Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 02:24:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231784.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_SRR6231784 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231784.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 02:24:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231784.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,444,448
Mapped reads	2,162,664 / 88.47%
Unmapped reads	281,784 / 11.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,228 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	128,482 / 5.26%
Duplication rate	2.54%
Clipped reads	1,251,339 / 51.19%

2.2. ACGT Content

Number/percentage of A's	40,045,958 / 29.03%
Number/percentage of C's	27,101,421 / 19.65%
Number/percentage of T's	38,219,526 / 27.71%
Number/percentage of G's	32,561,425 / 23.61%
Number/percentage of N's	10,729 / 0.01%
GC Percentage	43.25%

2.3. Coverage

Mean	0.0446

Standard Deviation	7.0042

2.4. Mapping Quality

Mean Mapping Quality	43.41

2.5. Mismatches and indels

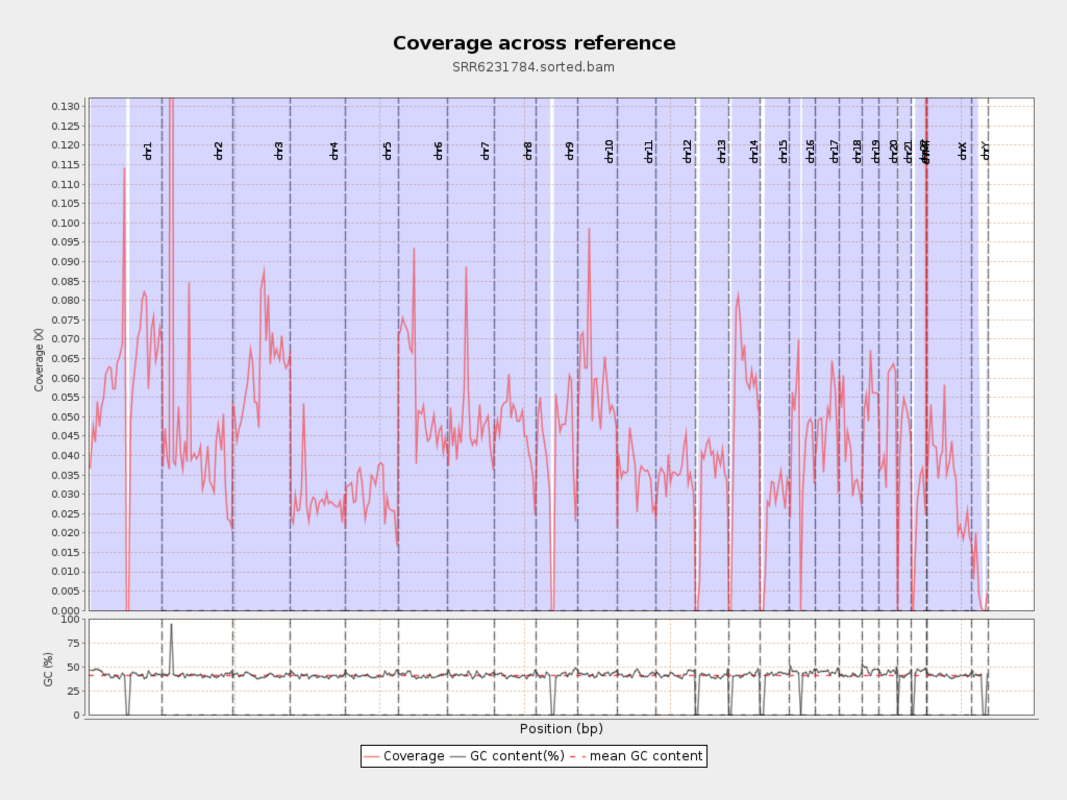
General error rate	0.66%
Mismatches	893,284
Insertions	10,051
Mapped reads with at least one insertion	0.46%
Deletions	30,923
Mapped reads with at least one deletion	1.41%
Homopolymer indels	43.63%

2.6. Chromosome stats

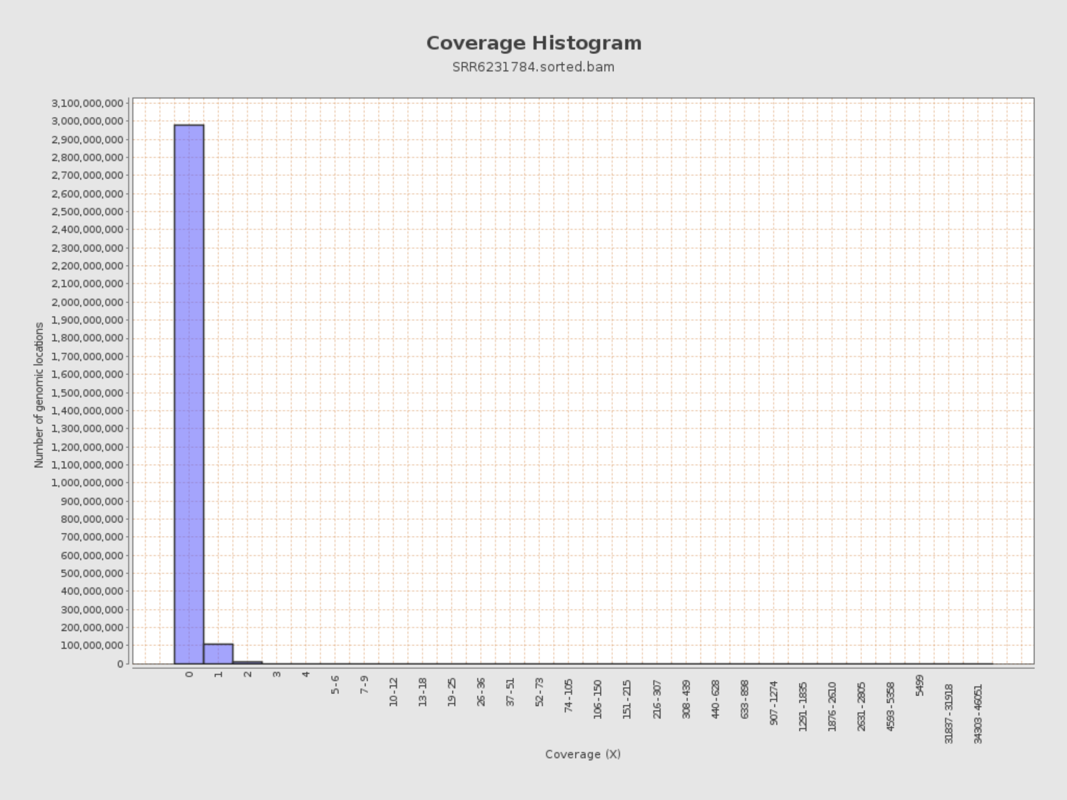
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14952833	0.06	1.1186
chr2	243199373	13390189	0.0551	24.9345
chr3	198022430	12334764	0.0623	0.2751
chr4	191154276	5400092	0.0282	0.2048
chr5	180915260	5468171	0.0302	0.1957
chr6	171115067	9567090	0.0559	0.3607
chr7	159138663	7681568	0.0483	0.6185

chr8	146364022	6897812	0.0471	0.5208
chr9	141213431	5869009	0.0416	0.3728
chr10	135534747	8110641	0.0598	0.4775
chr11	135006516	4744384	0.0351	0.3262
chr12	133851895	4722961	0.0353	0.2136
chr13	115169878	3758593	0.0326	0.1972
chr14	107349540	5853798	0.0545	0.3235
chr15	102531392	2554002	0.0249	0.1761
chr16	90354753	3927416	0.0435	0.2789
chr17	81195210	3907800	0.0481	0.2657
chr18	78077248	3191167	0.0409	0.7359
chr19	59128983	3237383	0.0548	0.7182
chr20	63025520	3083505	0.0489	0.2507
chr21	48129895	2103296	0.0437	0.247
chr22	51304566	1159821	0.0226	0.1627
chrMT	16571	298946	18.0403	10.1808
chrX	155270560	5403599	0.0348	0.2415
chrY	59373566	372259	0.0063	0.1301

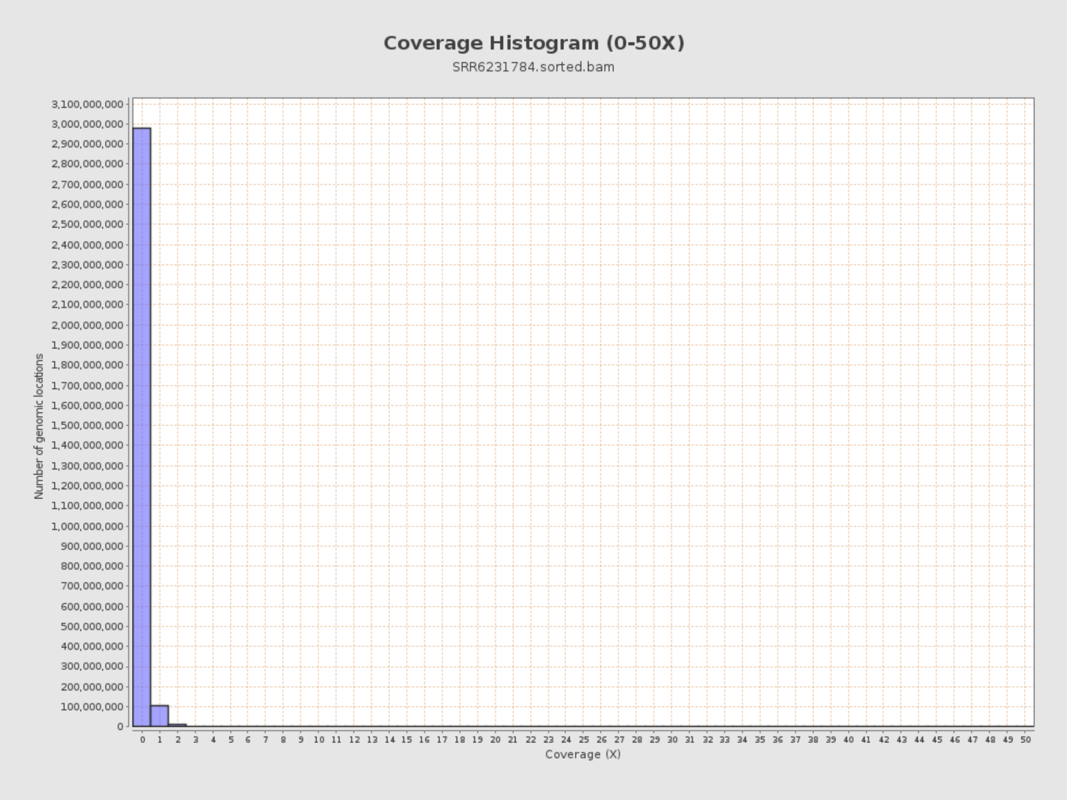
3. Results : Coverage across reference



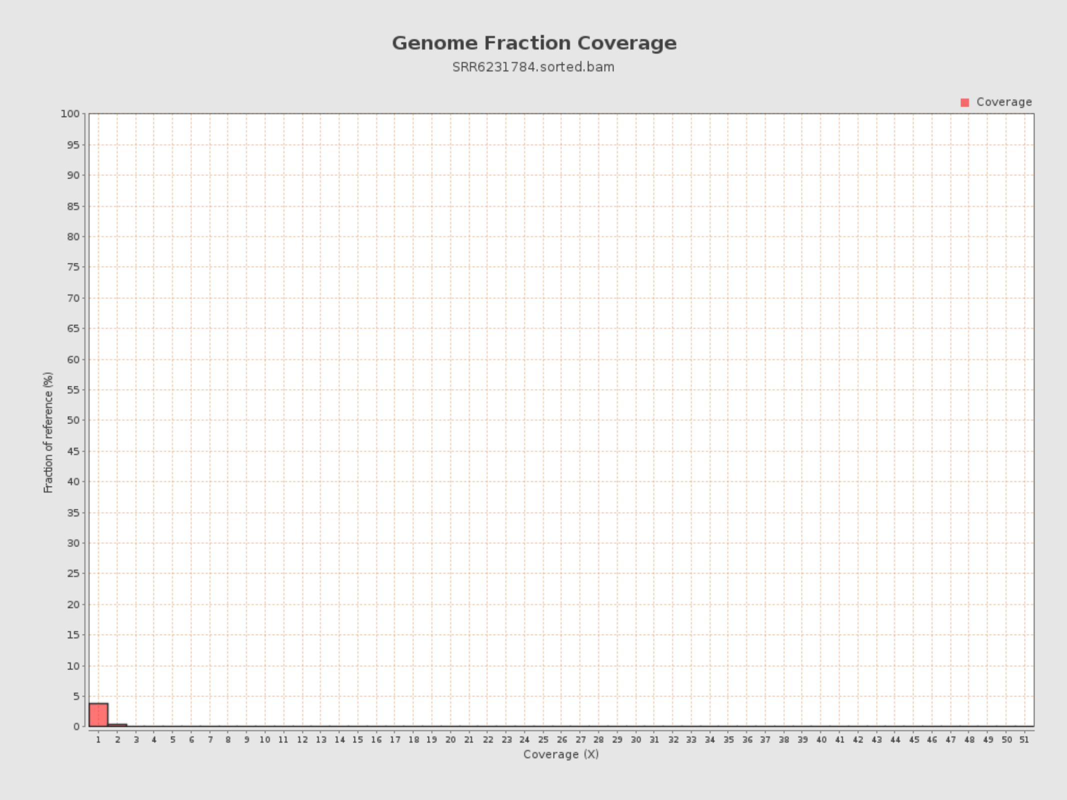
4. Results : Coverage Histogram



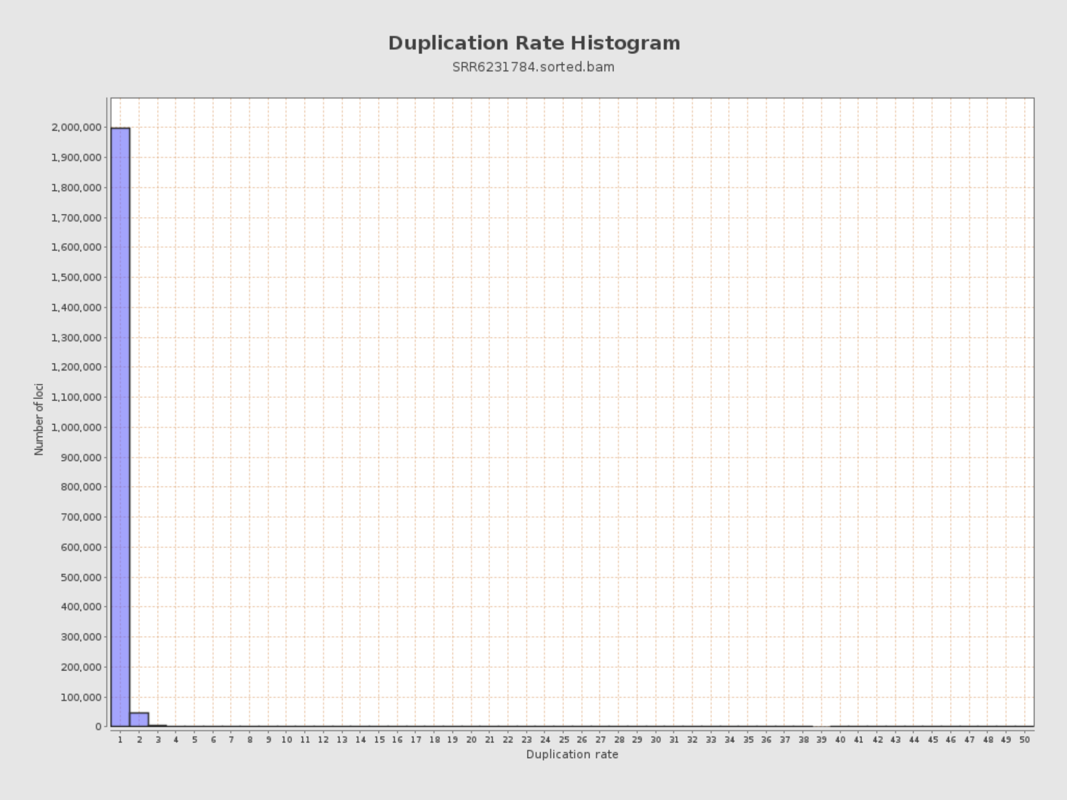
5. Results : Coverage Histogram (0-50X)



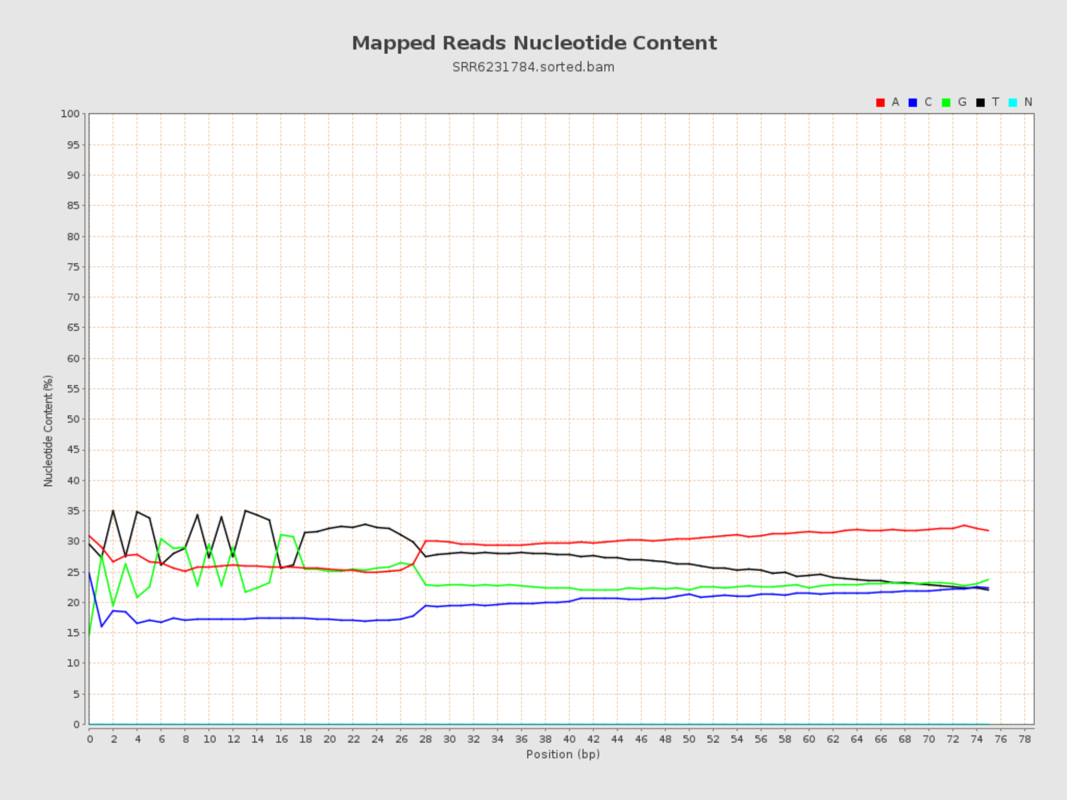
6. Results : Genome Fraction Coverage



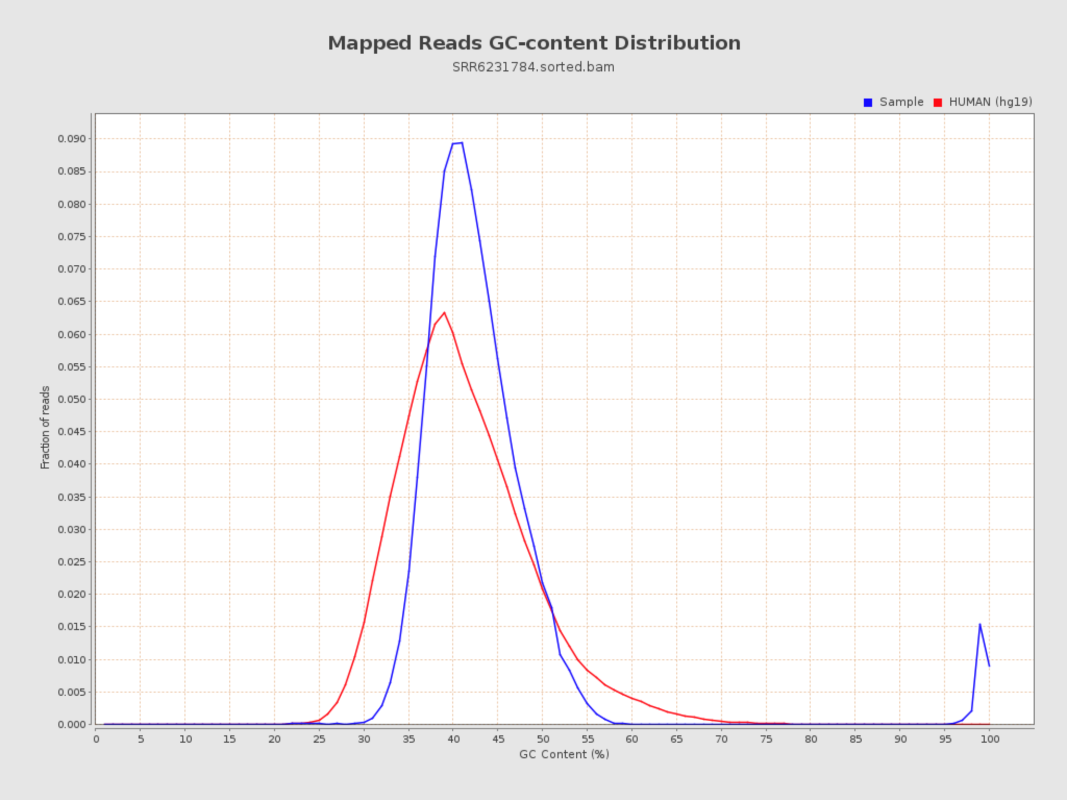
7. Results : Duplication Rate Histogram



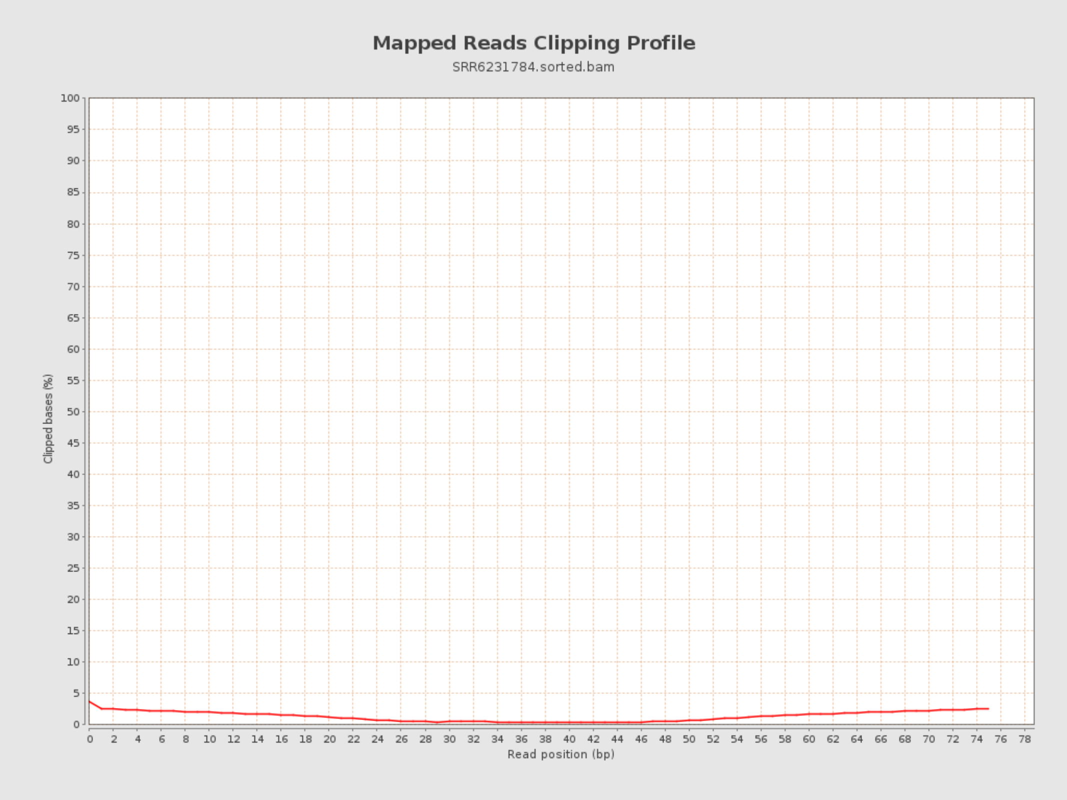
8. Results : Mapped Reads Nucleotide Content



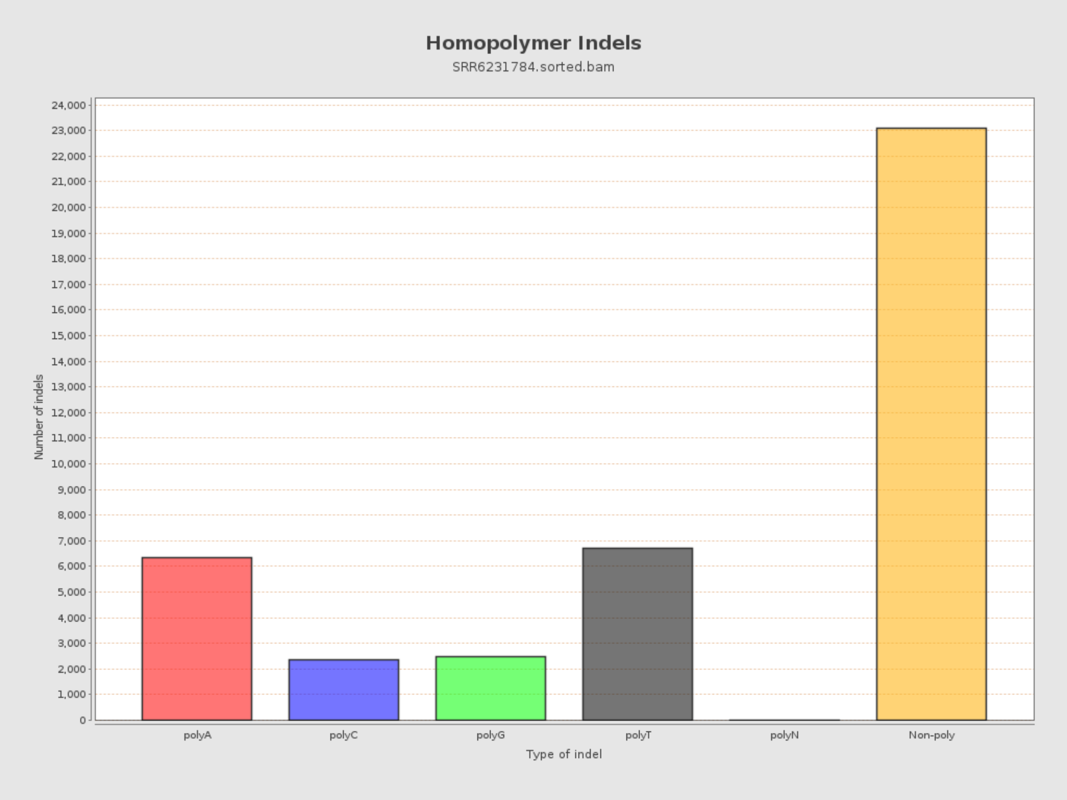
9. Results : Mapped Reads GC-content Distribution



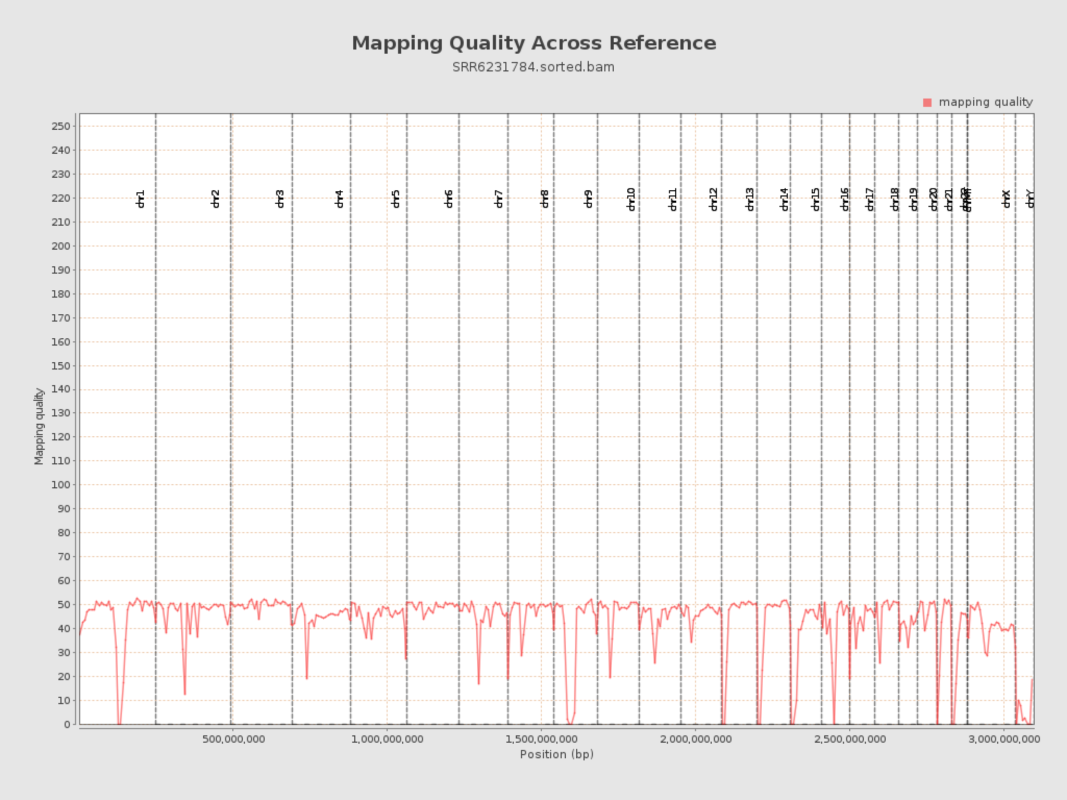
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram