Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:41:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231747.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_SRR6231747 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231747.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:41:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231747.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,731,516
Mapped reads	4,458,493 / 94.23%
Unmapped reads	273,023 / 5.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,271 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	506,701 / 10.71%
Duplication rate	4.91%
Clipped reads	1,632,460 / 34.5%

2.2. ACGT Content

Number/percentage of A's	81,085,934 / 26.51%
Number/percentage of C's	55,661,253 / 18.2%
Number/percentage of T's	87,880,400 / 28.74%
Number/percentage of G's	81,119,314 / 26.53%
Number/percentage of N's	67,247 / 0.02%
GC Percentage	44.73%

2.3. Coverage

Mean	0.0988

Standard Deviation	35.5438

2.4. Mapping Quality

Mean Mapping Quality	46.01

2.5. Mismatches and indels

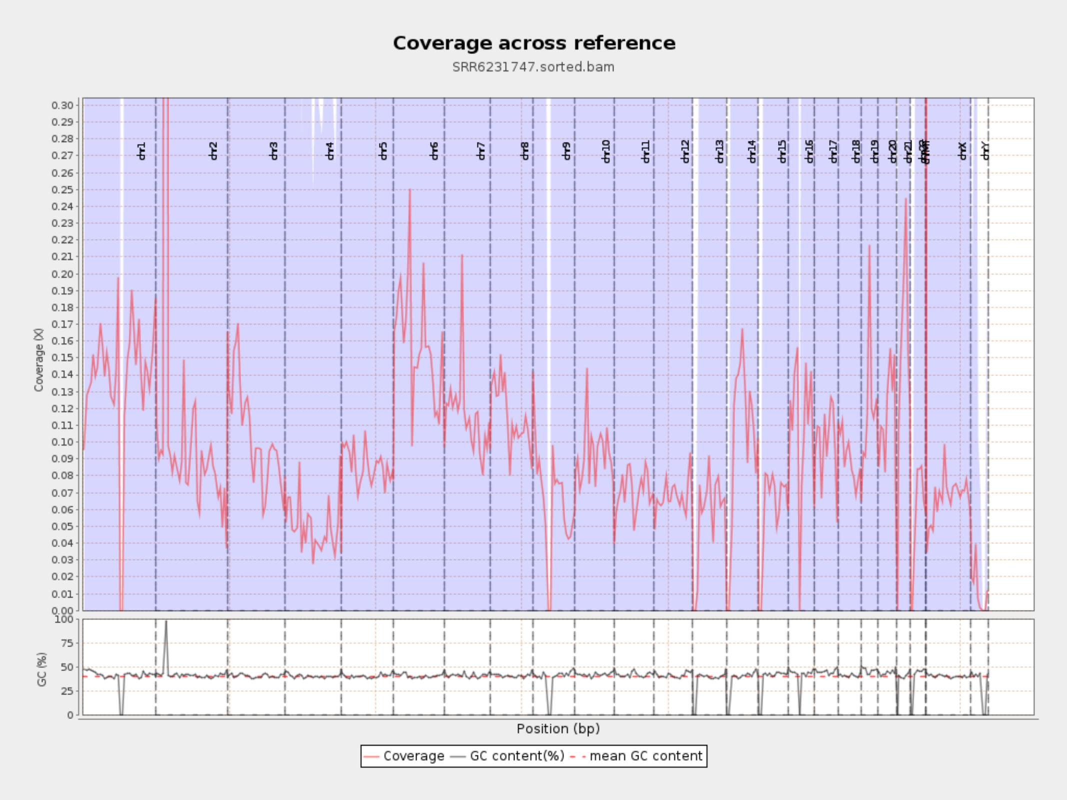
General error rate	0.66%
Mismatches	1,978,292
Insertions	20,936
Mapped reads with at least one insertion	0.47%
Deletions	70,305
Mapped reads with at least one deletion	1.56%
Homopolymer indels	46.97%

2.6. Chromosome stats

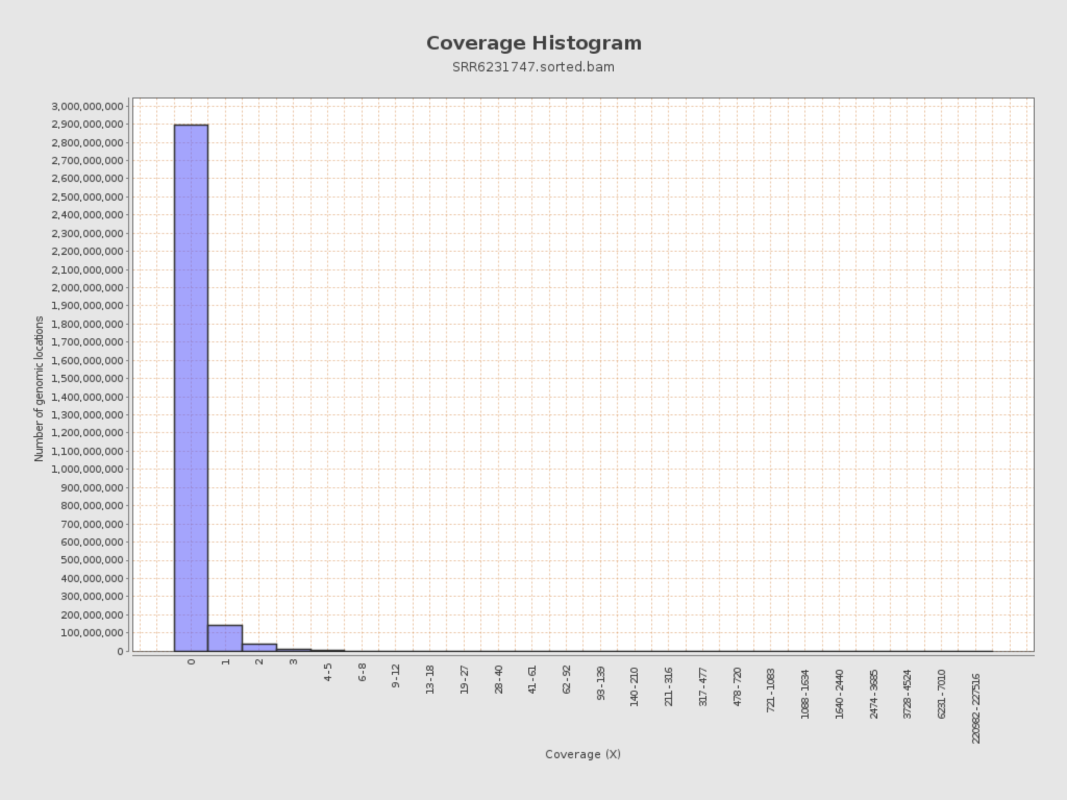
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34284325	0.1375	1.8362
chr2	243199373	39023902	0.1605	126.7777
chr3	198022430	20710049	0.1046	0.4365
chr4	191154276	9592146	0.0502	0.352
chr5	180915260	15567288	0.086	0.4063
chr6	171115067	27278193	0.1594	0.8137
chr7	159138663	18510927	0.1163	1.5652

chr8	146364022	16836613	0.115	0.8379
chr9	141213431	8862868	0.0628	0.5874
chr10	135534747	12547027	0.0926	0.7245
chr11	135006516	9598300	0.0711	0.7716
chr12	133851895	9045477	0.0676	0.3577
chr13	115169878	6431613	0.0558	0.3133
chr14	107349540	11100954	0.1034	0.5424
chr15	102531392	6018368	0.0587	0.322
chr16	90354753	9520403	0.1054	0.4897
chr17	81195210	8234441	0.1014	0.5667
chr18	78077248	7045086	0.0902	1.2668
chr19	59128983	7204197	0.1218	1.1709
chr20	63025520	7421344	0.1178	0.4789
chr21	48129895	7225892	0.1501	0.5746
chr22	51304566	2863063	0.0558	0.3144
chrMT	16571	15118	0.9123	1.4982
chrX	155270560	10301201	0.0663	0.4347
chrY	59373566	690612	0.0116	0.2217

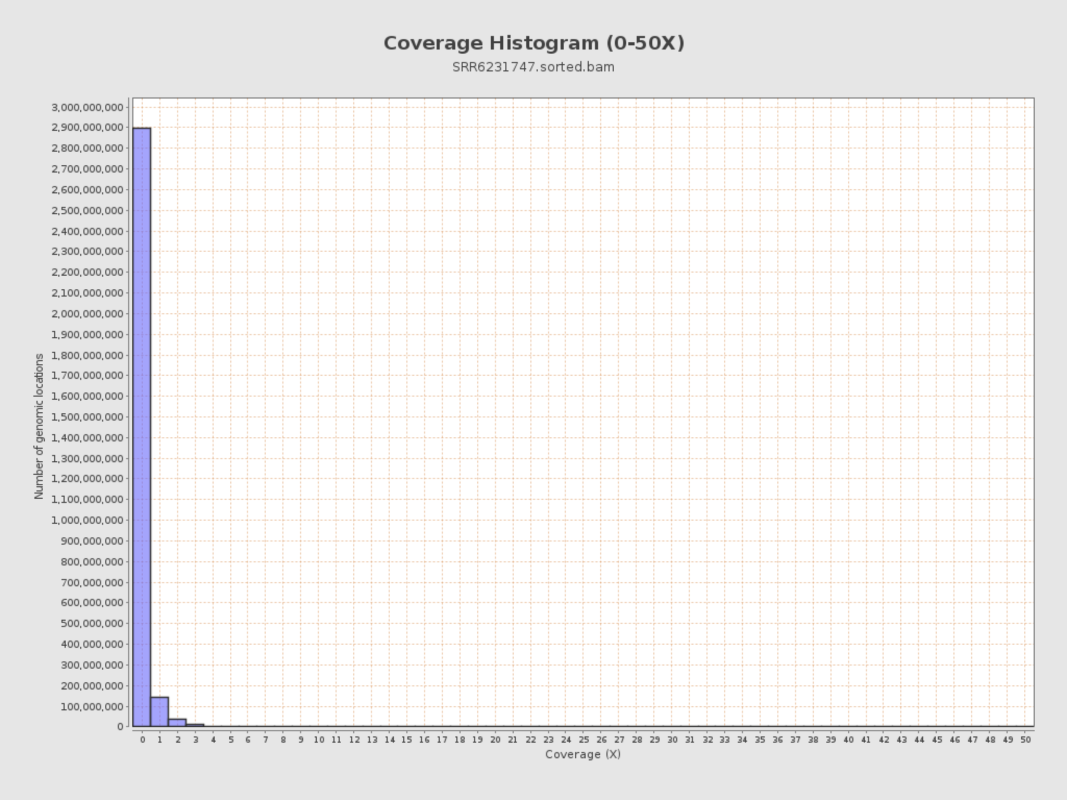
3. Results : Coverage across reference



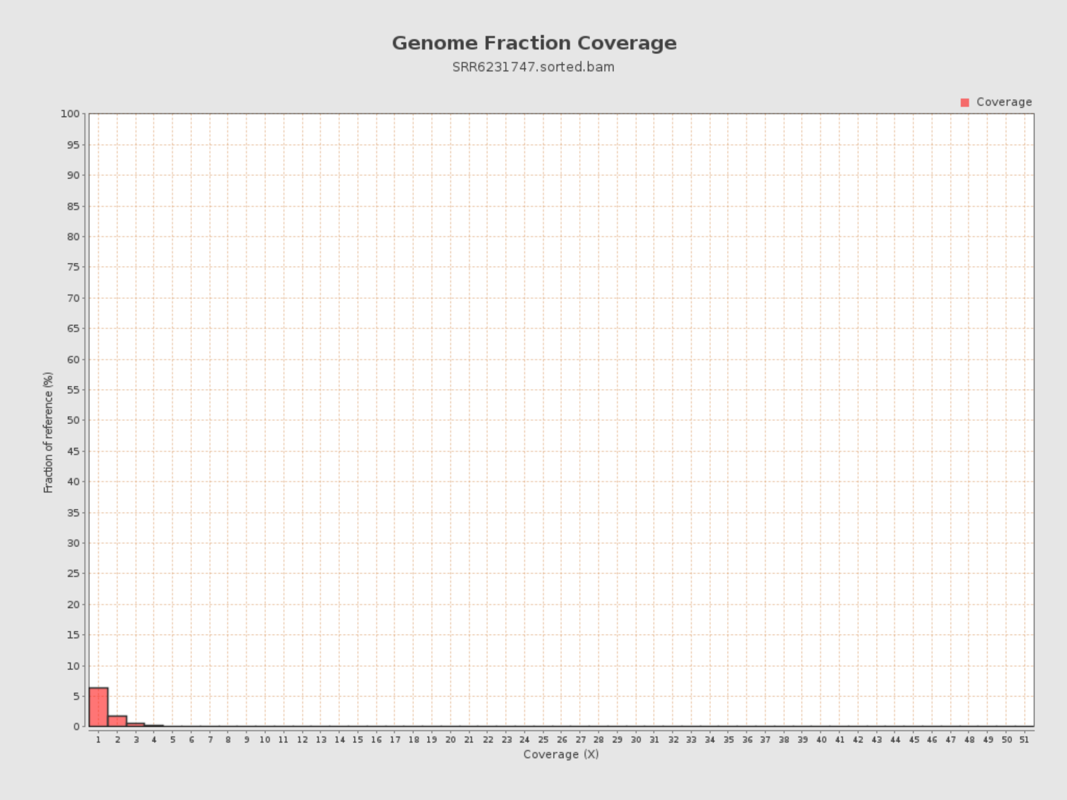
4. Results : Coverage Histogram



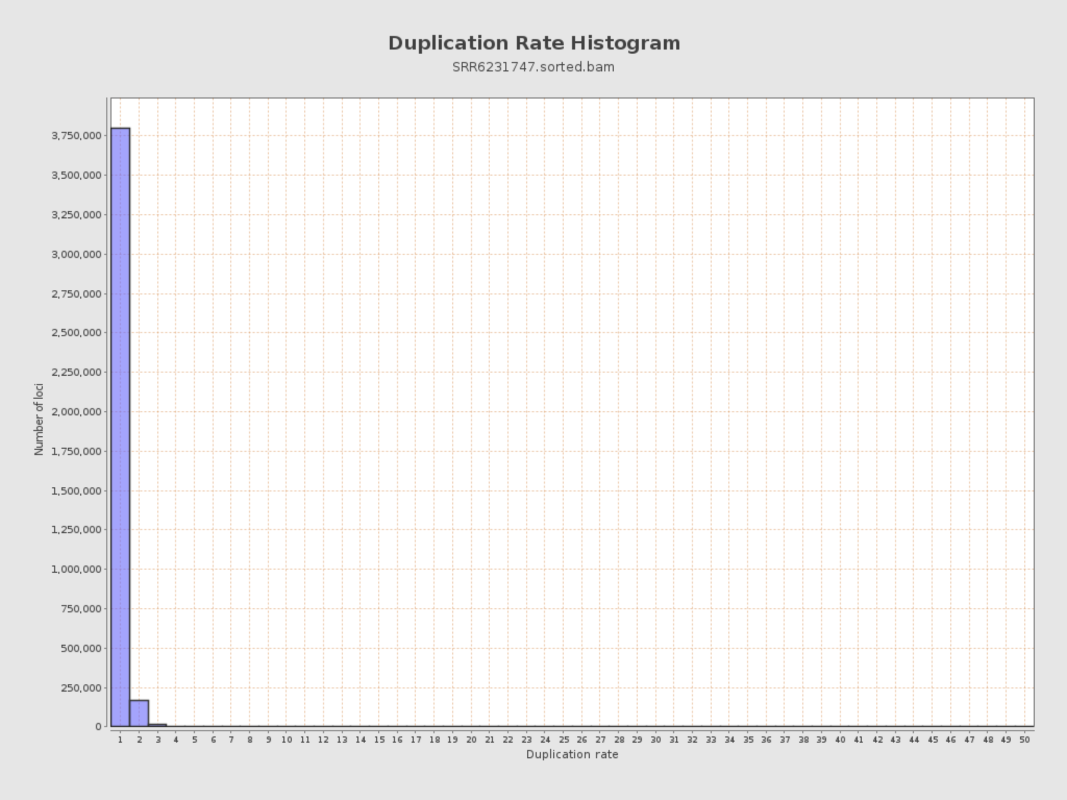
5. Results : Coverage Histogram (0-50X)



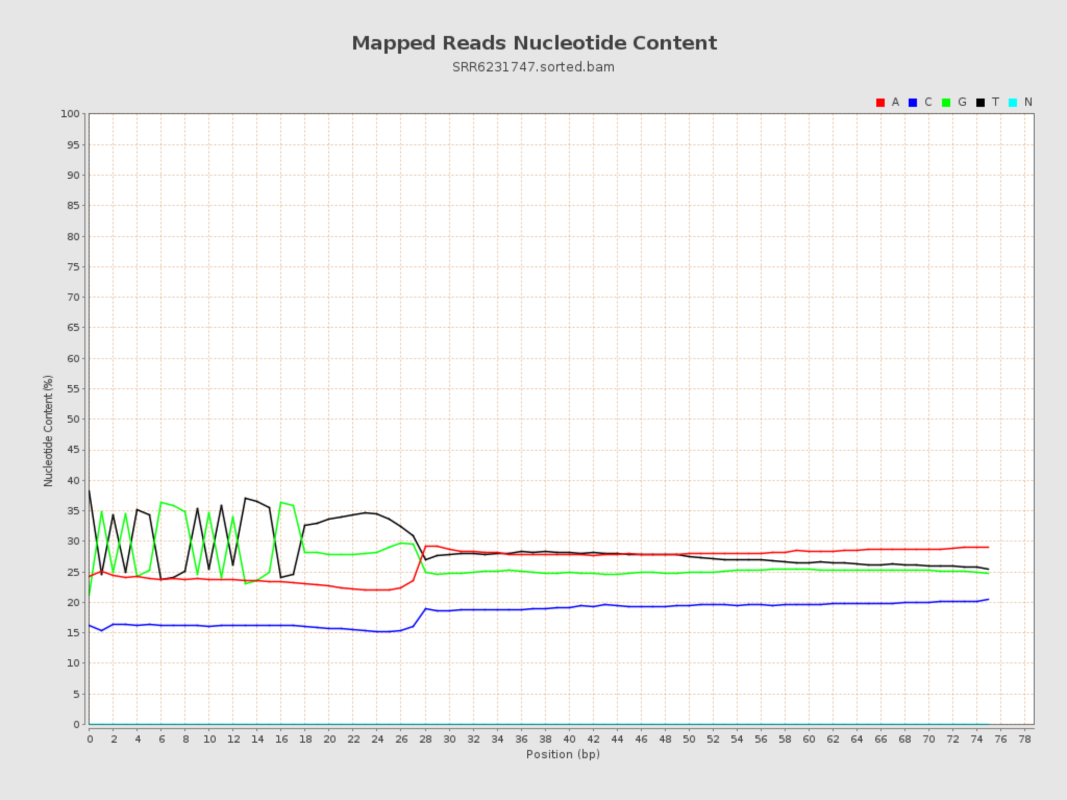
6. Results : Genome Fraction Coverage



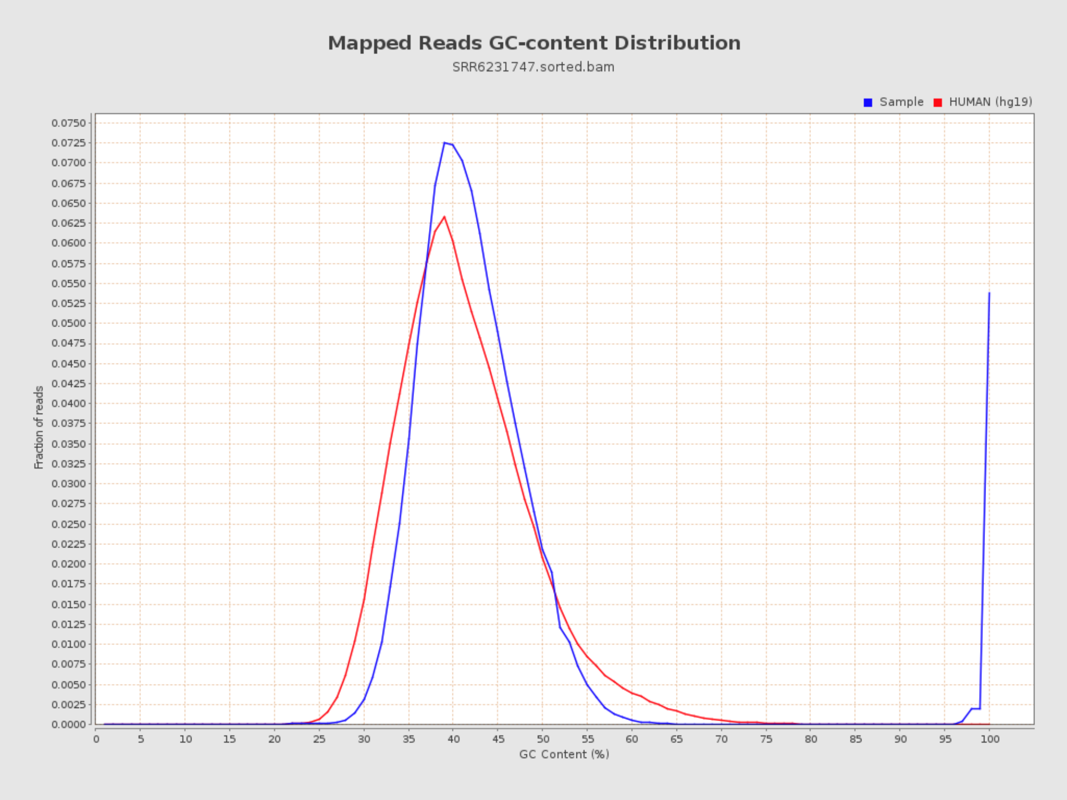
7. Results : Duplication Rate Histogram



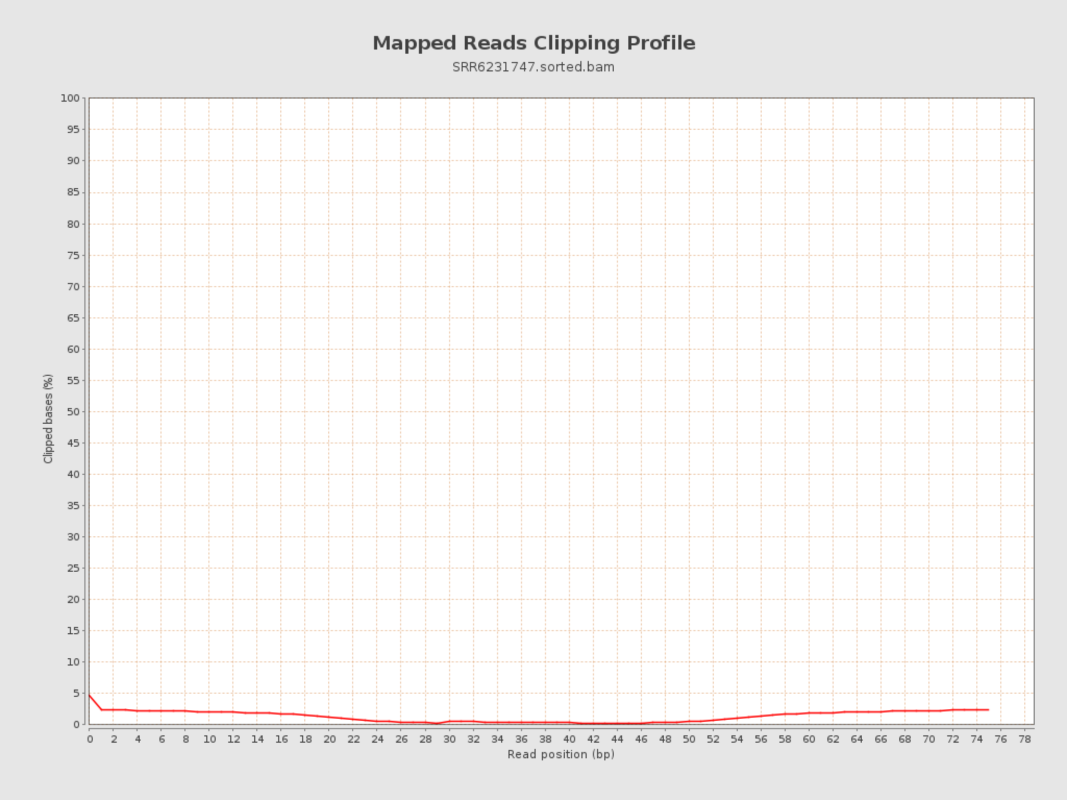
8. Results : Mapped Reads Nucleotide Content



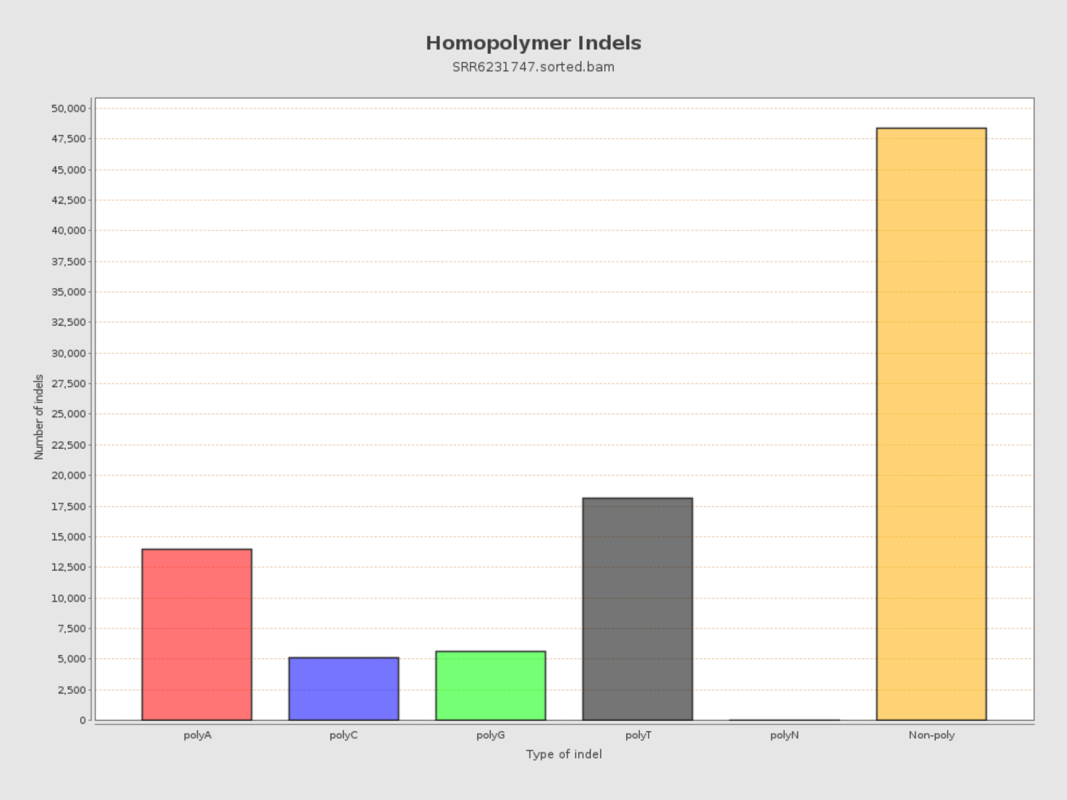
9. Results : Mapped Reads GC-content Distribution



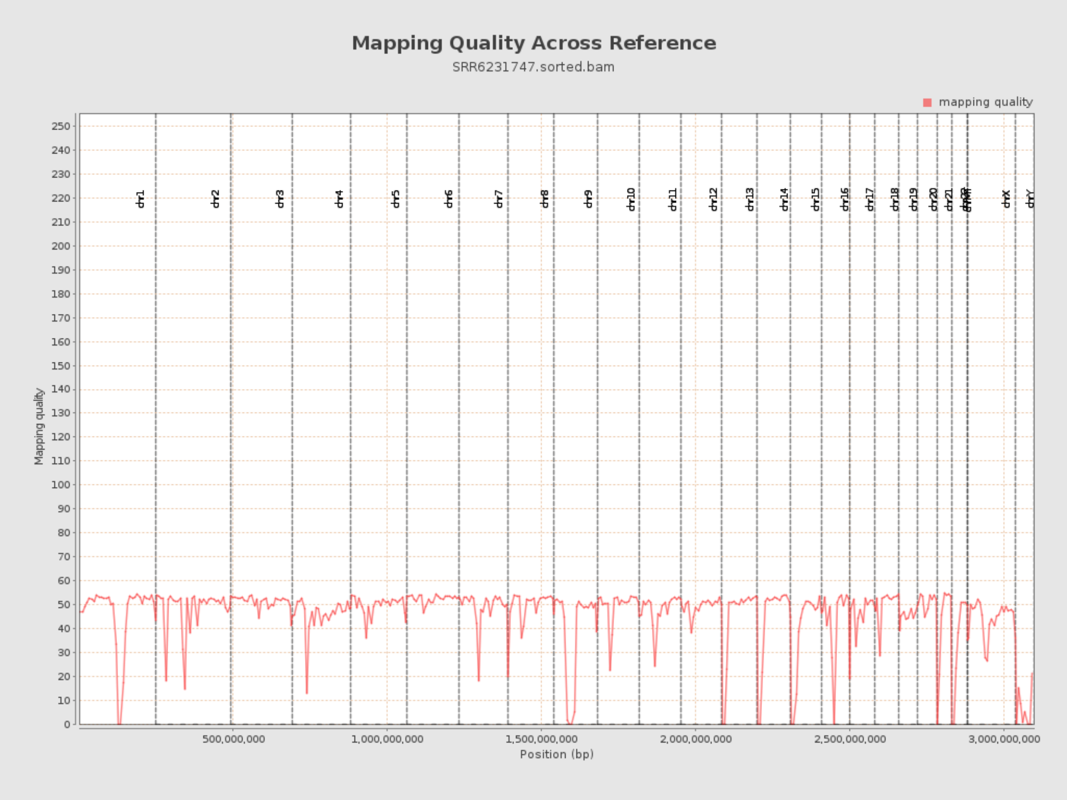
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram