Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:04:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231762.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_SRR6231762 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231762.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:04:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231762.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,781,333
Mapped reads	2,487,939 / 89.45%
Unmapped reads	293,394 / 10.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,003 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	145,756 / 5.24%
Duplication rate	2.35%
Clipped reads	1,213,910 / 43.64%

2.2. ACGT Content

Number/percentage of A's	45,318,333 / 27.69%
Number/percentage of C's	32,461,845 / 19.83%
Number/percentage of T's	45,787,798 / 27.97%
Number/percentage of G's	40,109,406 / 24.5%
Number/percentage of N's	11,884 / 0.01%
GC Percentage	44.33%

2.3. Coverage

Mean	0.0529

Standard Deviation	7.3507

2.4. Mapping Quality

Mean Mapping Quality	41.02

2.5. Mismatches and indels

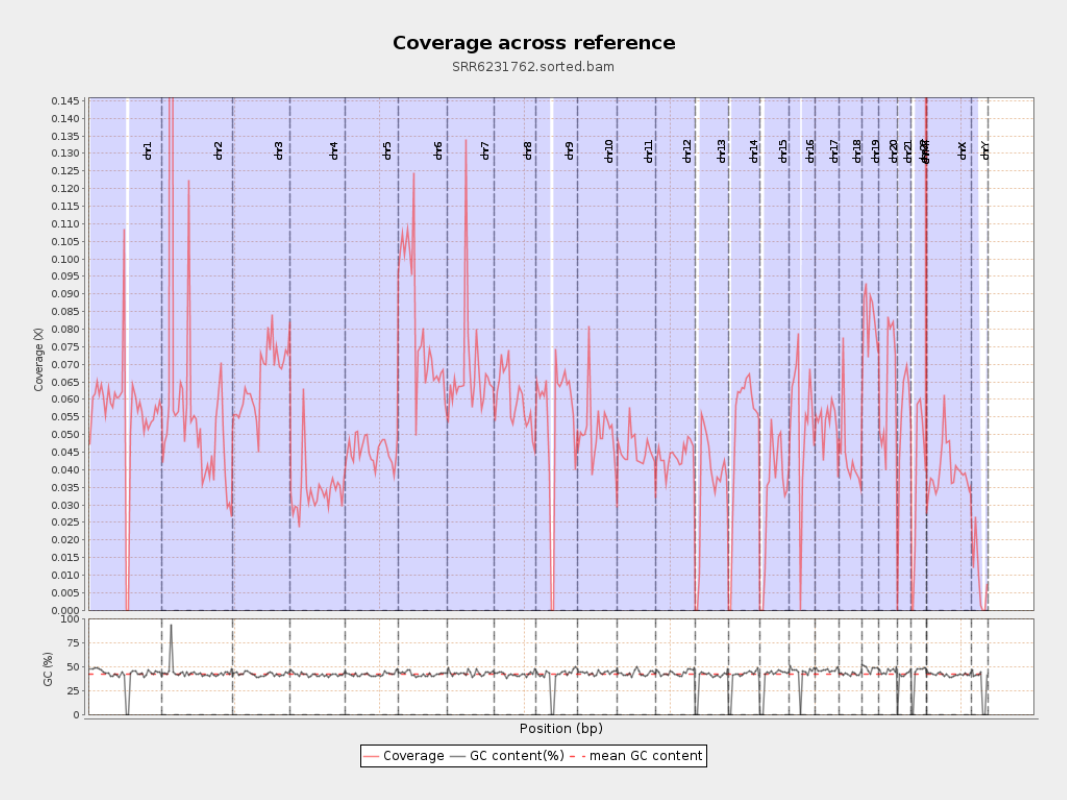
General error rate	0.69%
Mismatches	1,108,866
Insertions	13,562
Mapped reads with at least one insertion	0.54%
Deletions	37,949
Mapped reads with at least one deletion	1.51%
Homopolymer indels	44.6%

2.6. Chromosome stats

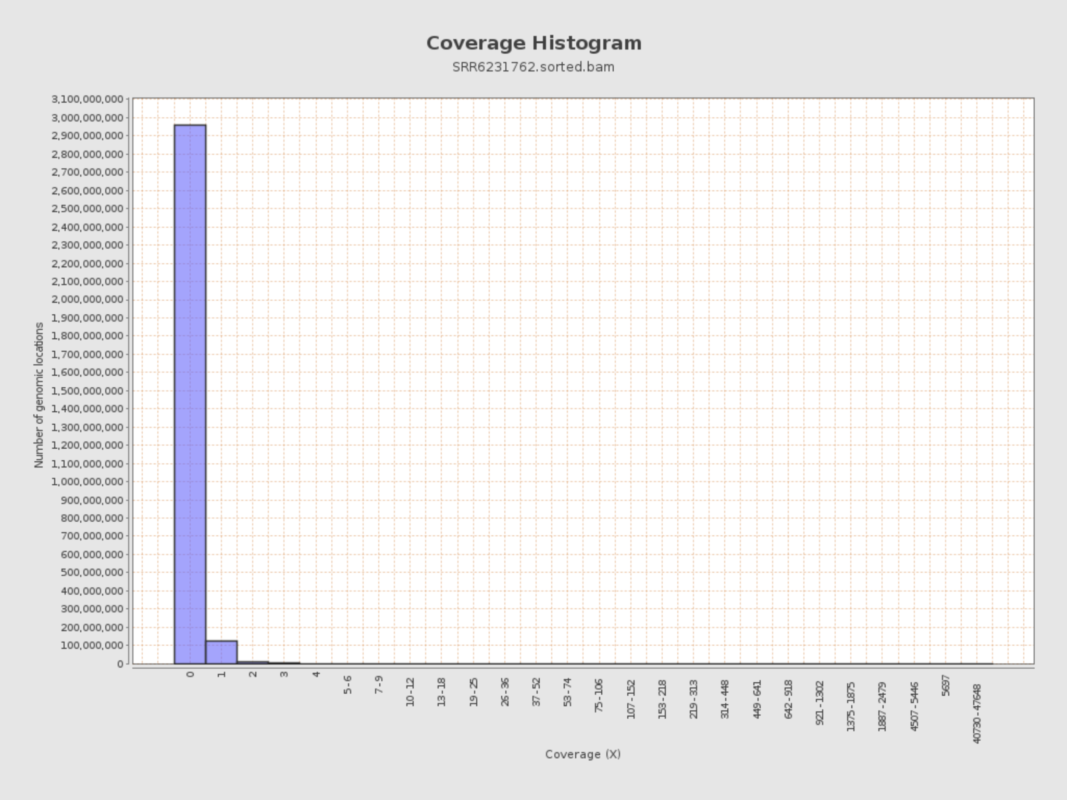
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13993290	0.0561	1.1508
chr2	243199373	16450327	0.0676	26.1498
chr3	198022430	12960921	0.0655	0.288
chr4	191154276	6467835	0.0338	0.2408
chr5	180915260	8208180	0.0454	0.2465
chr6	171115067	13785223	0.0806	0.4786
chr7	159138663	10832746	0.0681	1.0482

chr8	146364022	8688838	0.0594	0.6773
chr9	141213431	7648872	0.0542	0.5319
chr10	135534747	6909071	0.051	0.4414
chr11	135006516	6072353	0.045	0.4865
chr12	133851895	5865107	0.0438	0.2484
chr13	115169878	4096844	0.0356	0.2097
chr14	107349540	5482204	0.0511	0.3944
chr15	102531392	3412334	0.0333	0.218
chr16	90354753	4905513	0.0543	0.3341
chr17	81195210	4324481	0.0533	0.3017
chr18	78077248	3468679	0.0444	1.1313
chr19	59128983	4886868	0.0826	0.7666
chr20	63025520	3965583	0.0629	0.3095
chr21	48129895	2564933	0.0533	0.2982
chr22	51304566	1904087	0.0371	0.2153
chrMT	16571	165412	9.982	7.7576
chrX	155270560	6155747	0.0396	0.2917
chrY	59373566	537611	0.0091	0.1643

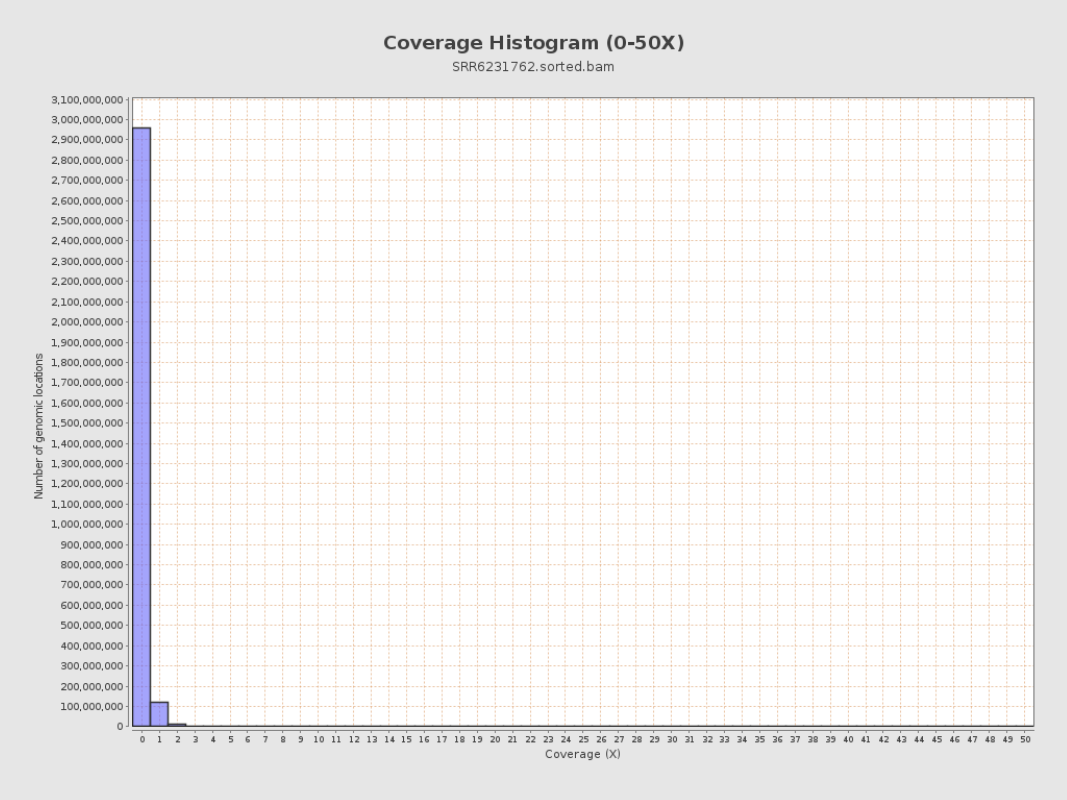
3. Results : Coverage across reference



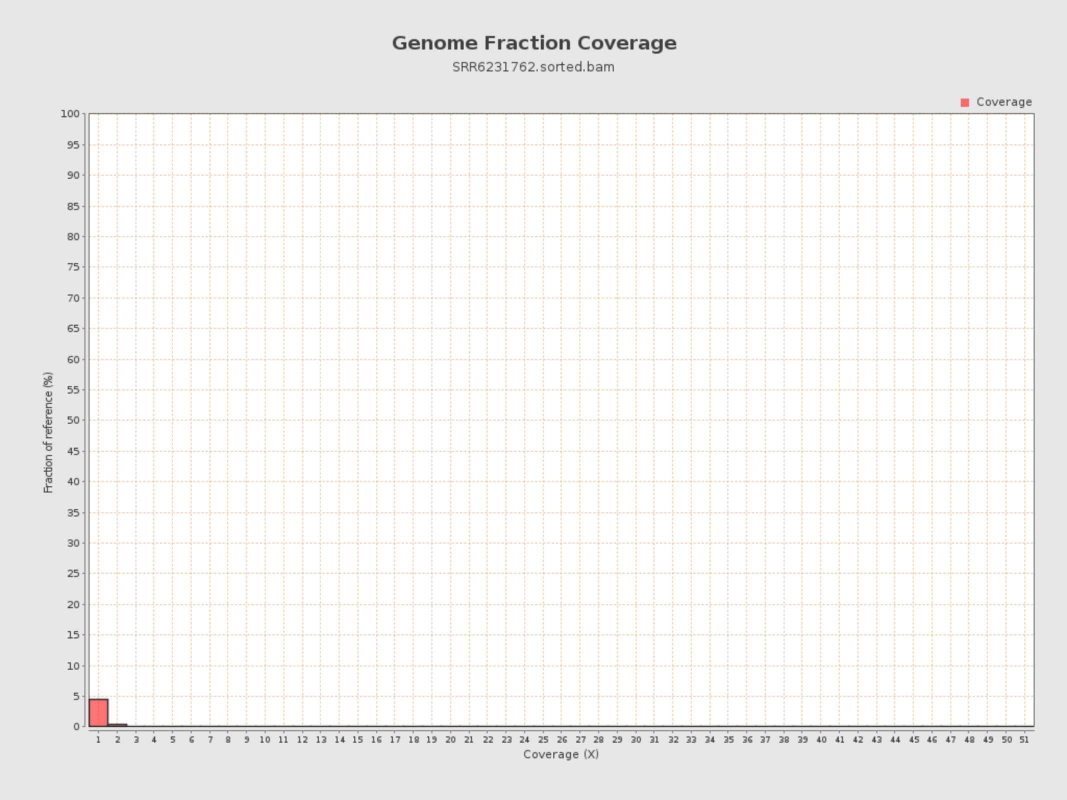
4. Results : Coverage Histogram



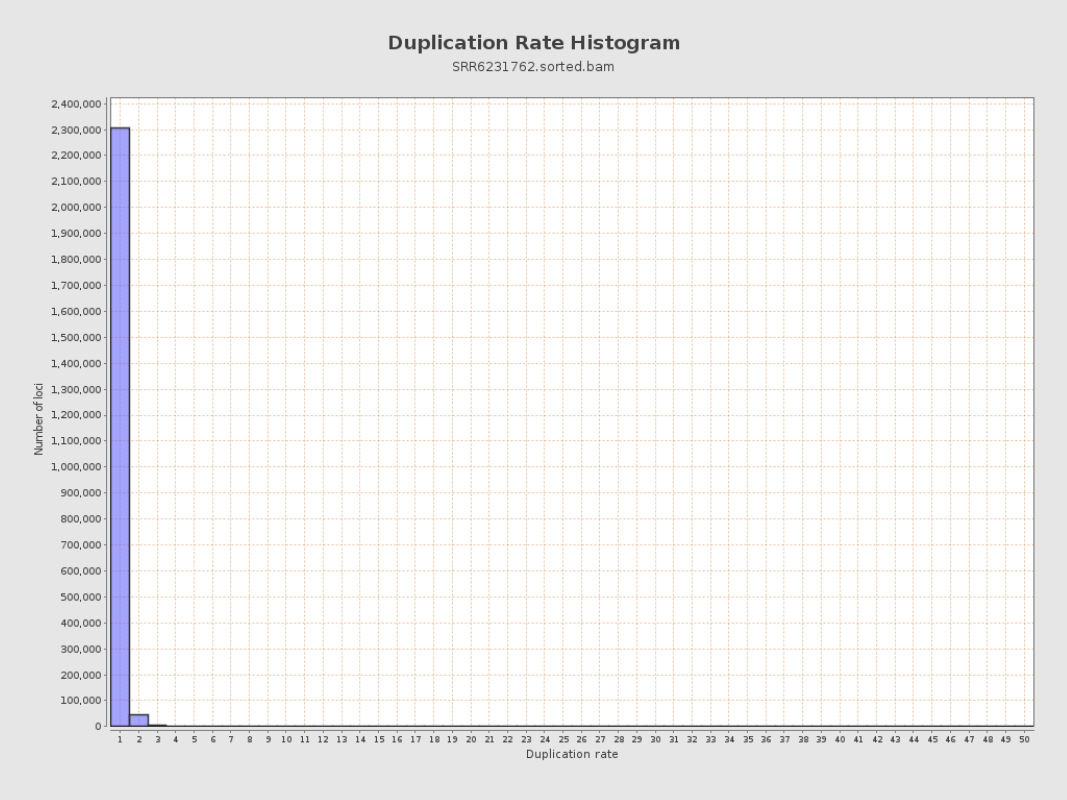
5. Results : Coverage Histogram (0-50X)



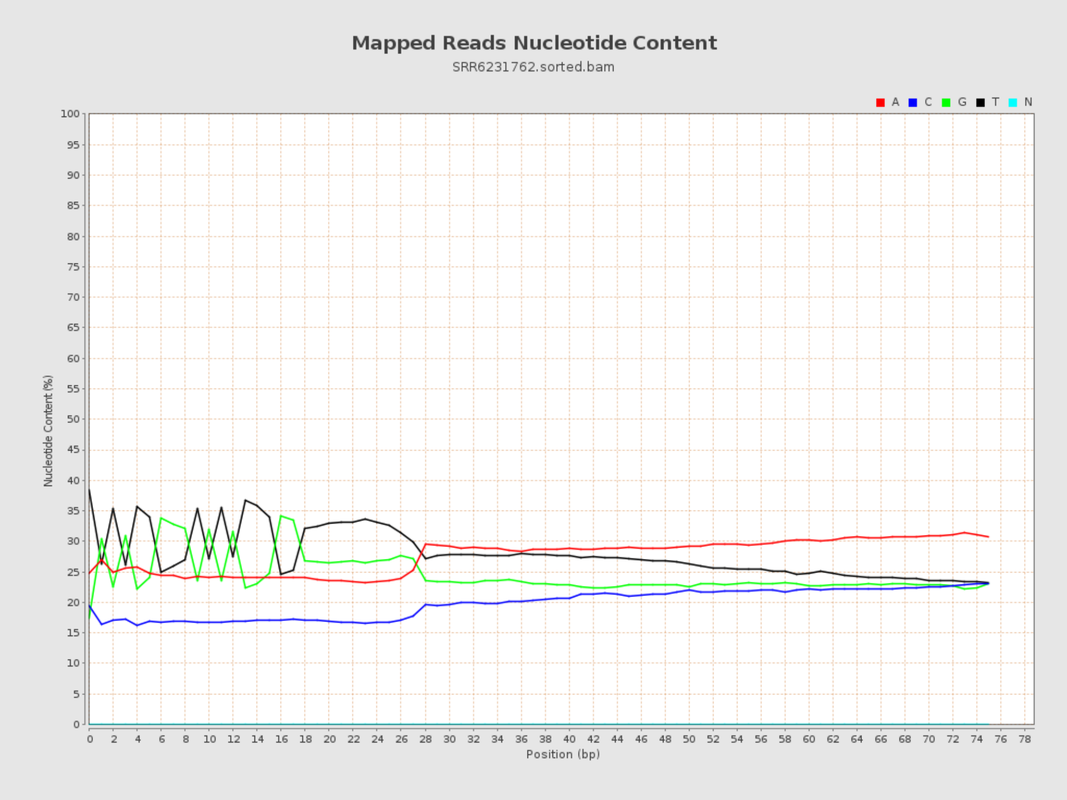
6. Results : Genome Fraction Coverage



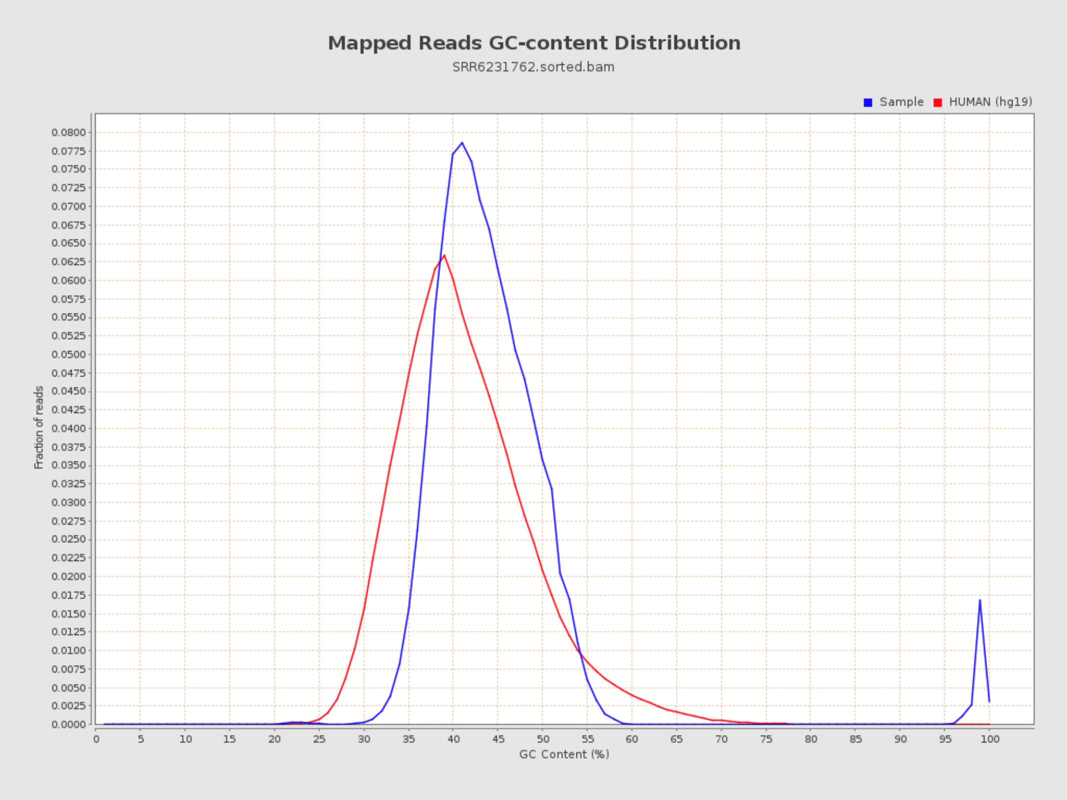
7. Results : Duplication Rate Histogram



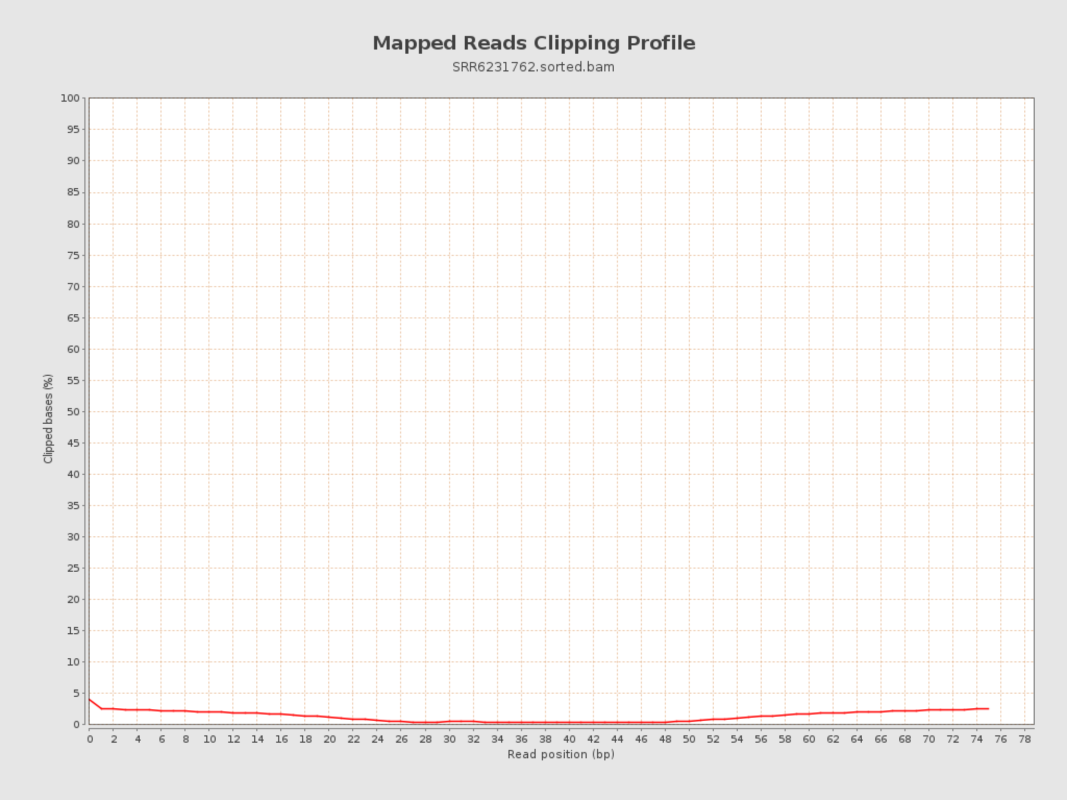
8. Results : Mapped Reads Nucleotide Content



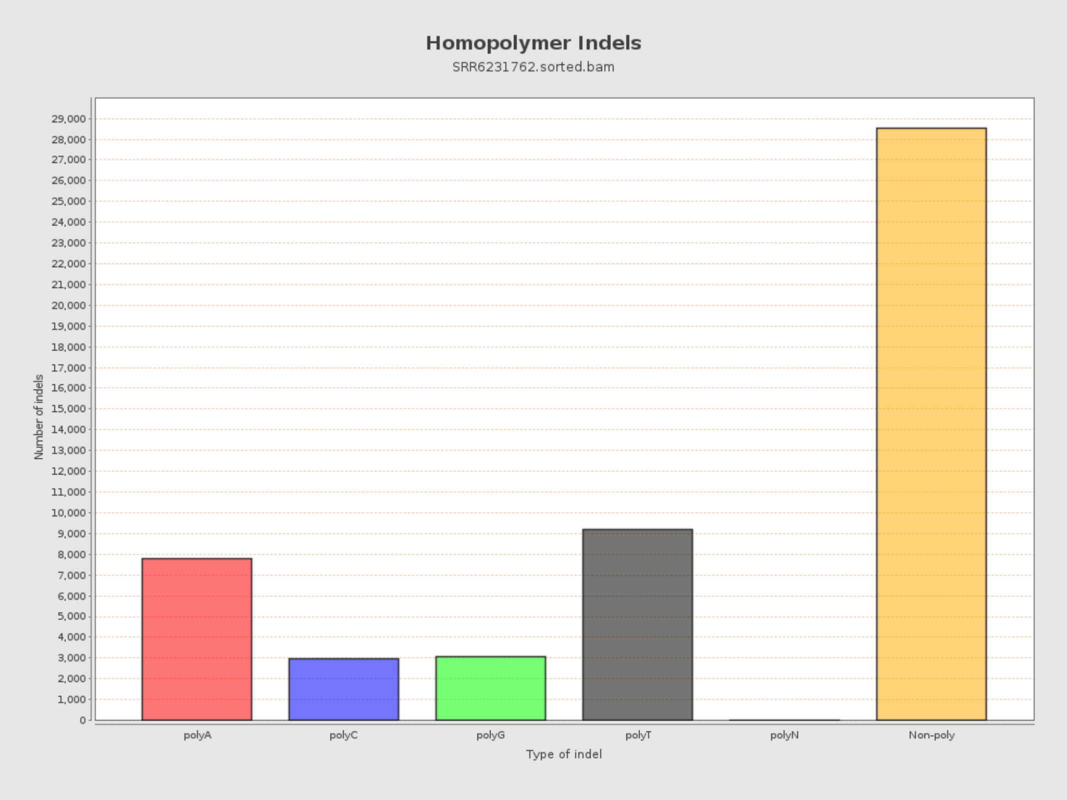
9. Results : Mapped Reads GC-content Distribution



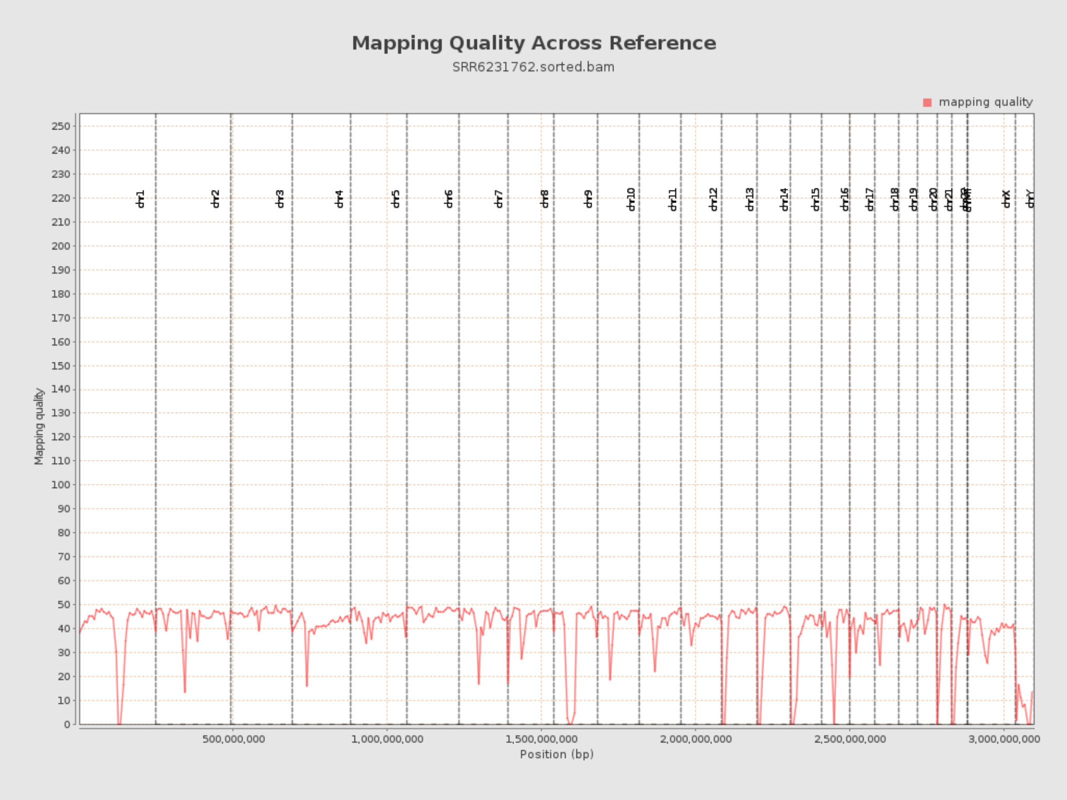
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram