Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 02:06:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231781.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_SRR6231781 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231781.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 02:06:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231781.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,013,254
Mapped reads	11,778,248 / 90.51%
Unmapped reads	1,235,006 / 9.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	99,180 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,130,105 / 8.68%
Duplication rate	6.3%
Clipped reads	5,085,683 / 39.08%

2.2. ACGT Content

Number/percentage of A's	227,260,180 / 28.82%
Number/percentage of C's	151,227,537 / 19.18%
Number/percentage of T's	236,125,584 / 29.94%
Number/percentage of G's	173,922,694 / 22.05%
Number/percentage of N's	59,993 / 0.01%
GC Percentage	41.23%

2.3. Coverage

Mean	0.2548

Standard Deviation	14.9642

2.4. Mapping Quality

Mean Mapping Quality	46.01

2.5. Mismatches and indels

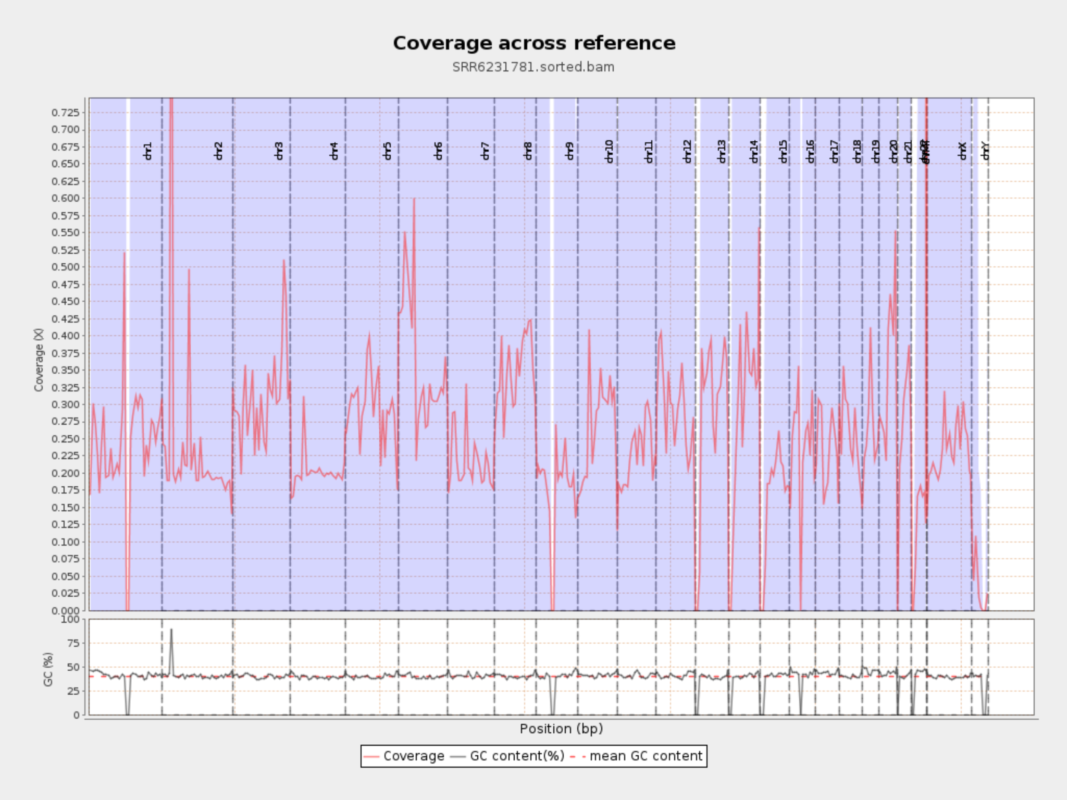
General error rate	0.61%
Mismatches	4,693,295
Insertions	56,510
Mapped reads with at least one insertion	0.47%
Deletions	184,061
Mapped reads with at least one deletion	1.55%
Homopolymer indels	46.4%

2.6. Chromosome stats

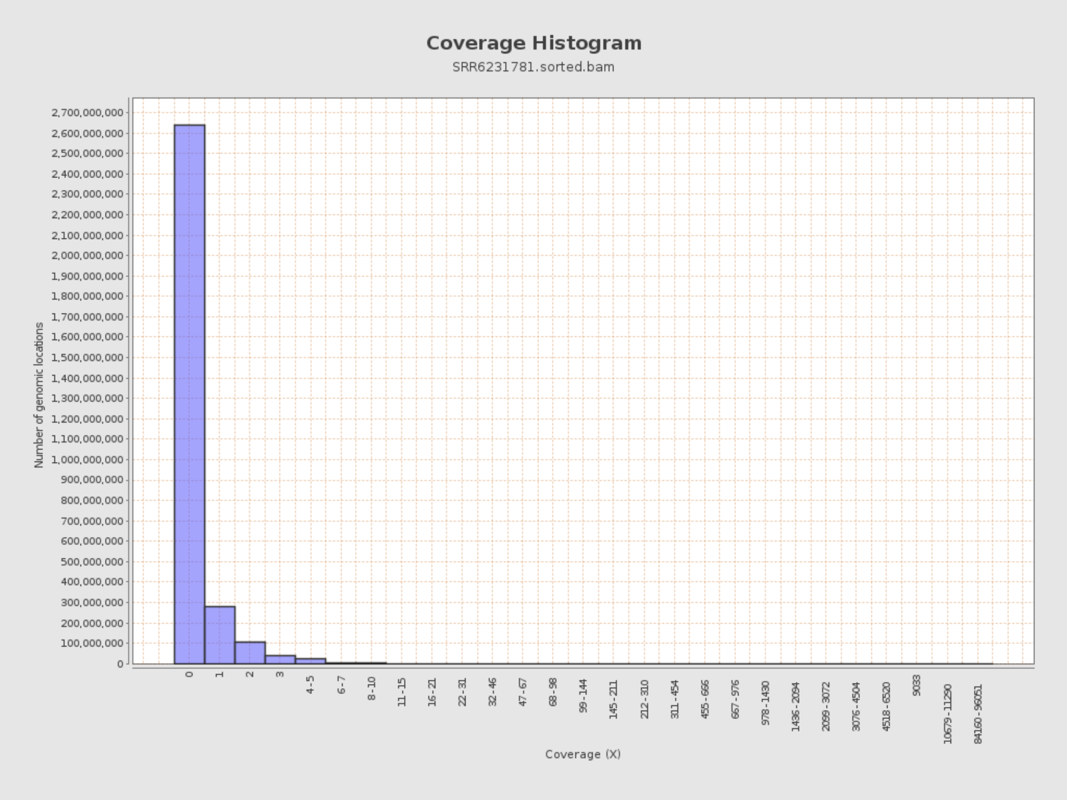
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	60078270	0.241	5.6786
chr2	243199373	59265661	0.2437	52.8116
chr3	198022430	61820339	0.3122	0.8516
chr4	191154276	38429291	0.201	0.8559
chr5	180915260	53437293	0.2954	0.8467
chr6	171115067	62384314	0.3646	1.8653
chr7	159138663	34574271	0.2173	1.8173

chr8	146364022	51366503	0.351	3.2346
chr9	141213431	24672402	0.1747	1.6377
chr10	135534747	36679174	0.2706	2.0437
chr11	135006516	30379410	0.225	1.3422
chr12	133851895	39369868	0.2941	0.8731
chr13	115169878	32609918	0.2831	0.7992
chr14	107349540	29866324	0.2782	1.0712
chr15	102531392	16777229	0.1636	0.6235
chr16	90354753	21510354	0.2381	1.0913
chr17	81195210	18853204	0.2322	1.0124
chr18	78077248	20339896	0.2605	3.4567
chr19	59128983	15811651	0.2674	3.5572
chr20	63025520	22399882	0.3554	1.0176
chr21	48129895	12871420	0.2674	0.9321
chr22	51304566	6051982	0.118	0.4985
chrMT	16571	1151896	69.5128	33.1483
chrX	155270560	36304586	0.2338	0.98
chrY	59373566	1909544	0.0322	0.7165

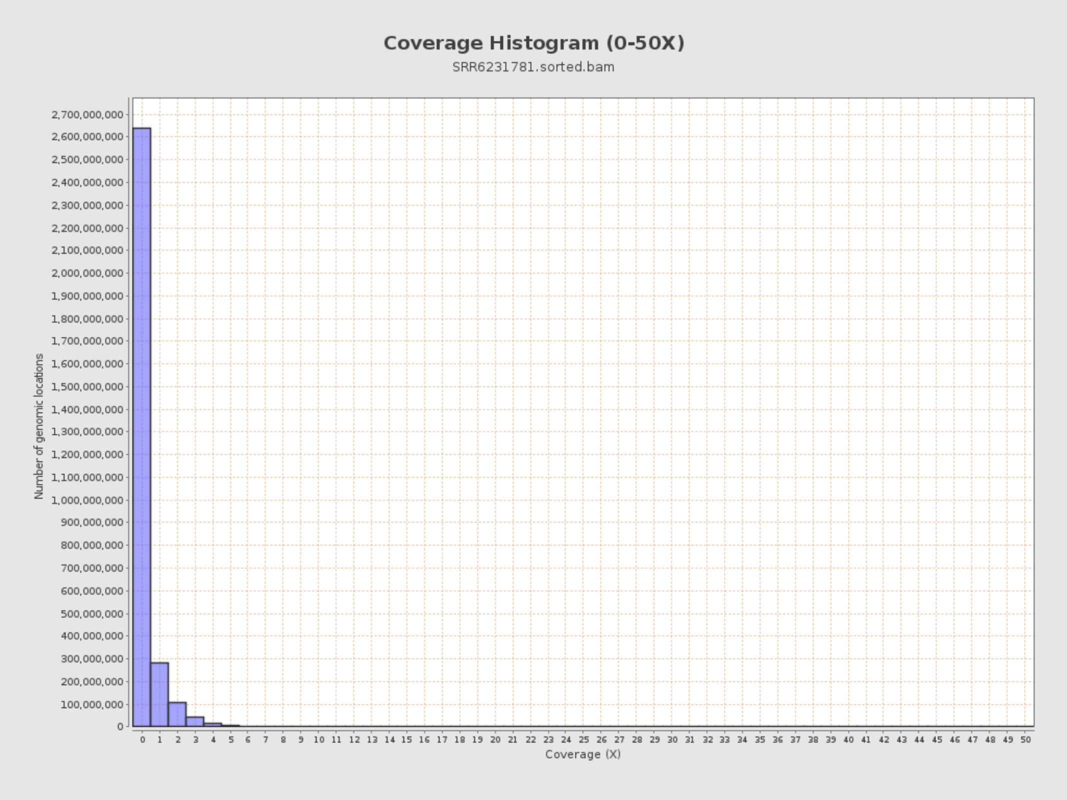
3. Results : Coverage across reference



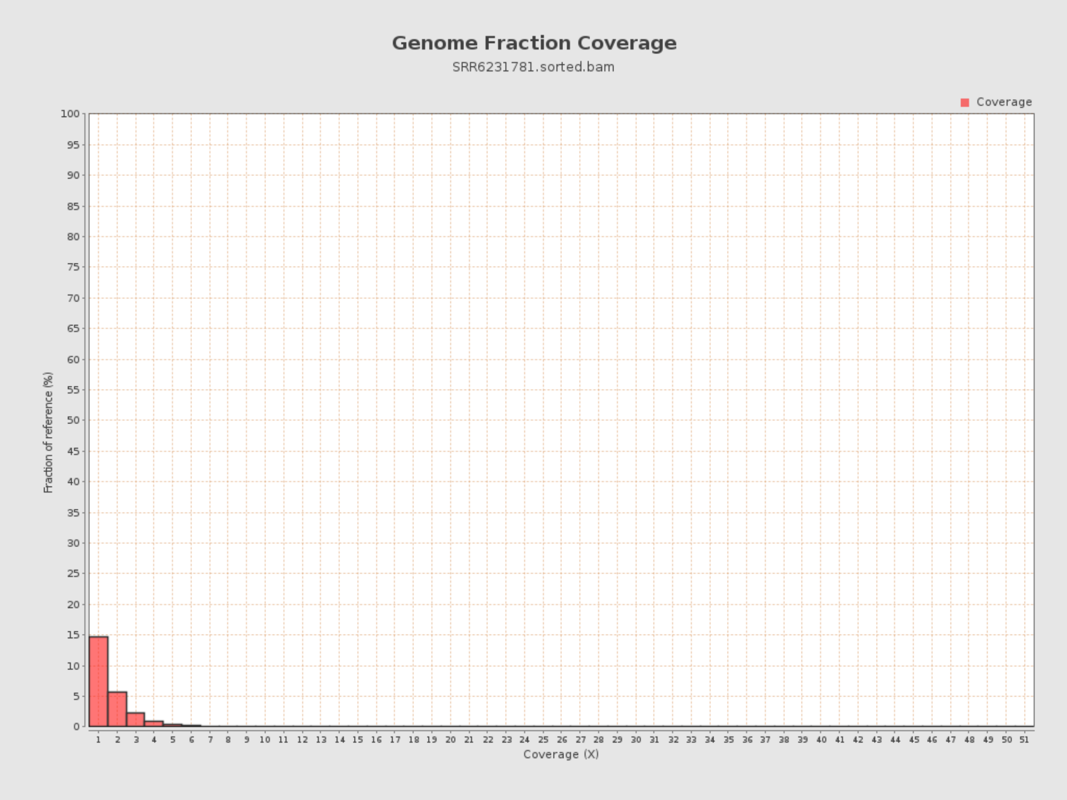
4. Results : Coverage Histogram



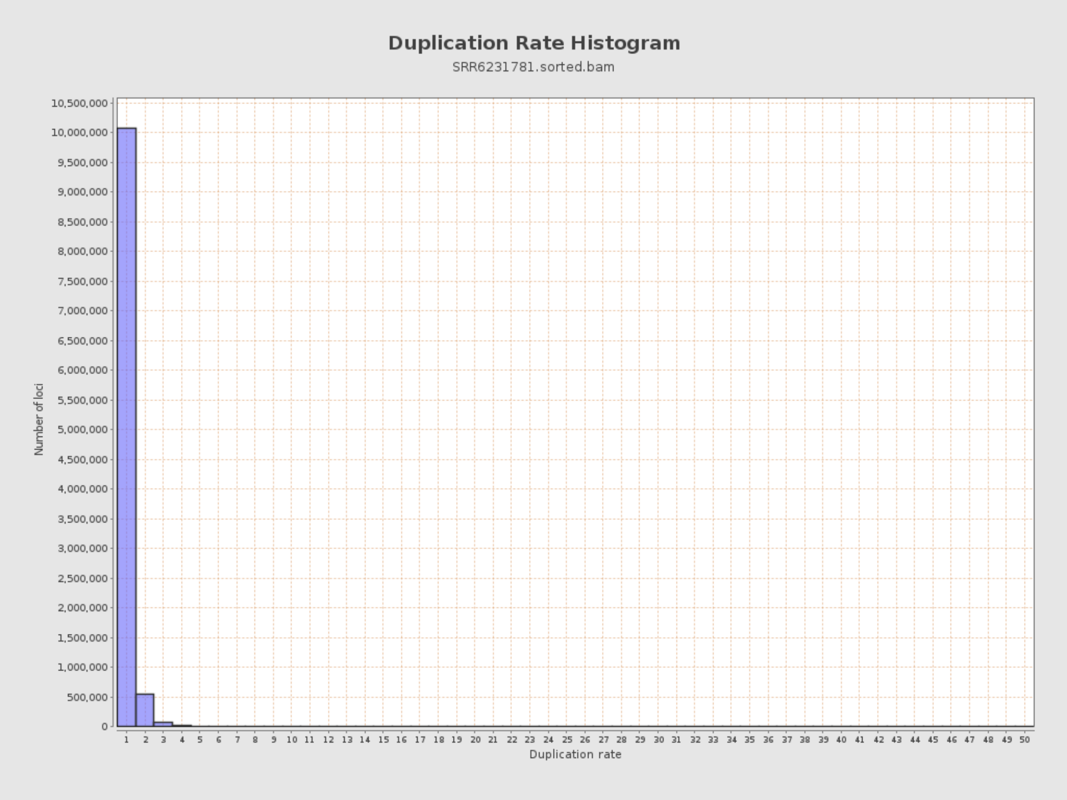
5. Results : Coverage Histogram (0-50X)



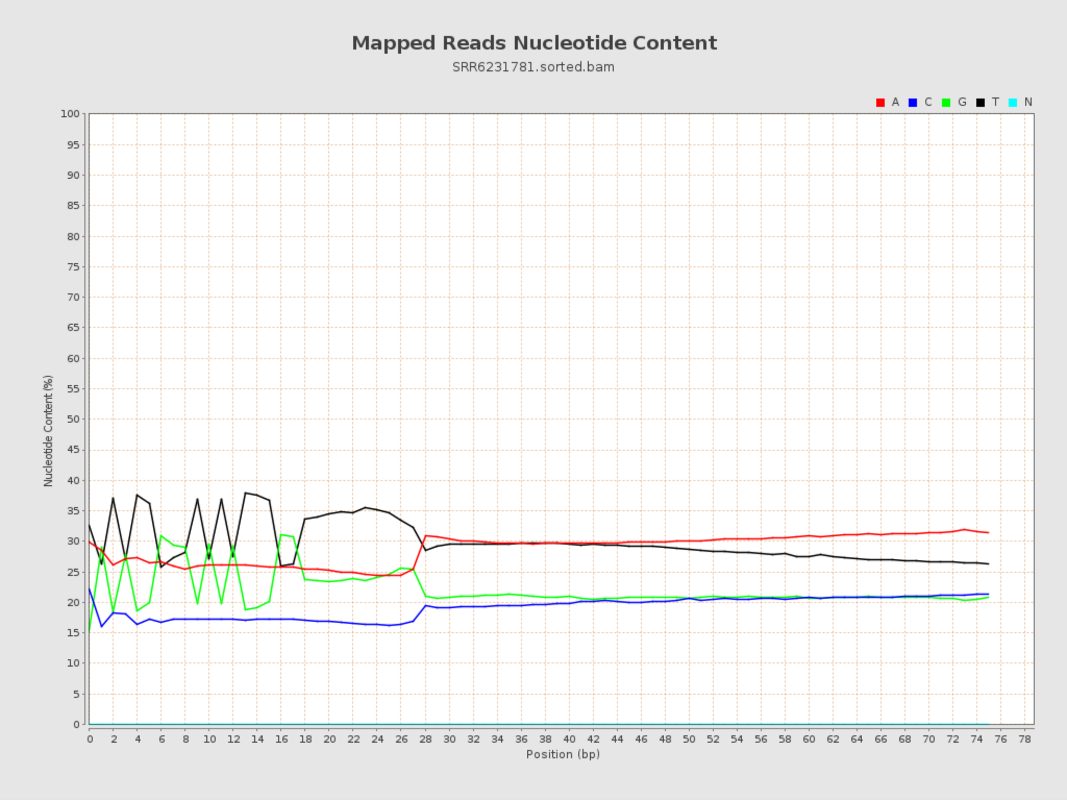
6. Results : Genome Fraction Coverage



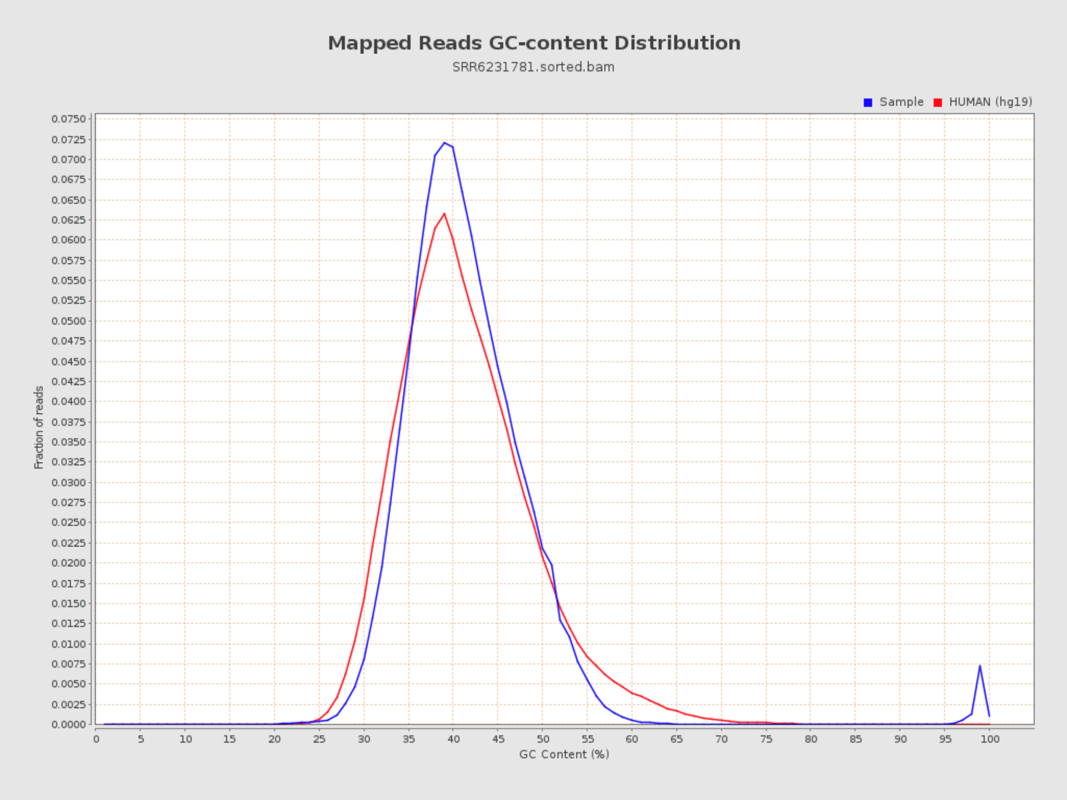
7. Results : Duplication Rate Histogram



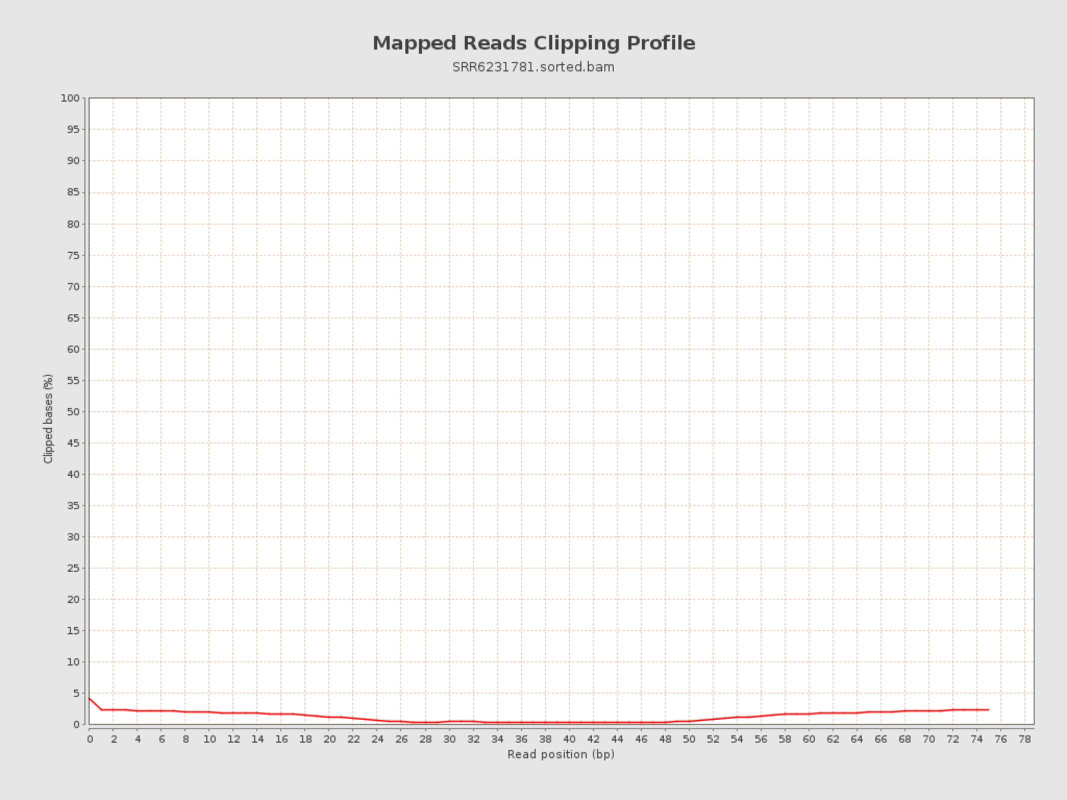
8. Results : Mapped Reads Nucleotide Content



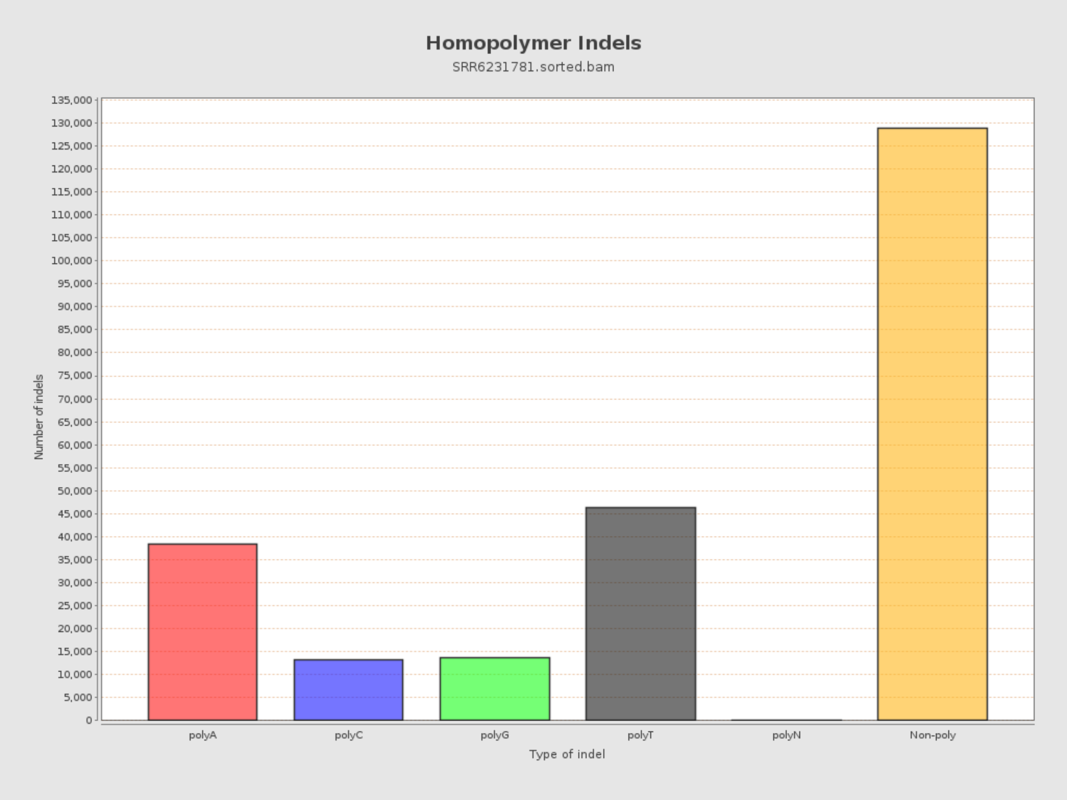
9. Results : Mapped Reads GC-content Distribution



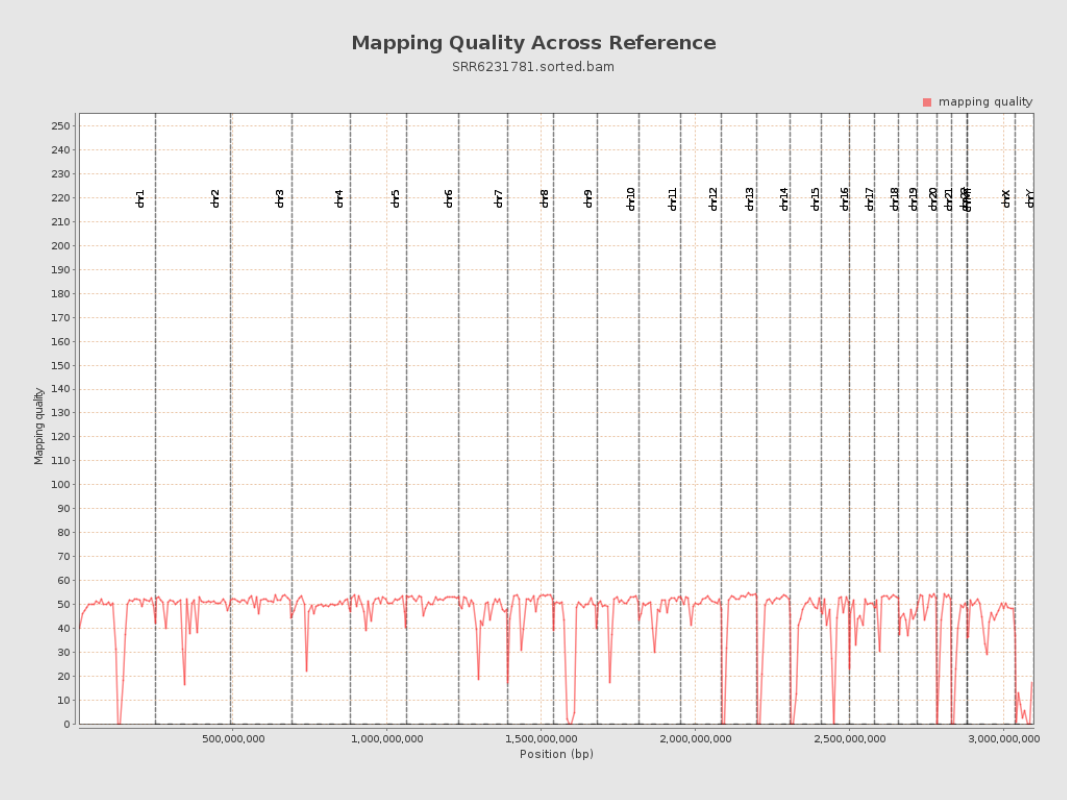
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram