Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 02:31:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231786.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_SRR6231786 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231786.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 02:31:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231786.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,188,348
Mapped reads	3,313,156 / 79.1%
Unmapped reads	875,192 / 20.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,951 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	523,231 / 12.49%
Duplication rate	10.18%
Clipped reads	1,689,604 / 40.34%

2.2. ACGT Content

Number/percentage of A's	60,723,369 / 28.23%
Number/percentage of C's	41,468,654 / 19.28%
Number/percentage of T's	63,403,119 / 29.48%
Number/percentage of G's	49,484,726 / 23.01%
Number/percentage of N's	14,997 / 0.01%
GC Percentage	42.29%

2.3. Coverage

Mean	0.0695

Standard Deviation	7.1861

2.4. Mapping Quality

Mean Mapping Quality	41.6

2.5. Mismatches and indels

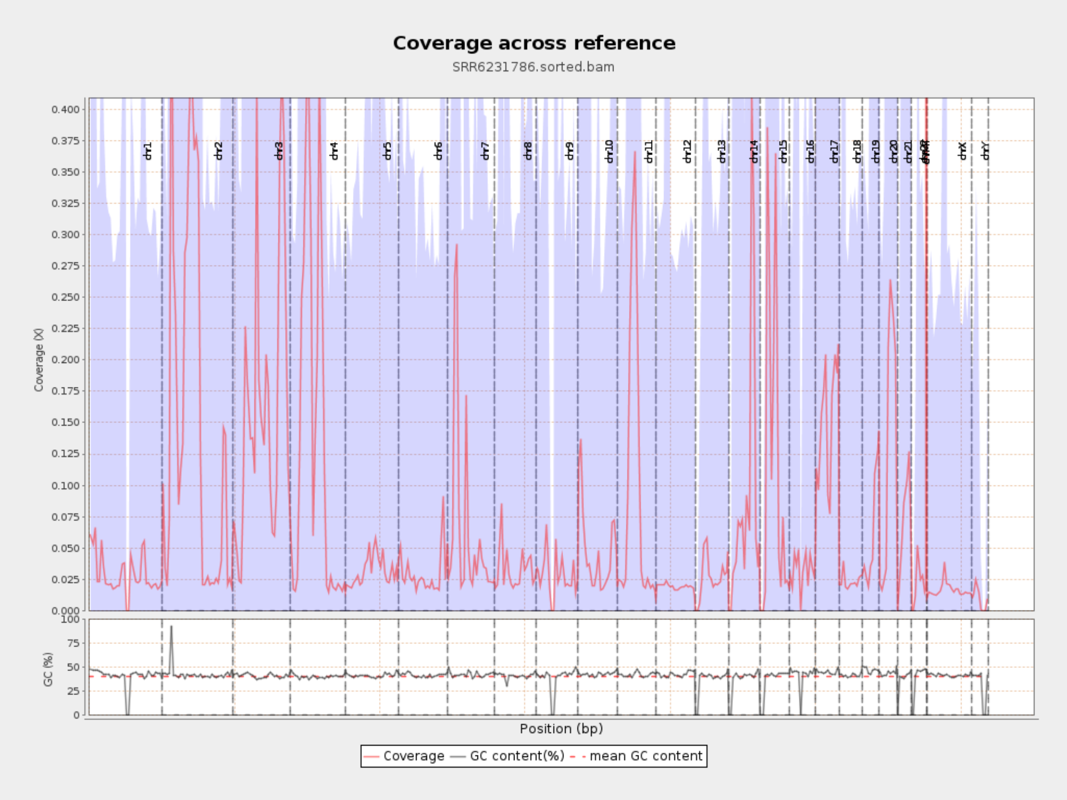
General error rate	0.65%
Mismatches	1,370,444
Insertions	14,209
Mapped reads with at least one insertion	0.42%
Deletions	58,932
Mapped reads with at least one deletion	1.76%
Homopolymer indels	45.77%

2.6. Chromosome stats

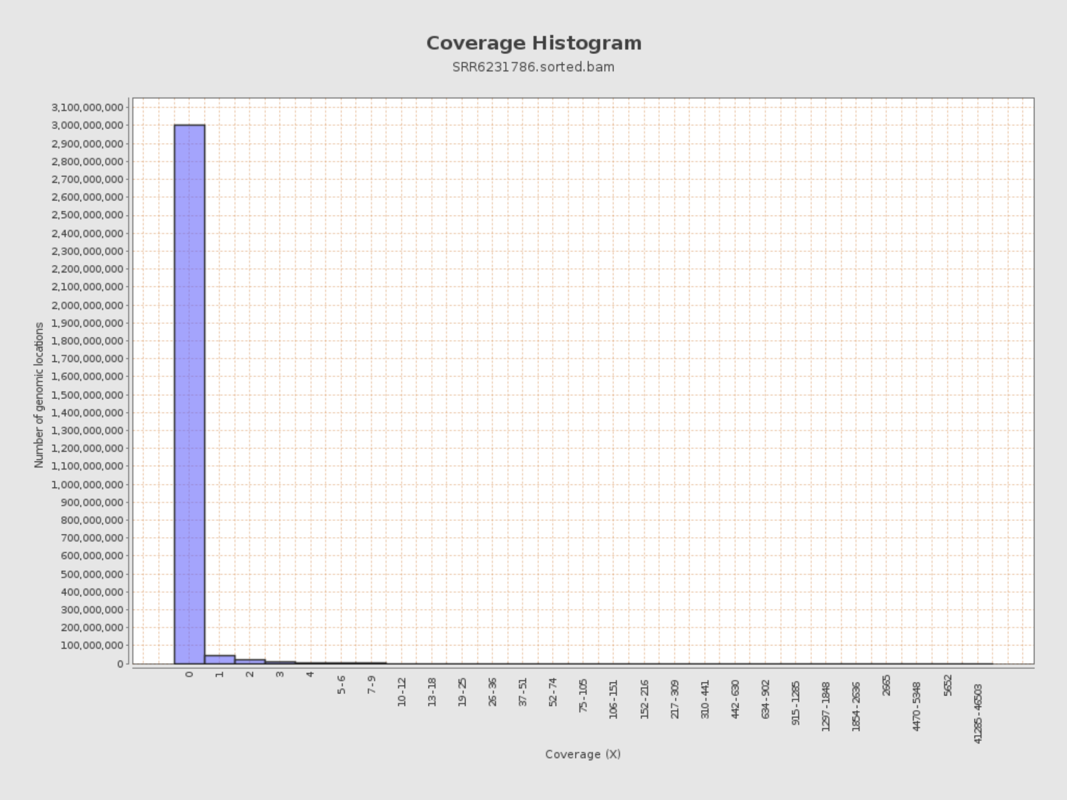
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7207572	0.0289	0.4197
chr2	243199373	37339747	0.1535	25.4994
chr3	198022430	32631029	0.1648	0.7582
chr4	191154276	25114271	0.1314	0.6766
chr5	180915260	5803043	0.0321	0.3552
chr6	171115067	5111763	0.0299	0.3574
chr7	159138663	10561305	0.0664	1.4413

chr8	146364022	4837853	0.0331	1.4417
chr9	141213431	3883879	0.0275	0.5124
chr10	135534747	6535964	0.0482	0.4379
chr11	135006516	12436714	0.0921	1.6915
chr12	133851895	2575397	0.0192	0.3508
chr13	115169878	2971150	0.0258	0.317
chr14	107349540	10040545	0.0935	0.6684
chr15	102531392	11875702	0.1158	0.6369
chr16	90354753	2906437	0.0322	0.3471
chr17	81195210	12321357	0.1517	1.0126
chr18	78077248	1822674	0.0233	0.6854
chr19	59128983	3428627	0.058	0.4738
chr20	63025520	8077517	0.1282	0.7046
chr21	48129895	3325566	0.0691	0.5009
chr22	51304566	1049955	0.0205	0.2739
chrMT	16571	232900	14.0547	9.433
chrX	155270560	2566766	0.0165	0.4575
chrY	59373566	536367	0.009	0.18

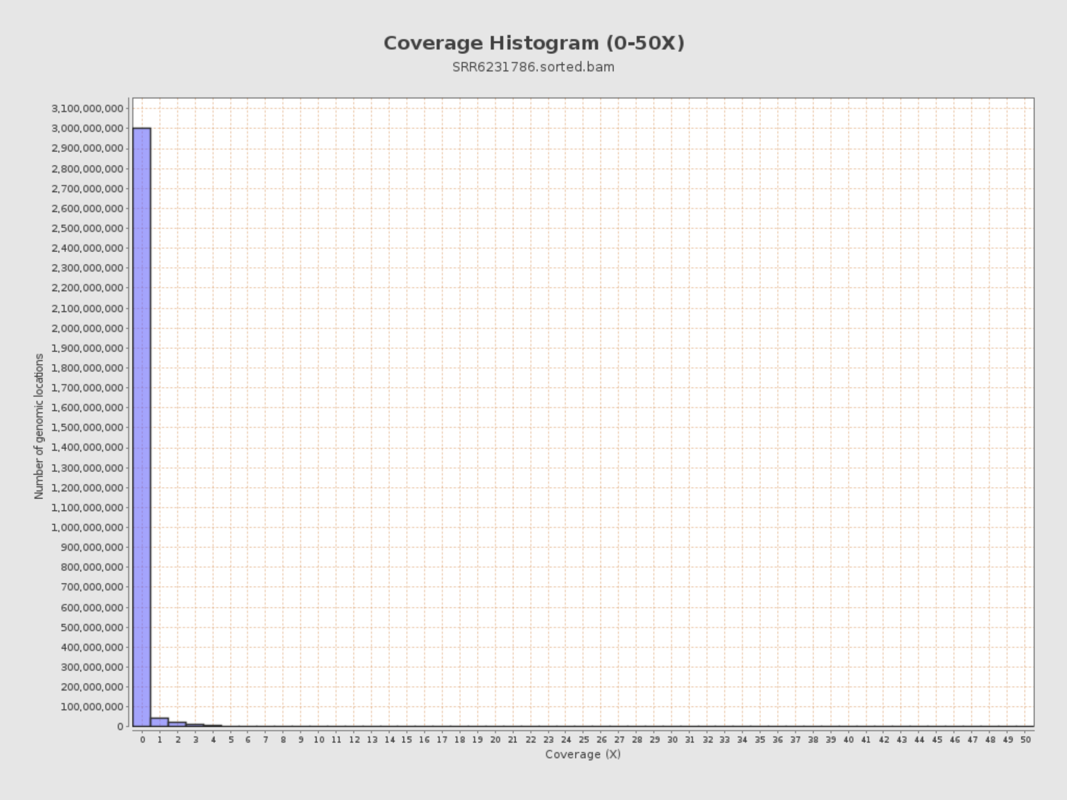
3. Results : Coverage across reference



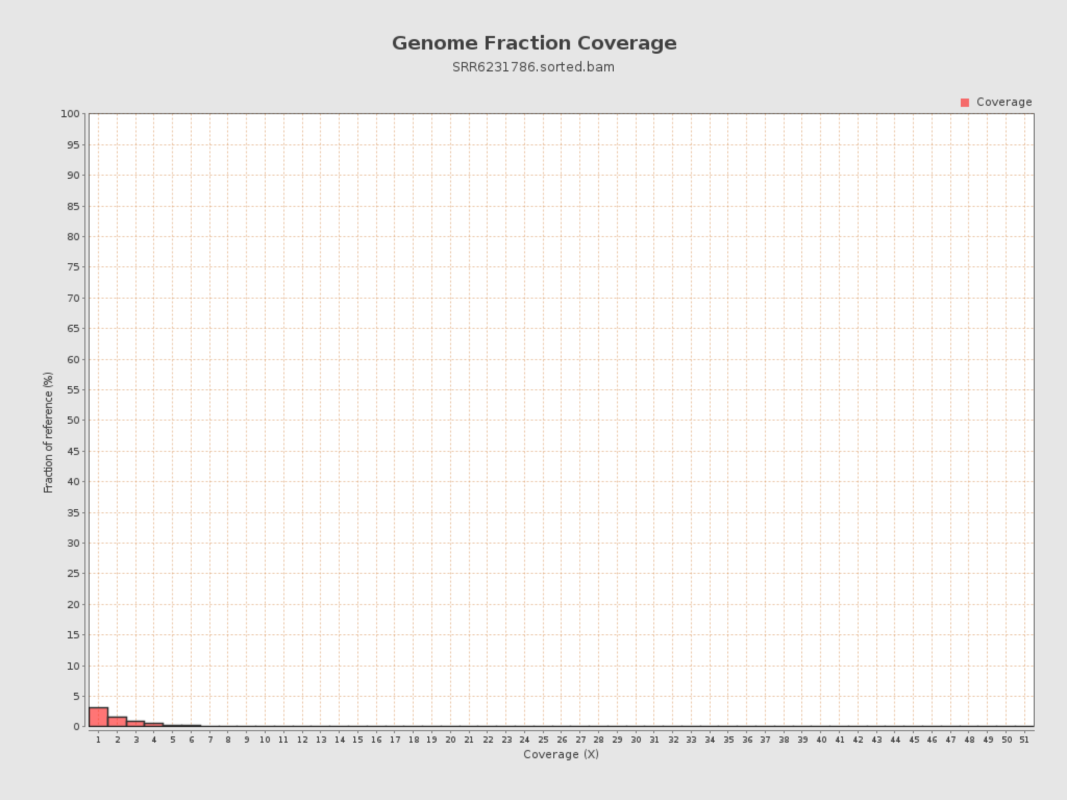
4. Results : Coverage Histogram



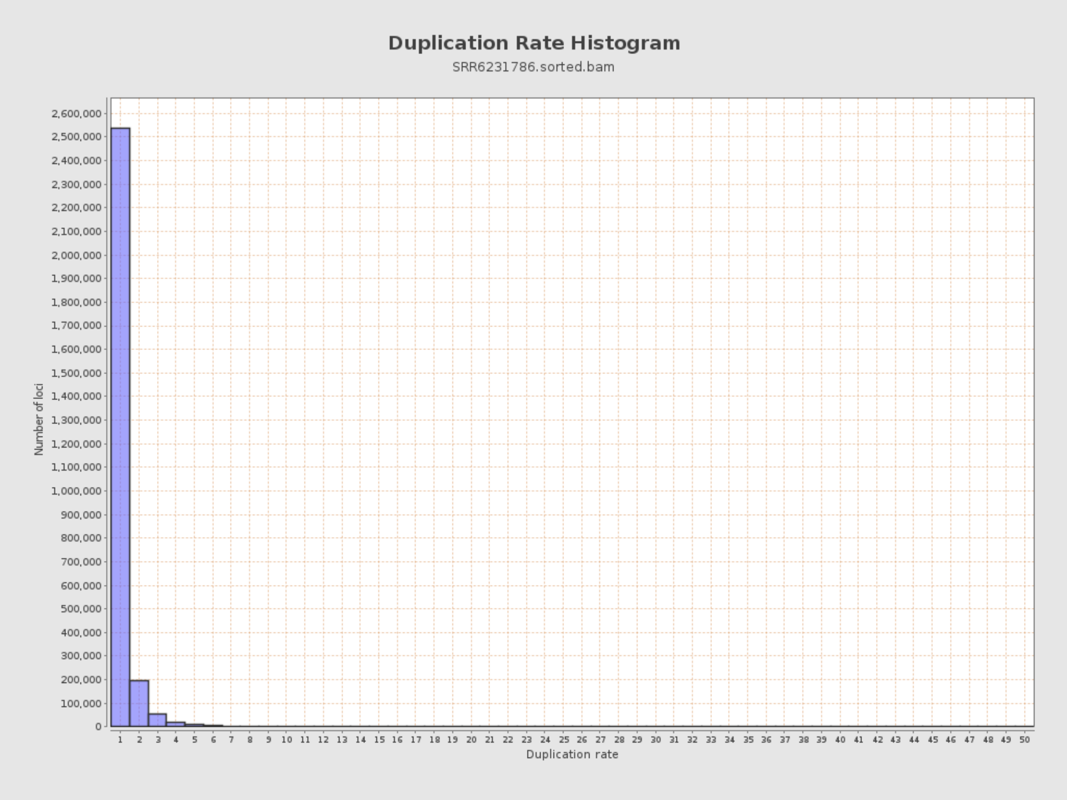
5. Results : Coverage Histogram (0-50X)



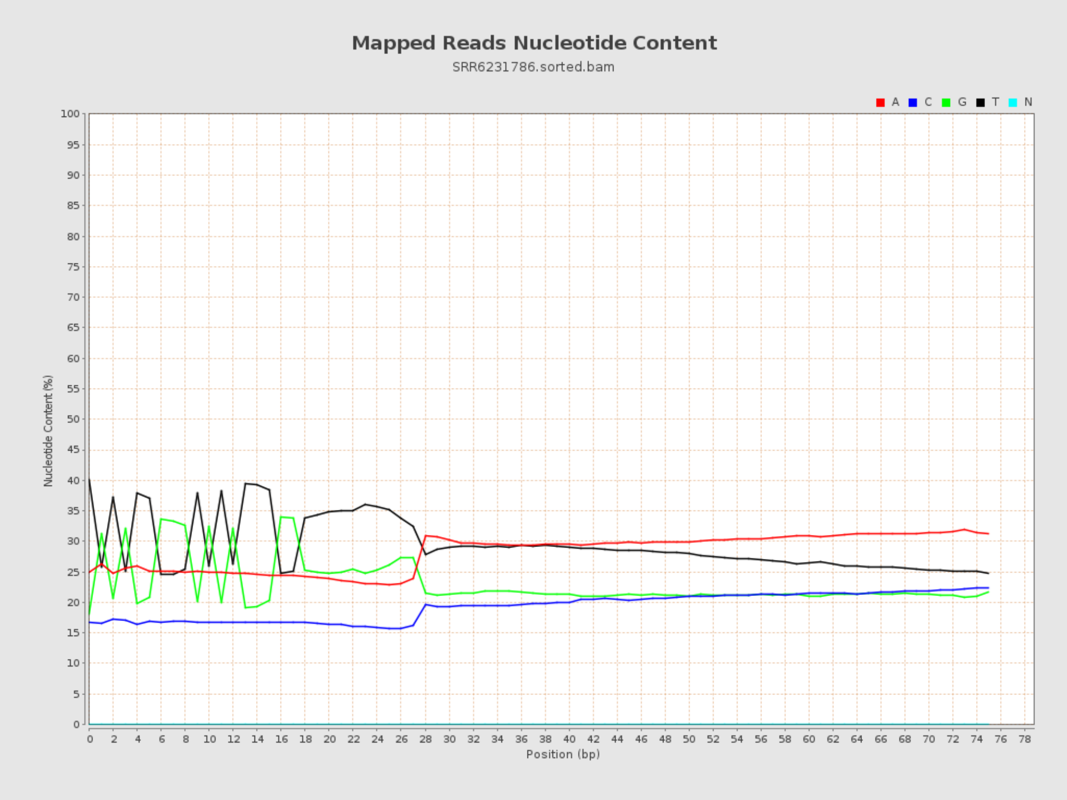
6. Results : Genome Fraction Coverage



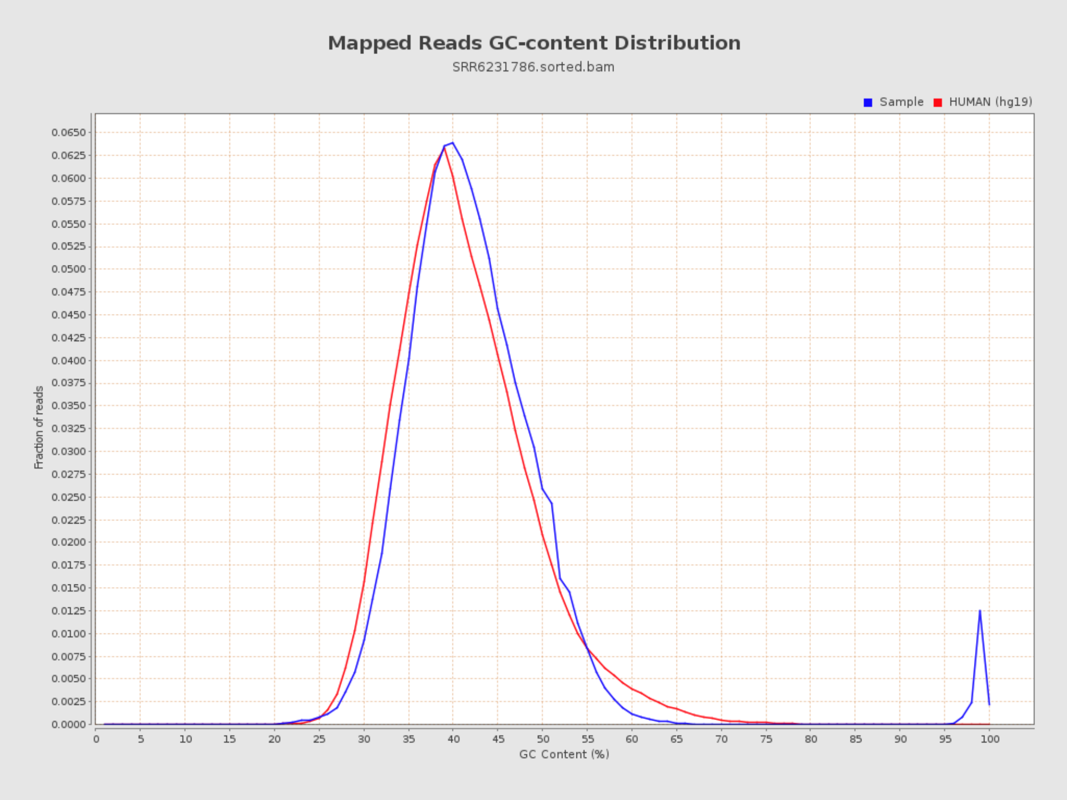
7. Results : Duplication Rate Histogram



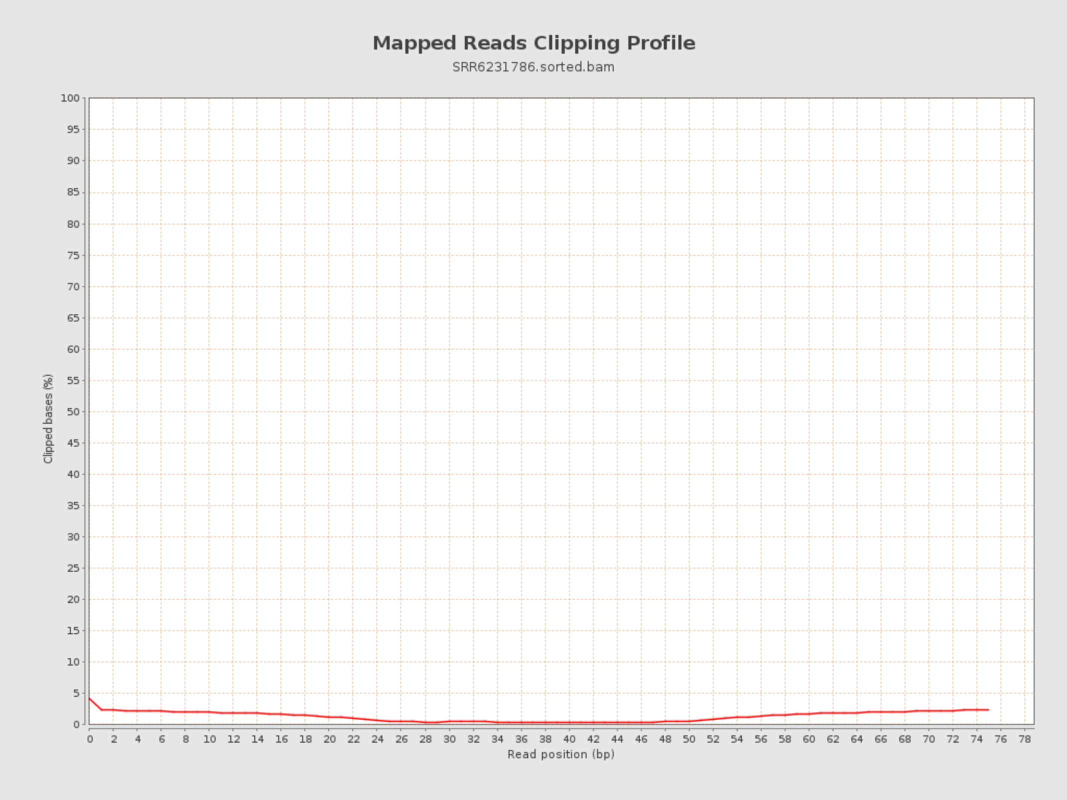
8. Results : Mapped Reads Nucleotide Content



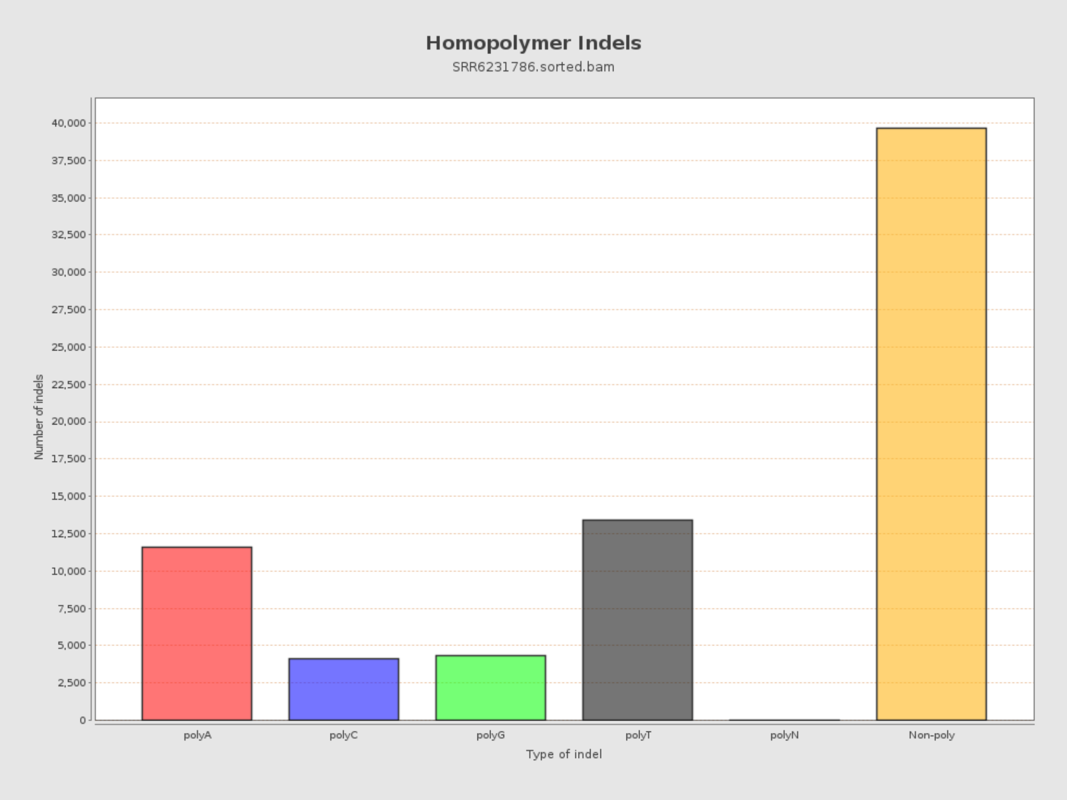
9. Results : Mapped Reads GC-content Distribution



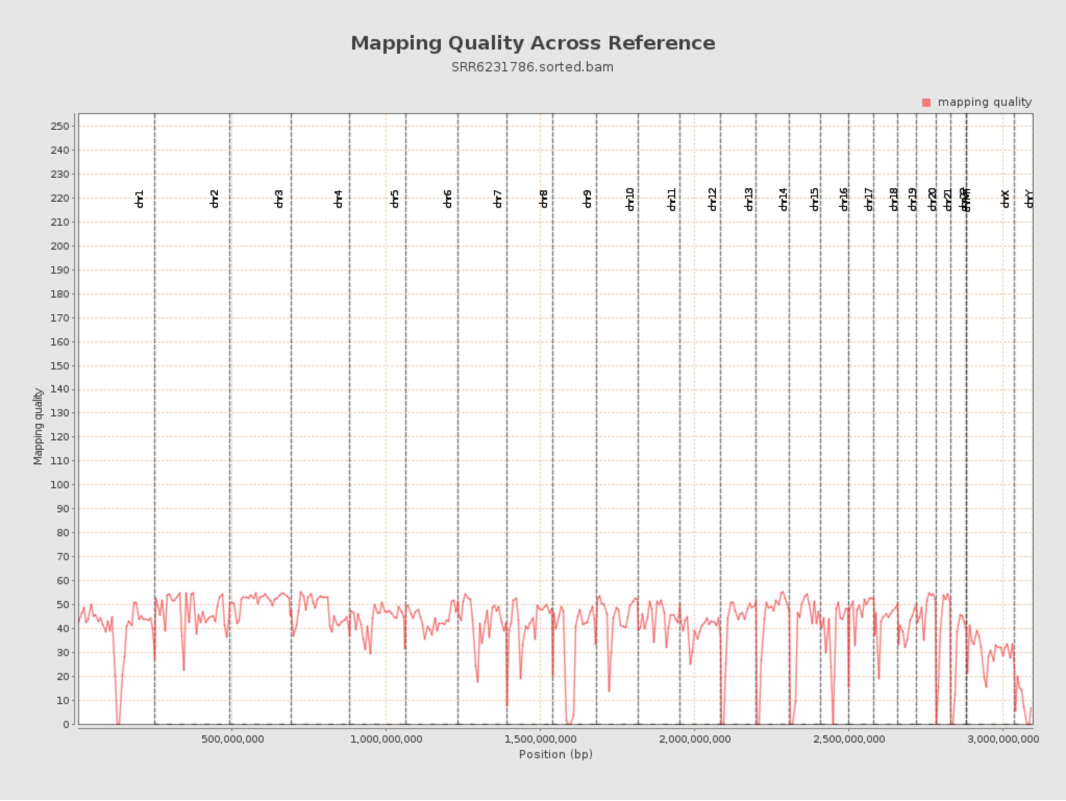
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram