Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:46:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231748.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_SRR6231748 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231748.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:46:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231748.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,335,934
Mapped reads	4,092,751 / 94.39%
Unmapped reads	243,183 / 5.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,278 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	299,349 / 6.9%
Duplication rate	3.38%
Clipped reads	1,602,093 / 36.95%

2.2. ACGT Content

Number/percentage of A's	73,638,299 / 26.51%
Number/percentage of C's	52,976,034 / 19.07%
Number/percentage of T's	80,449,755 / 28.97%
Number/percentage of G's	70,608,957 / 25.42%
Number/percentage of N's	60,223 / 0.02%
GC Percentage	44.5%

2.3. Coverage

Mean	0.0897

Standard Deviation	17.0898

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

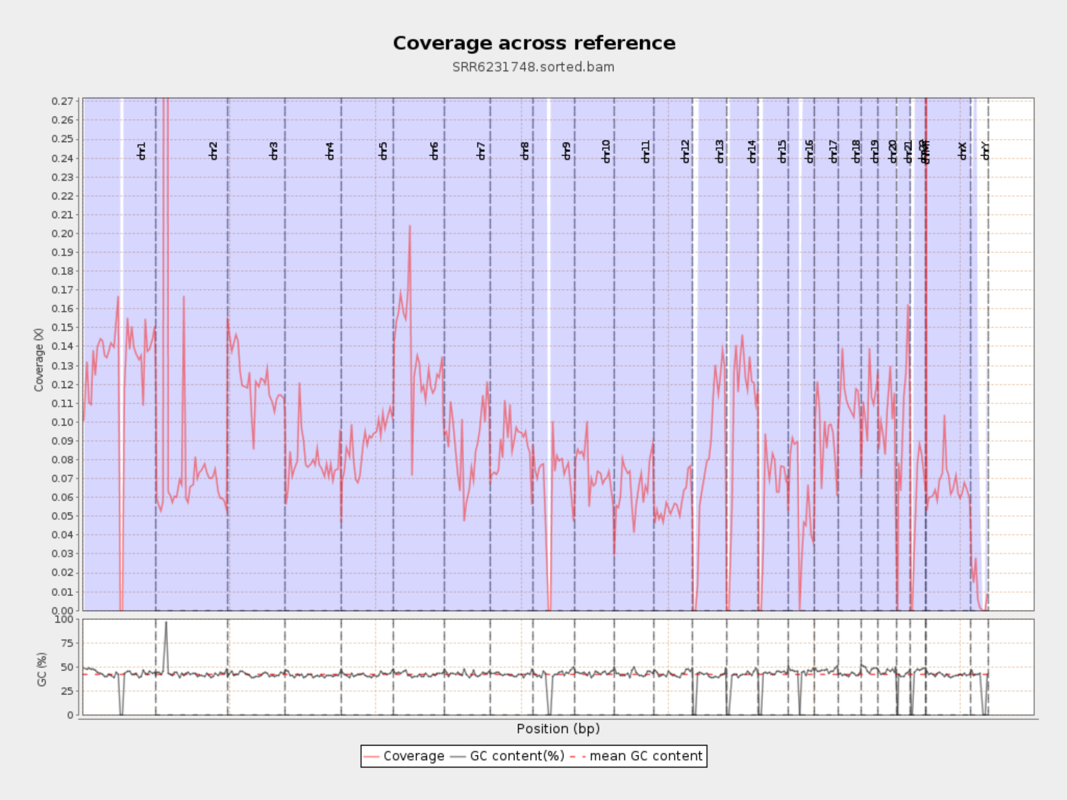
General error rate	0.67%
Mismatches	1,814,129
Insertions	18,779
Mapped reads with at least one insertion	0.45%
Deletions	58,557
Mapped reads with at least one deletion	1.42%
Homopolymer indels	46.83%

2.6. Chromosome stats

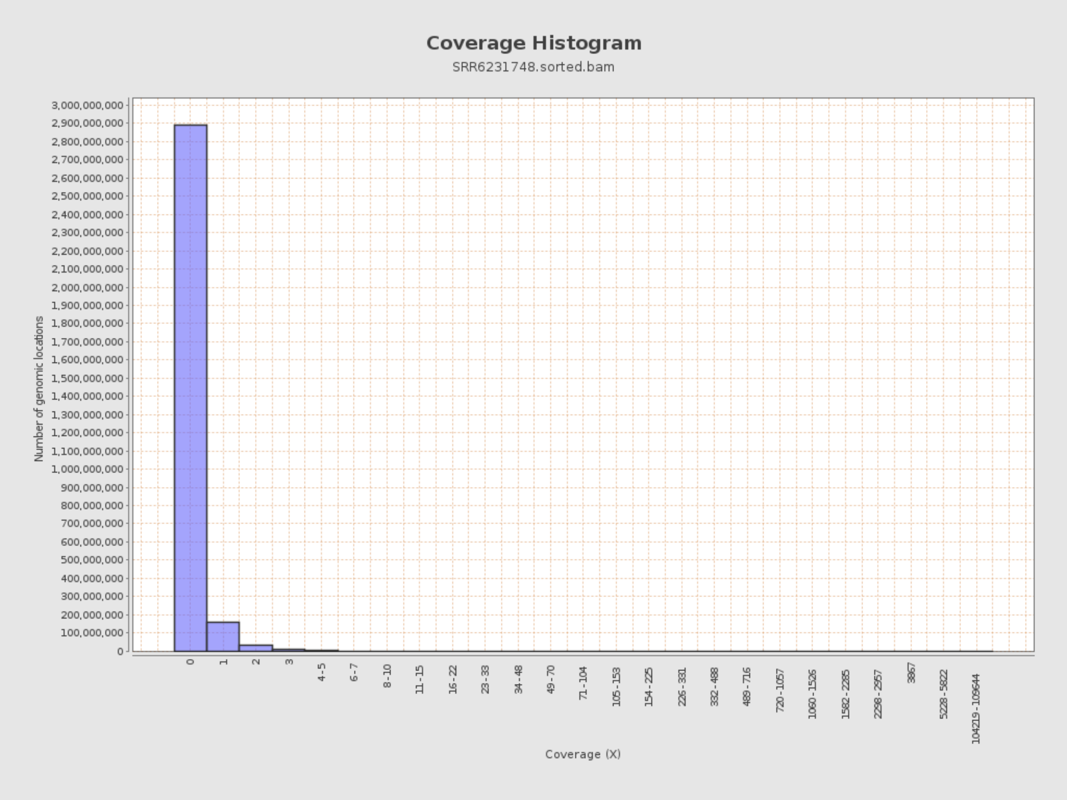
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31871698	0.1279	0.9947
chr2	243199373	25381452	0.1044	60.935
chr3	198022430	24113560	0.1218	0.444
chr4	191154276	15150416	0.0793	0.3864
chr5	180915260	16132554	0.0892	0.3812
chr6	171115067	23066931	0.1348	0.7102
chr7	159138663	13872714	0.0872	0.8196

chr8	146364022	12747720	0.0871	0.6451
chr9	141213431	9277069	0.0657	0.6983
chr10	135534747	10001160	0.0738	0.4882
chr11	135006516	8794445	0.0651	0.6516
chr12	133851895	7598191	0.0568	0.3109
chr13	115169878	9447232	0.082	0.3622
chr14	107349540	11288886	0.1052	0.5418
chr15	102531392	6285850	0.0613	0.3159
chr16	90354753	5035201	0.0557	0.3964
chr17	81195210	7592338	0.0935	0.4661
chr18	78077248	8828912	0.1131	1.4603
chr19	59128983	6544558	0.1107	0.7449
chr20	63025520	6306868	0.1001	0.423
chr21	48129895	4759638	0.0989	0.4681
chr22	51304566	2882454	0.0562	0.2987
chrMT	16571	11683	0.705	1.3238
chrX	155270560	10254120	0.066	0.4607
chrY	59373566	583440	0.0098	0.1783

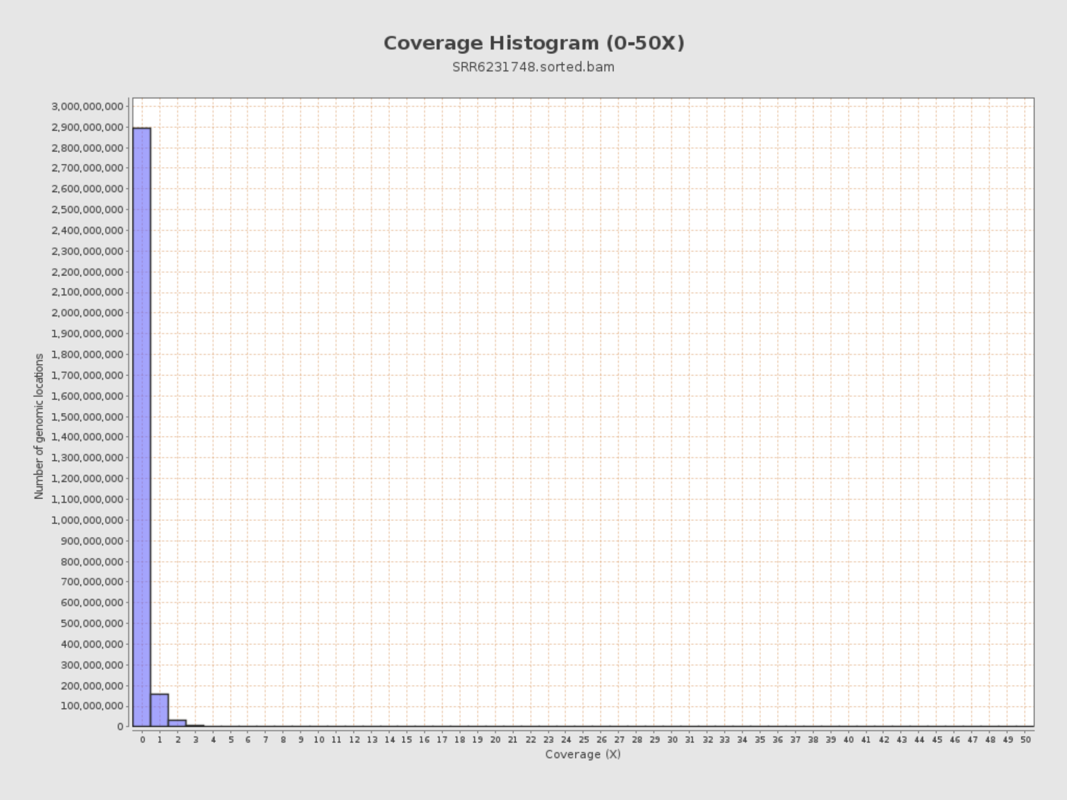
3. Results : Coverage across reference



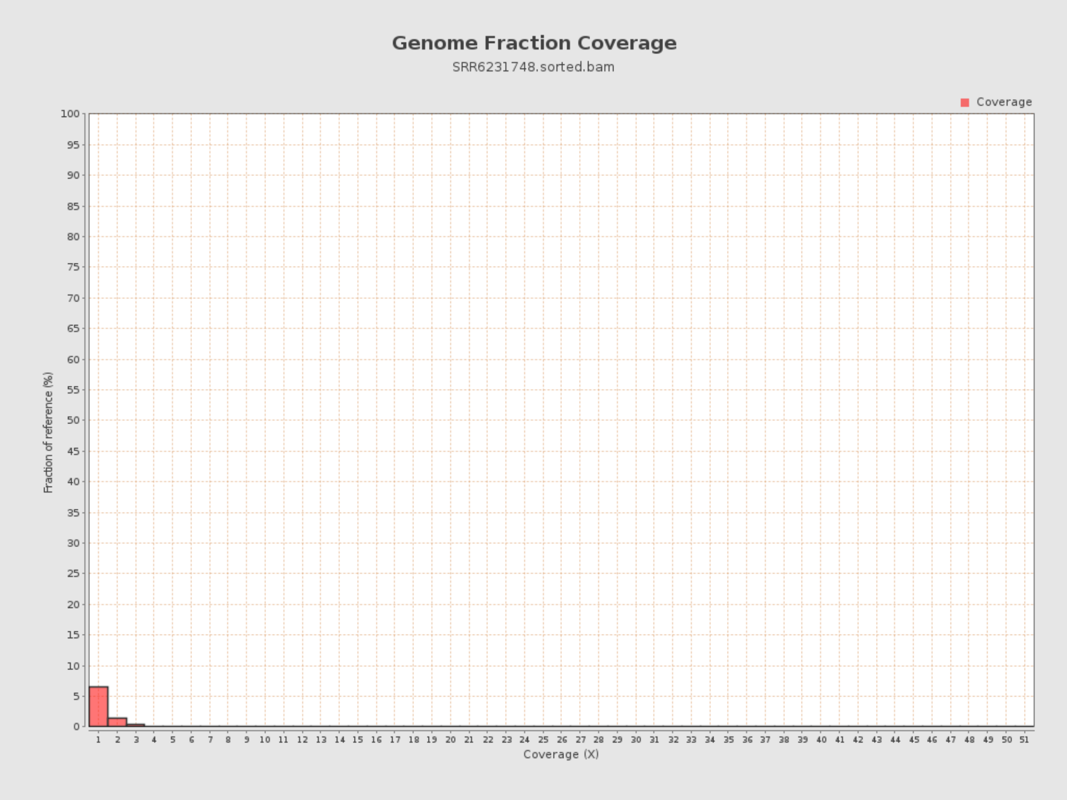
4. Results : Coverage Histogram



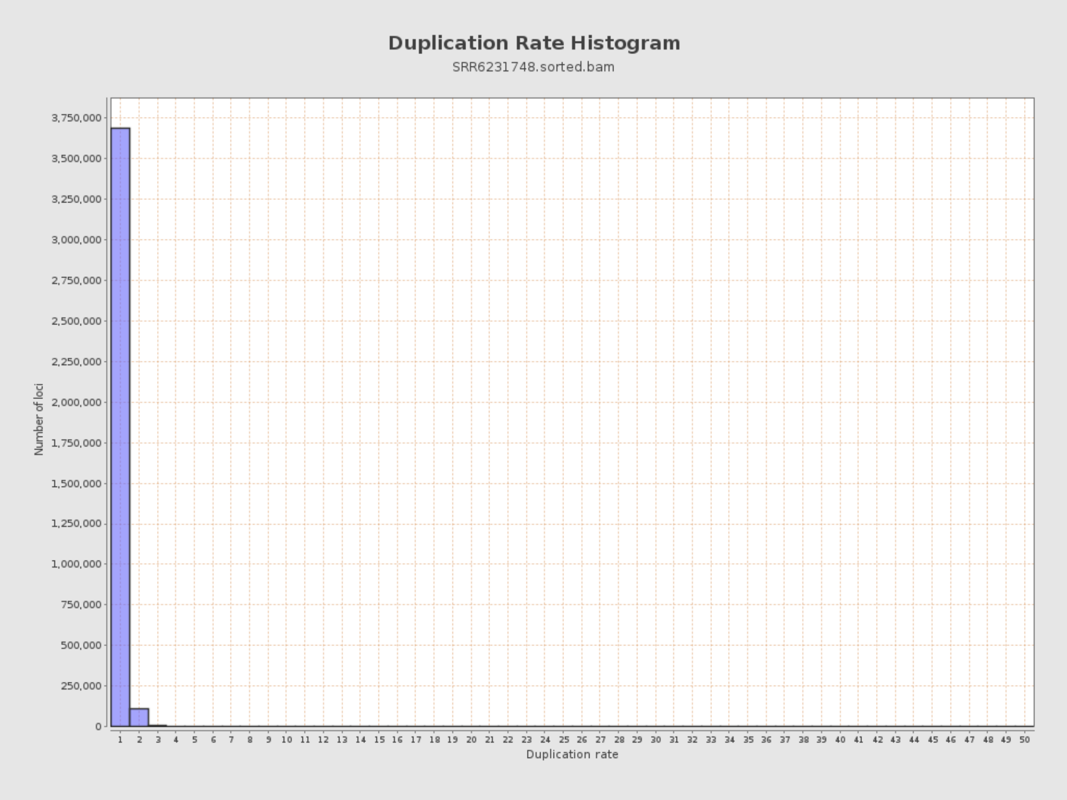
5. Results : Coverage Histogram (0-50X)



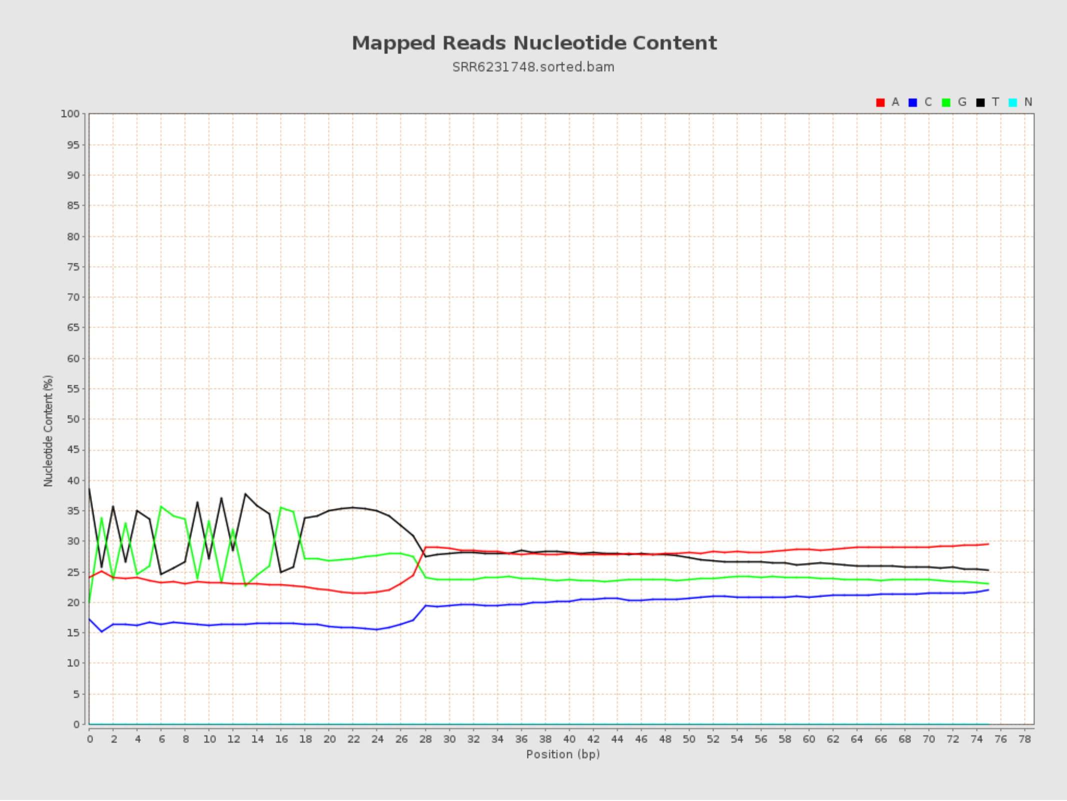
6. Results : Genome Fraction Coverage



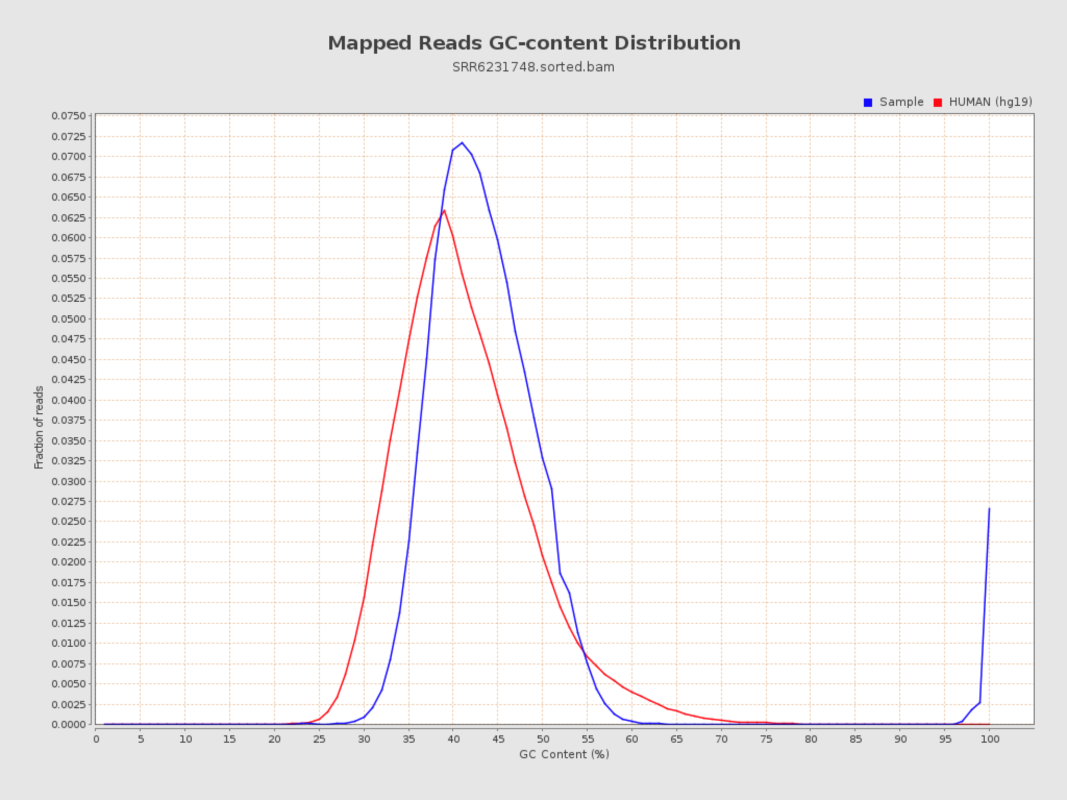
7. Results : Duplication Rate Histogram



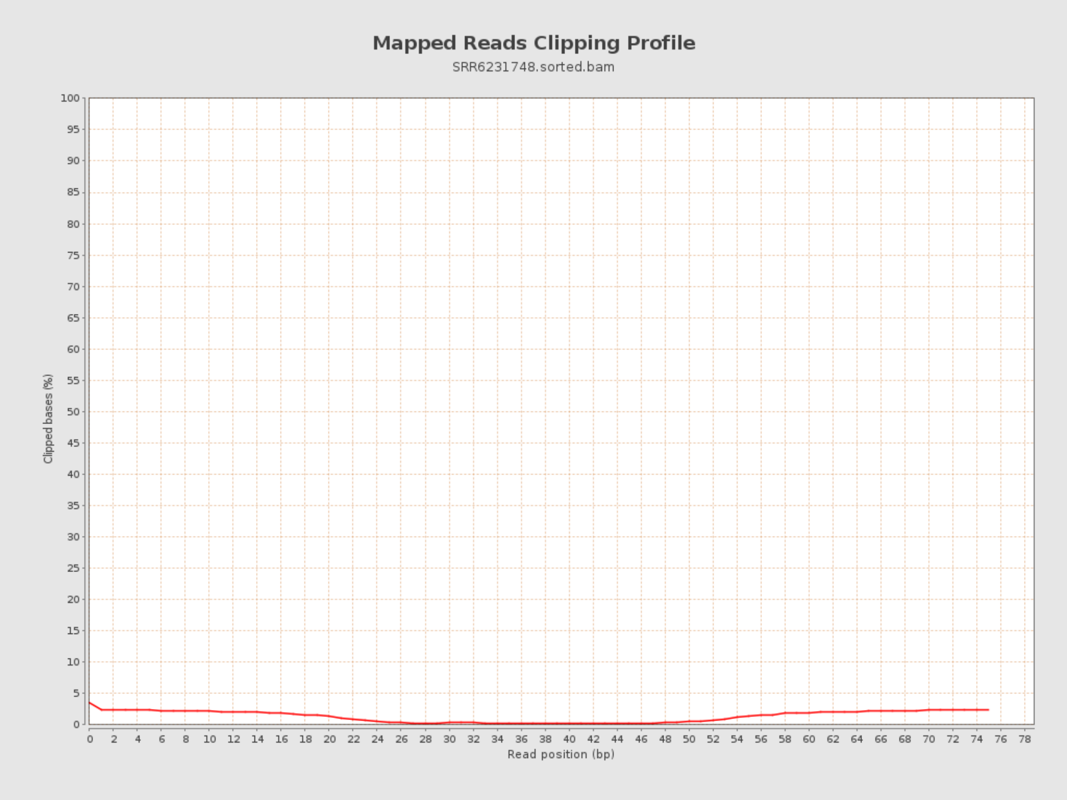
8. Results : Mapped Reads Nucleotide Content



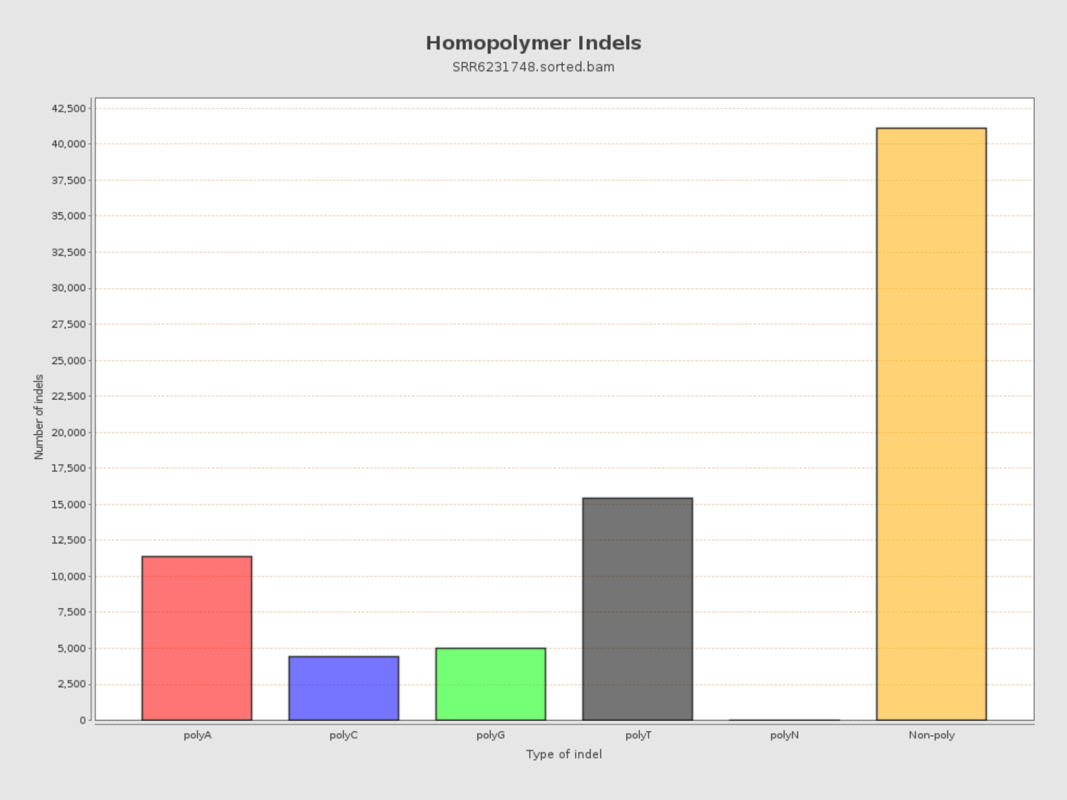
9. Results : Mapped Reads GC-content Distribution



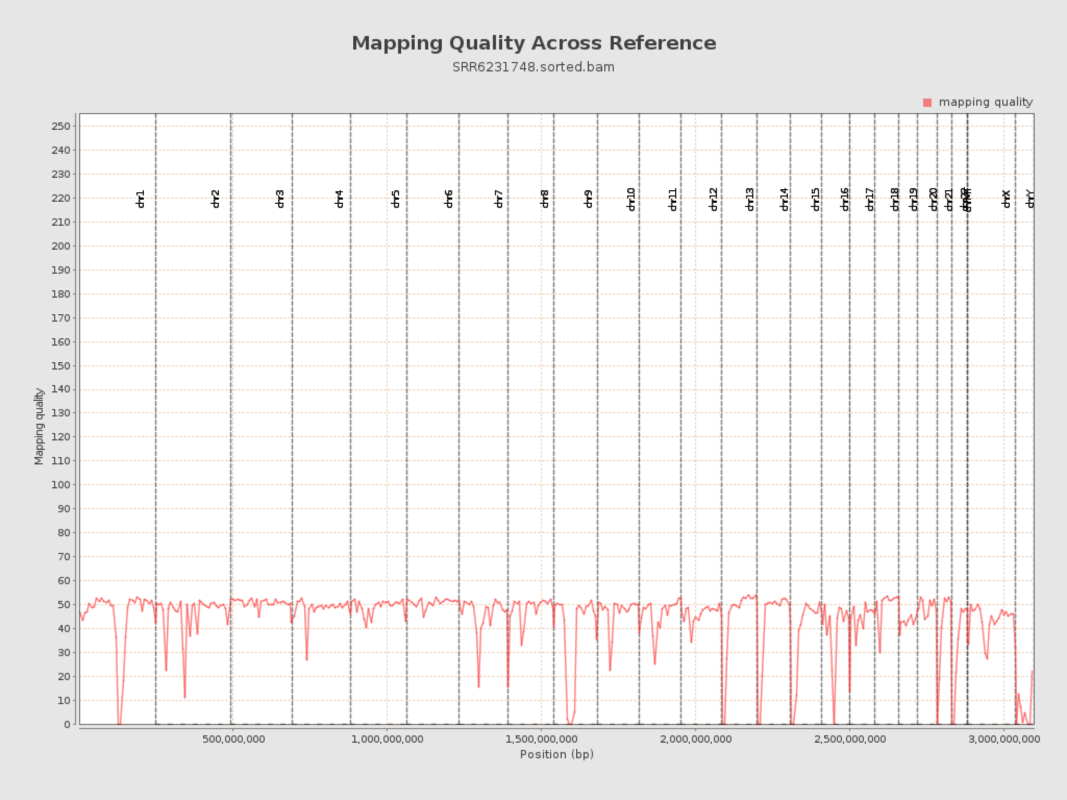
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram