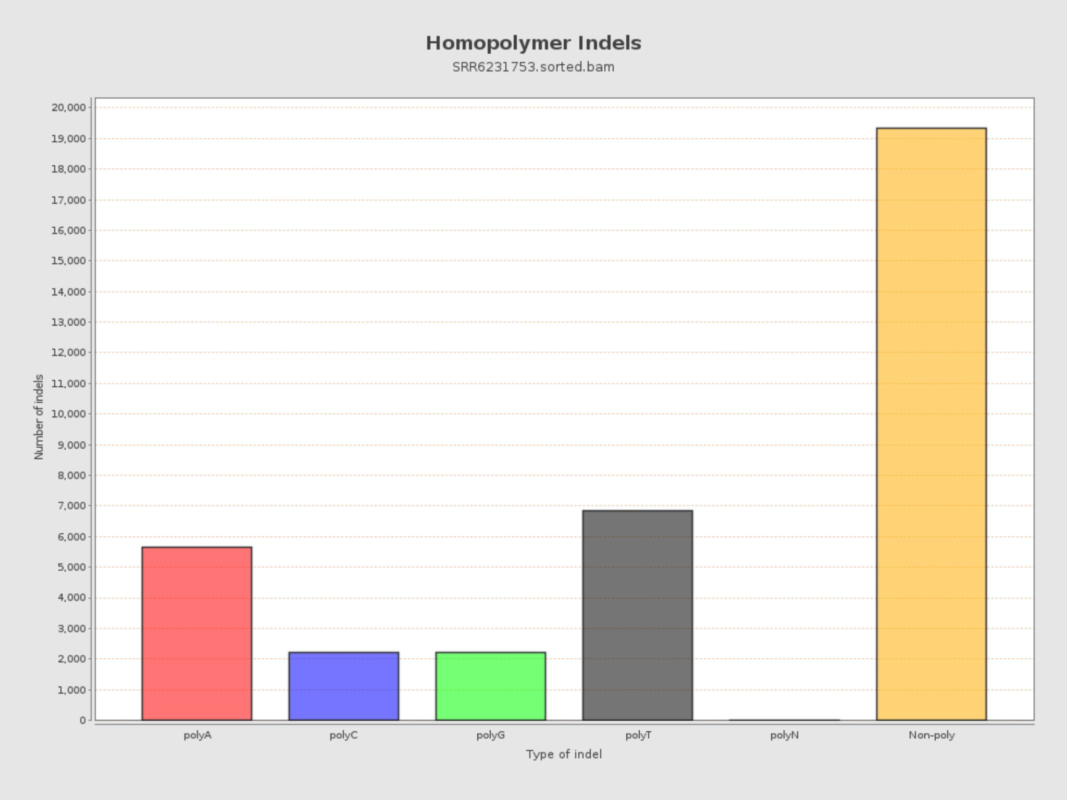
9. Results : Mapped Reads GC-content Distribution



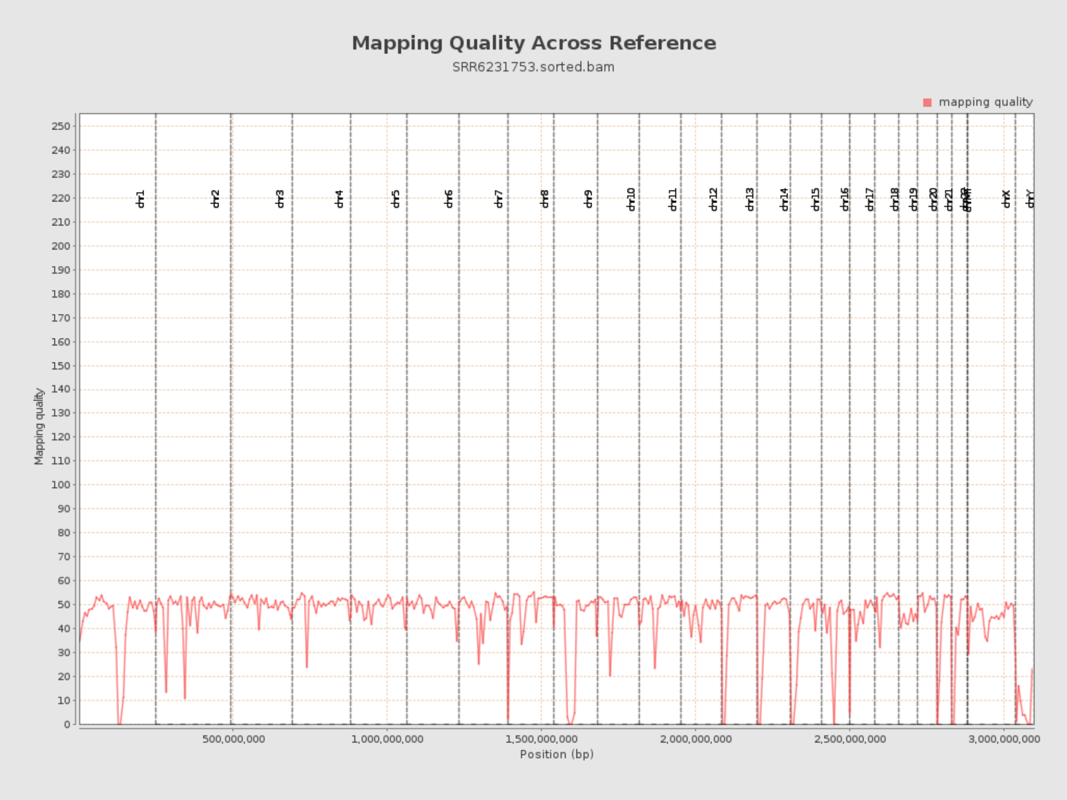
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram