Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:05:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081122.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_SRR3081122 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081122.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:05:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081122.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,529,577
Mapped reads	2,335,178 / 92.31%
Unmapped reads	194,399 / 7.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,260 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	105,319 / 4.16%
Duplication rate	2.87%
Clipped reads	874,911 / 34.59%

2.2. ACGT Content

Number/percentage of A's	45,360,134 / 28.32%
Number/percentage of C's	30,926,174 / 19.31%
Number/percentage of T's	48,998,514 / 30.6%
Number/percentage of G's	34,858,829 / 21.77%
Number/percentage of N's	1,840 / 0%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0518

Standard Deviation	0.5822

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

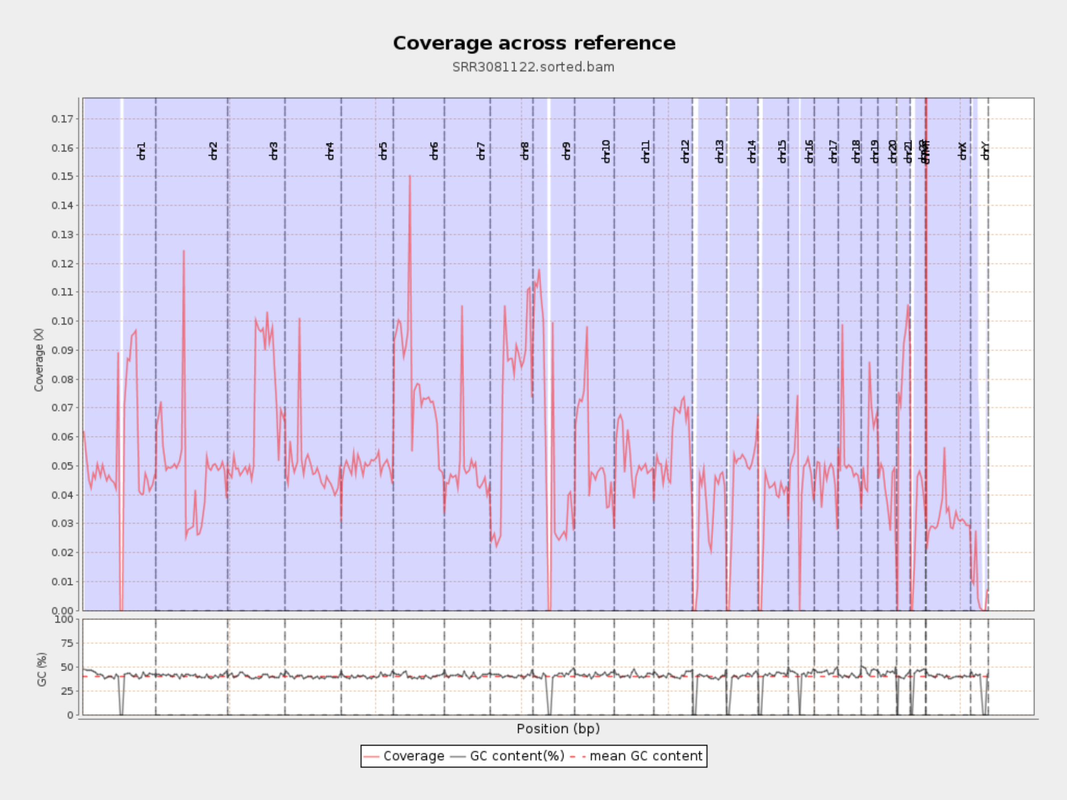
General error rate	0.92%
Mismatches	1,446,064
Insertions	13,201
Mapped reads with at least one insertion	0.56%
Deletions	35,196
Mapped reads with at least one deletion	1.49%
Homopolymer indels	46.48%

2.6. Chromosome stats

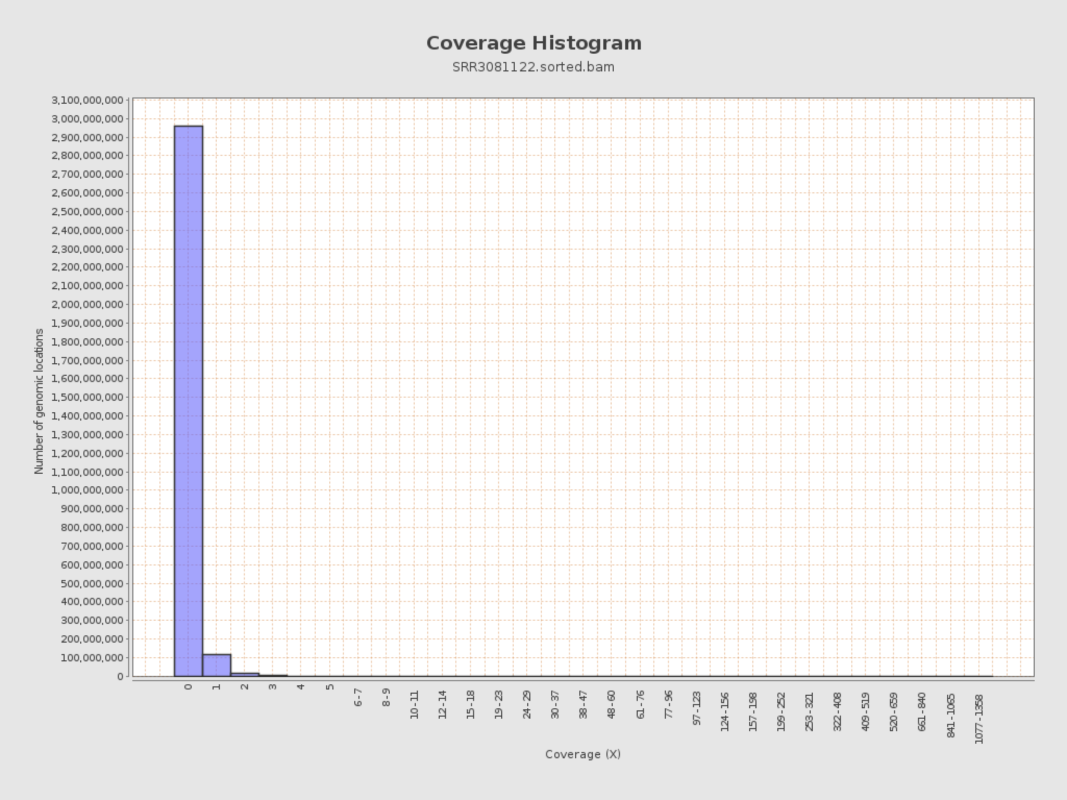
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13070807	0.0524	0.9081
chr2	243199373	11783767	0.0485	0.6733
chr3	198022430	13415973	0.0677	0.301
chr4	191154276	9524433	0.0498	0.3175
chr5	180915260	9072924	0.0502	0.2654
chr6	171115067	13624635	0.0796	0.6358
chr7	159138663	7765015	0.0488	0.7744

chr8	146364022	10667654	0.0729	0.5591
chr9	141213431	7685920	0.0544	0.778
chr10	135534747	7403392	0.0546	0.4765
chr11	135006516	7072277	0.0524	0.4682
chr12	133851895	7743588	0.0579	0.3248
chr13	115169878	3826179	0.0332	0.2022
chr14	107349540	4754413	0.0443	0.4243
chr15	102531392	3609473	0.0352	0.222
chr16	90354753	4125155	0.0457	0.4039
chr17	81195210	3743902	0.0461	0.2784
chr18	78077248	4175320	0.0535	1.5899
chr19	59128983	3488521	0.059	0.7008
chr20	63025520	2682322	0.0426	0.2932
chr21	48129895	3875192	0.0805	0.4618
chr22	51304566	1566122	0.0305	0.1944
chrMT	16571	159192	9.6067	6.0065
chrX	155270560	4936663	0.0318	0.2964
chrY	59373566	435710	0.0073	0.2187

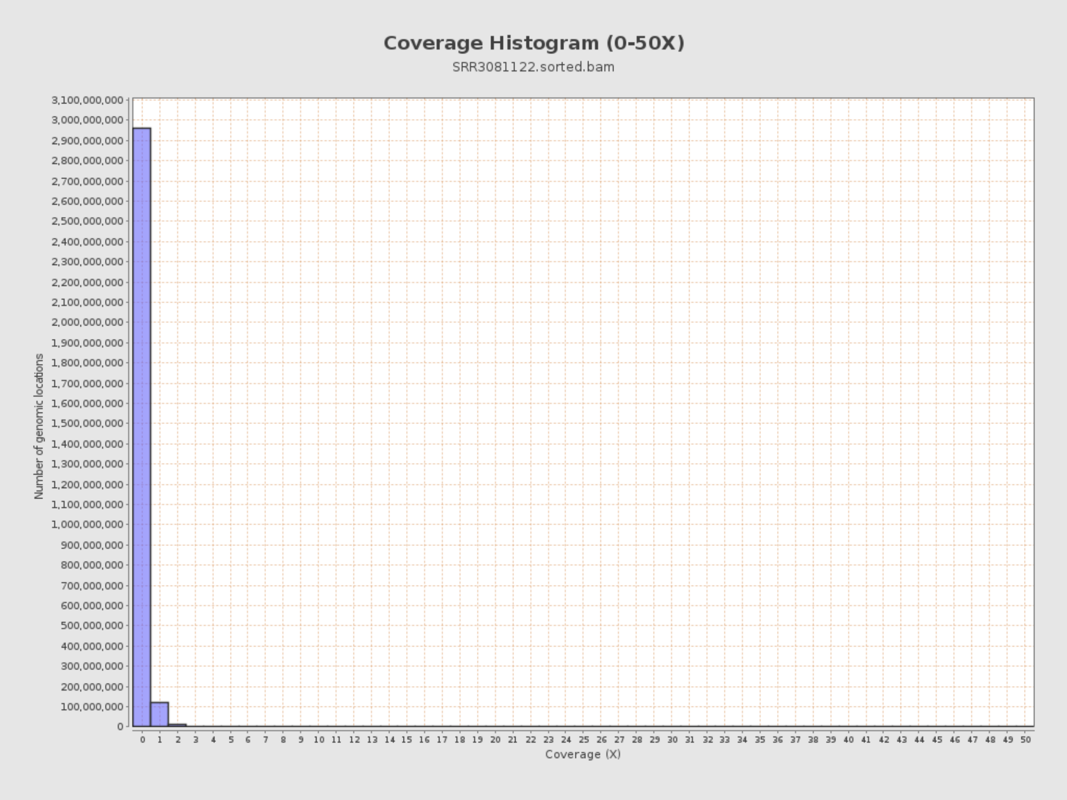
3. Results : Coverage across reference



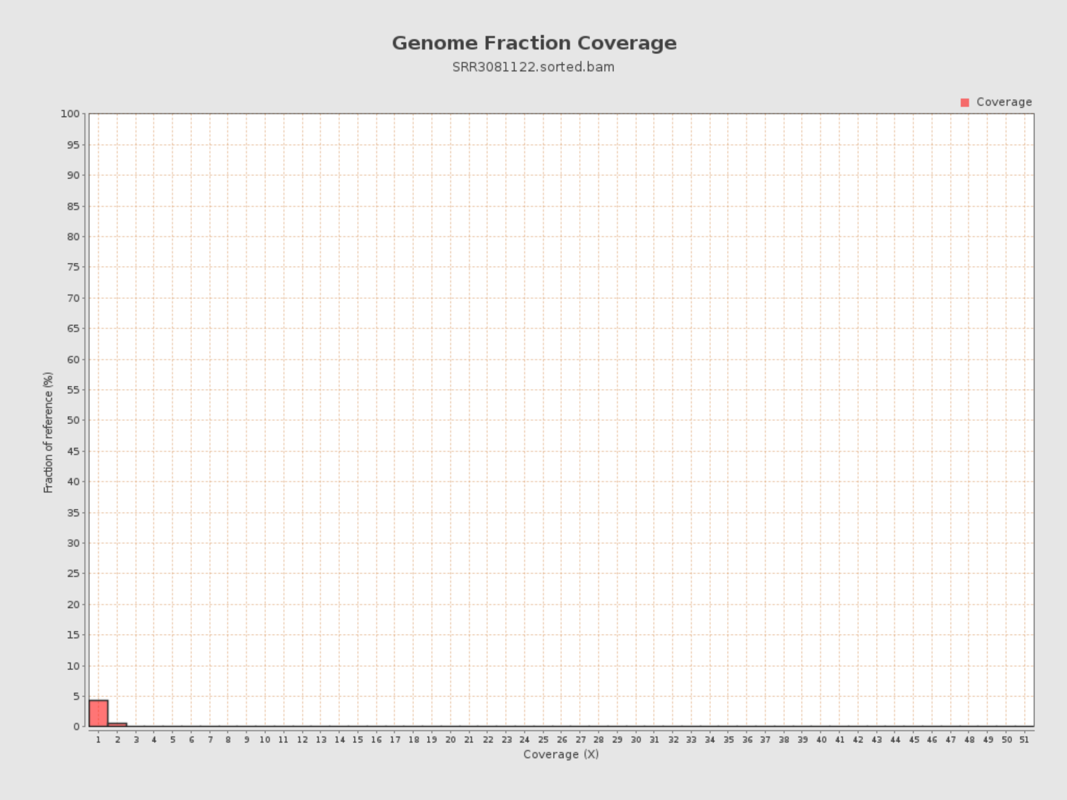
4. Results : Coverage Histogram



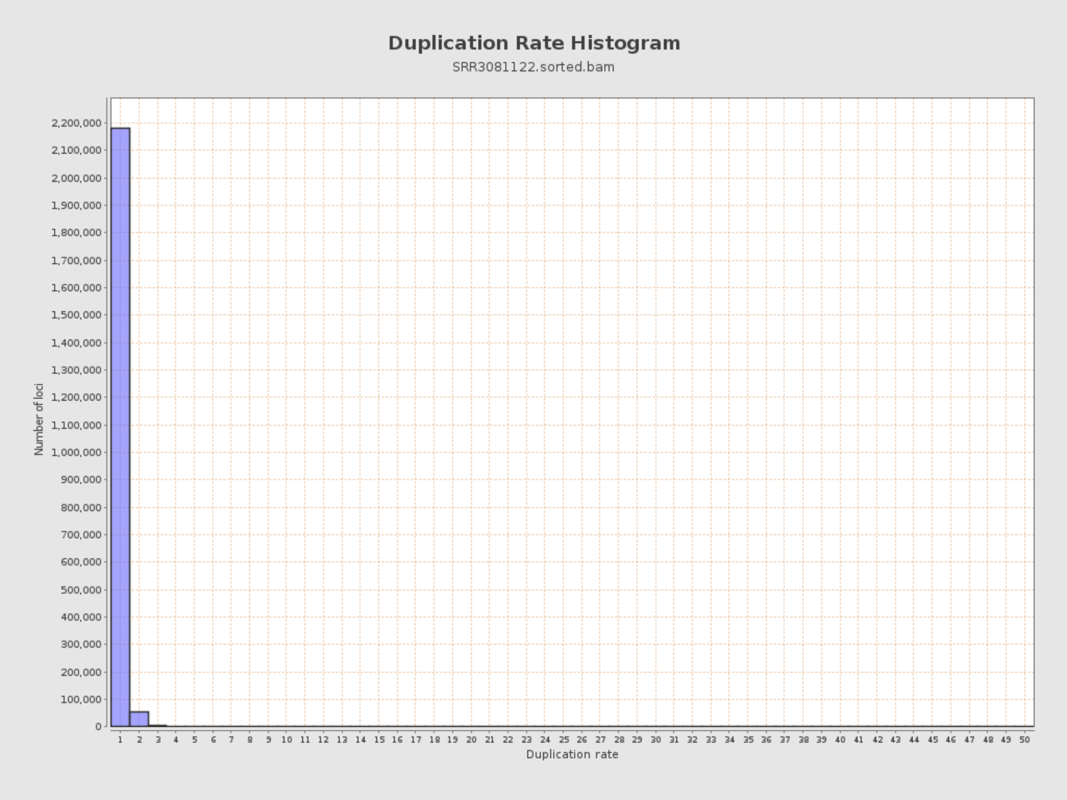
5. Results : Coverage Histogram (0-50X)



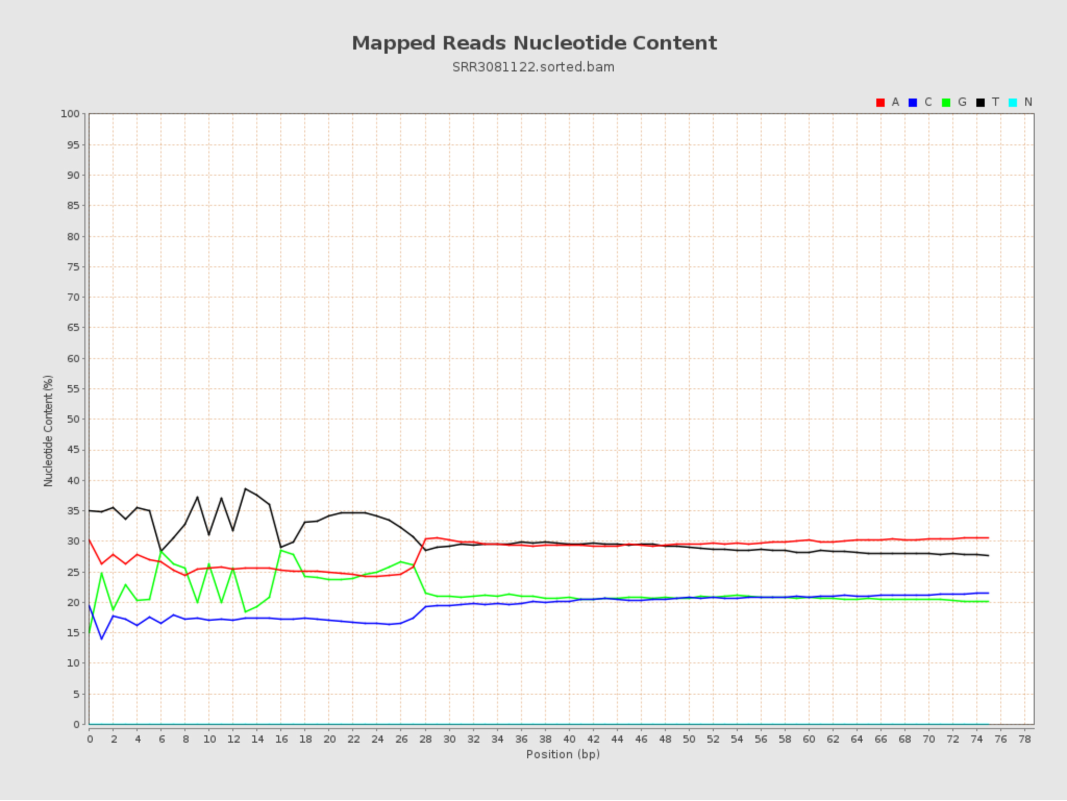
6. Results : Genome Fraction Coverage



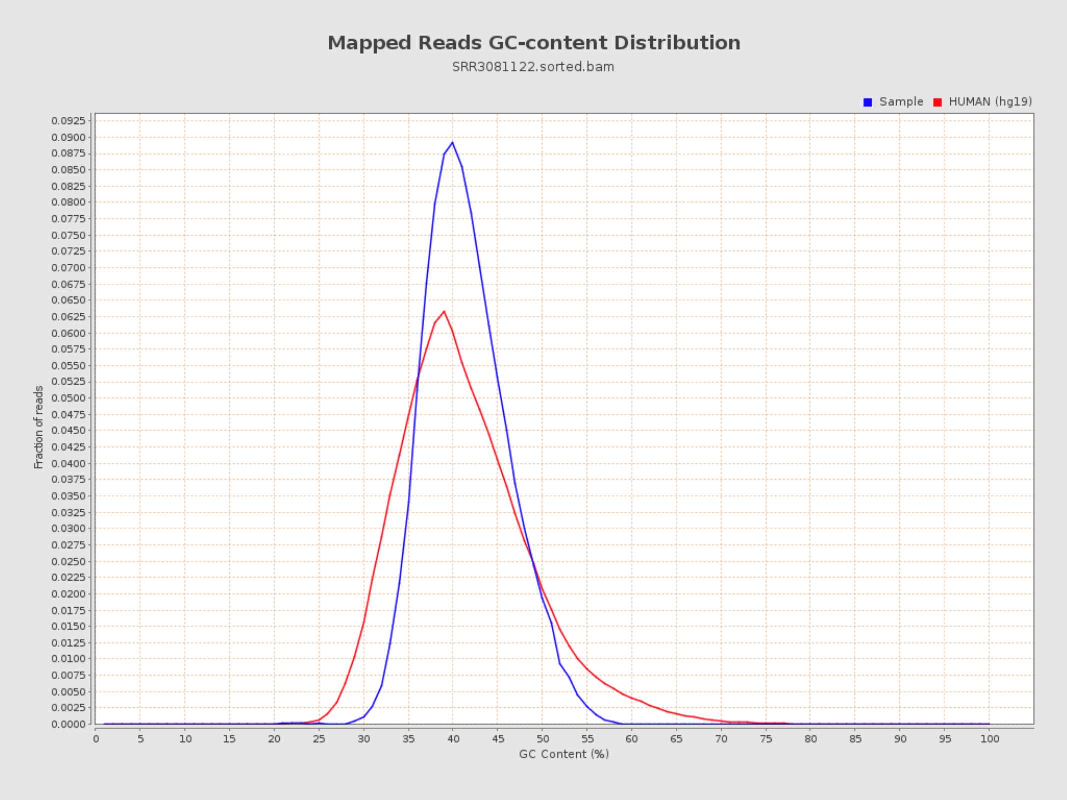
7. Results : Duplication Rate Histogram



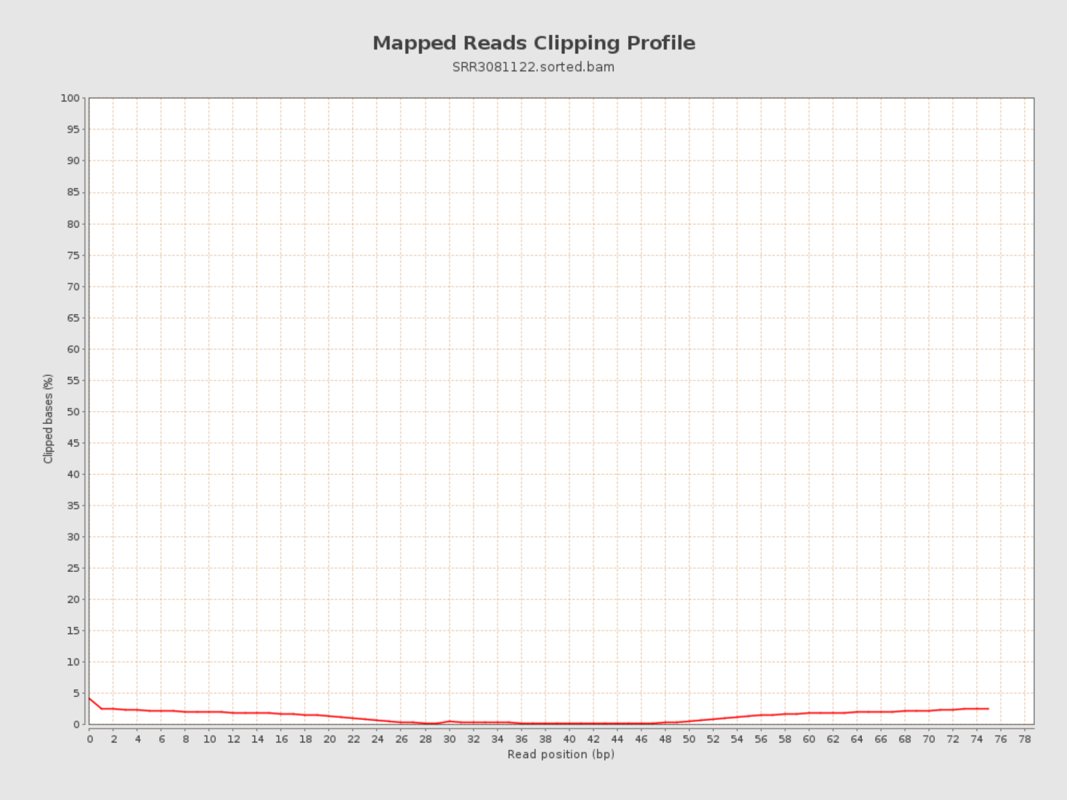
8. Results : Mapped Reads Nucleotide Content



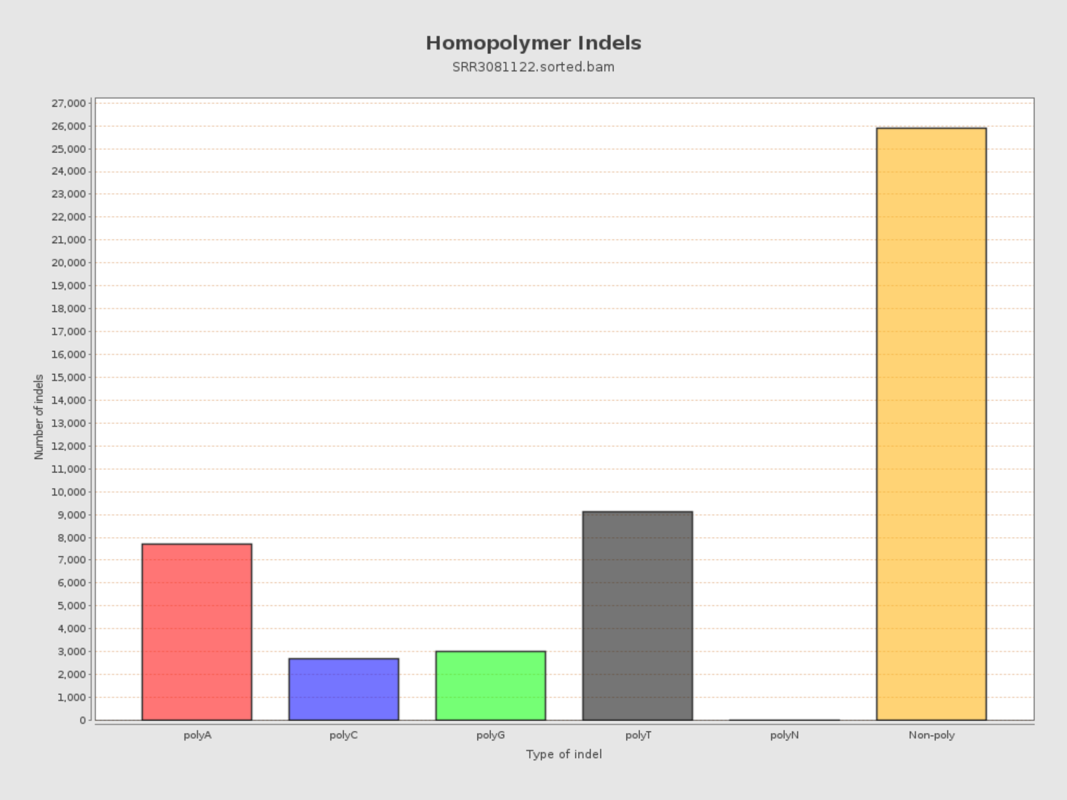
9. Results : Mapped Reads GC-content Distribution



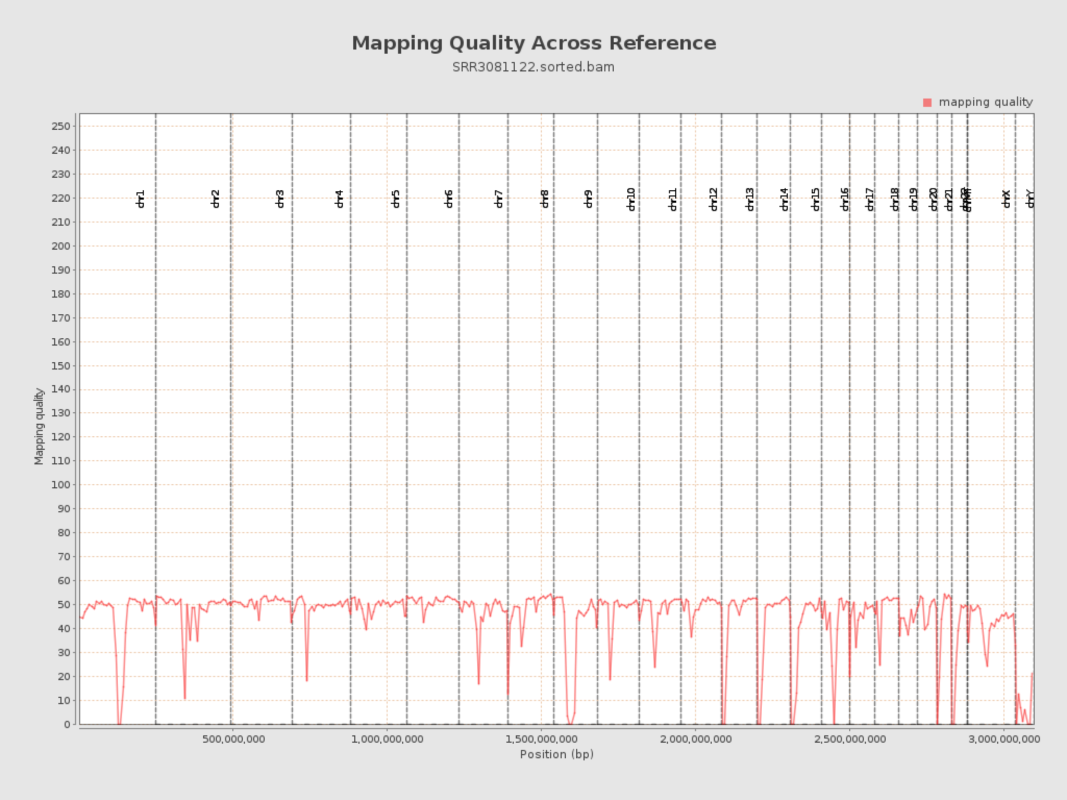
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram