Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:16:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081960.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_SRR3081960 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081960.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:16:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081960.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,605,771
Mapped reads	3,328,757 / 92.32%
Unmapped reads	277,014 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,116 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	149,404 / 4.14%
Duplication rate	3.38%
Clipped reads	1,021,735 / 28.34%

2.2. ACGT Content

Number/percentage of A's	67,876,731 / 29.21%
Number/percentage of C's	43,121,566 / 18.56%
Number/percentage of T's	73,591,530 / 31.67%
Number/percentage of G's	47,738,028 / 20.55%
Number/percentage of N's	30,447 / 0.01%
GC Percentage	39.1%

2.3. Coverage

Mean	0.0751

Standard Deviation	0.634

2.4. Mapping Quality

Mean Mapping Quality	47.4

2.5. Mismatches and indels

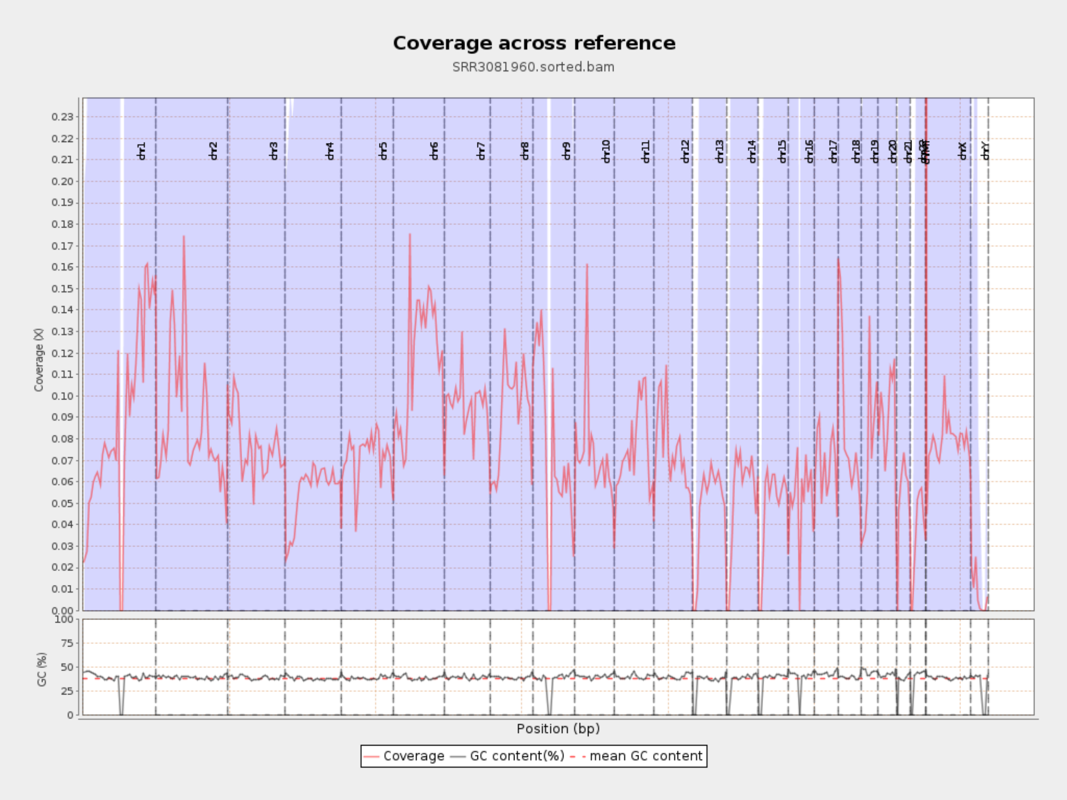
General error rate	0.77%
Mismatches	1,750,774
Insertions	16,497
Mapped reads with at least one insertion	0.49%
Deletions	52,172
Mapped reads with at least one deletion	1.55%
Homopolymer indels	48.02%

2.6. Chromosome stats

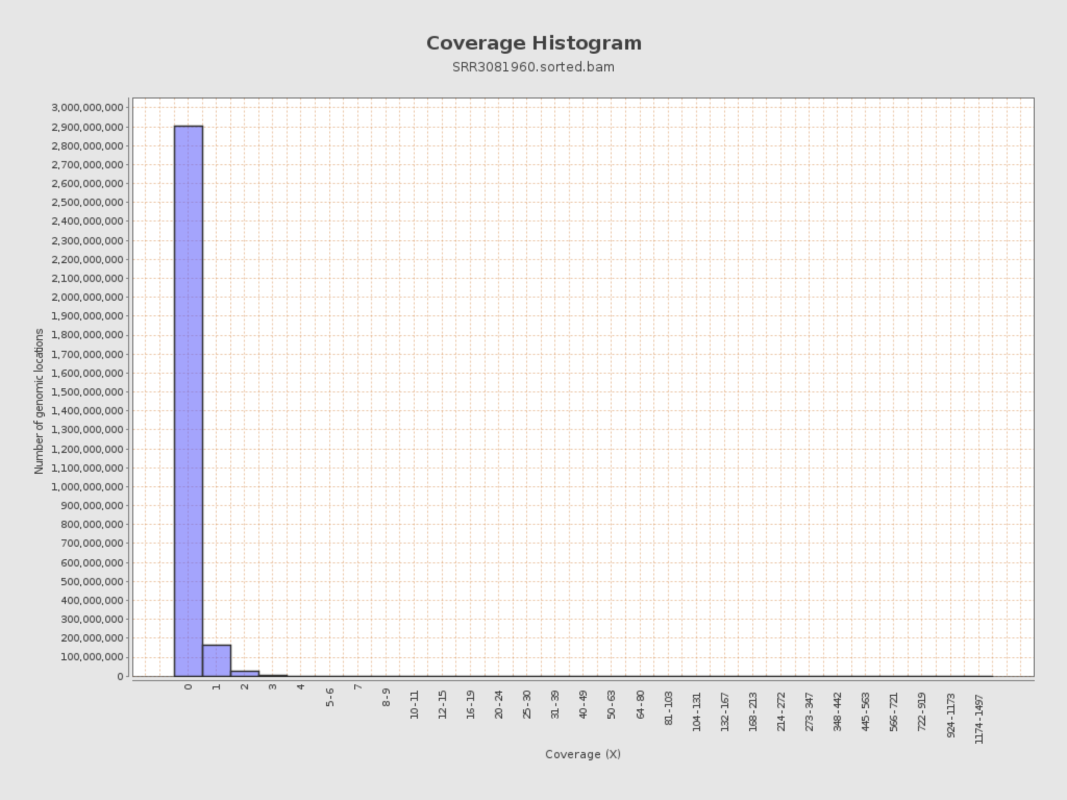
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21913614	0.0879	1.347
chr2	243199373	21435521	0.0881	0.7328
chr3	198022430	15326708	0.0774	0.3286
chr4	191154276	10580107	0.0553	0.297
chr5	180915260	12860115	0.0711	0.3113
chr6	171115067	20215365	0.1181	0.5688
chr7	159138663	15185401	0.0954	0.7321

chr8	146364022	13585402	0.0928	0.8815
chr9	141213431	10573691	0.0749	0.5876
chr10	135534747	9961475	0.0735	0.7181
chr11	135006516	10230725	0.0758	0.4118
chr12	133851895	9938804	0.0743	0.3266
chr13	115169878	5560236	0.0483	0.2504
chr14	107349540	5819902	0.0542	0.2954
chr15	102531392	4866557	0.0475	0.2502
chr16	90354753	4594467	0.0508	0.341
chr17	81195210	5665961	0.0698	0.3458
chr18	78077248	6706612	0.0859	0.8855
chr19	59128983	4367317	0.0739	0.9099
chr20	63025520	5857986	0.0929	0.3585
chr21	48129895	2540446	0.0528	0.3064
chr22	51304566	1830591	0.0357	0.2131
chrMT	16571	113694	6.861	4.2023
chrX	155270560	12245844	0.0789	0.3841
chrY	59373566	473211	0.008	0.1869

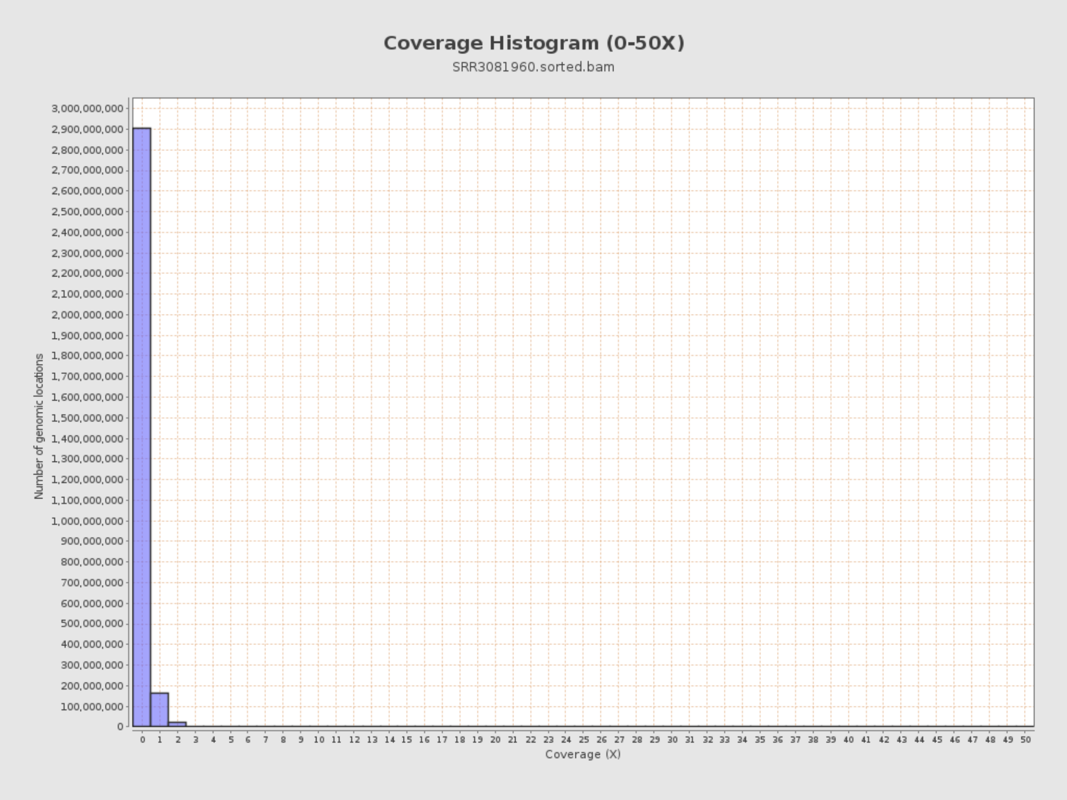
3. Results : Coverage across reference



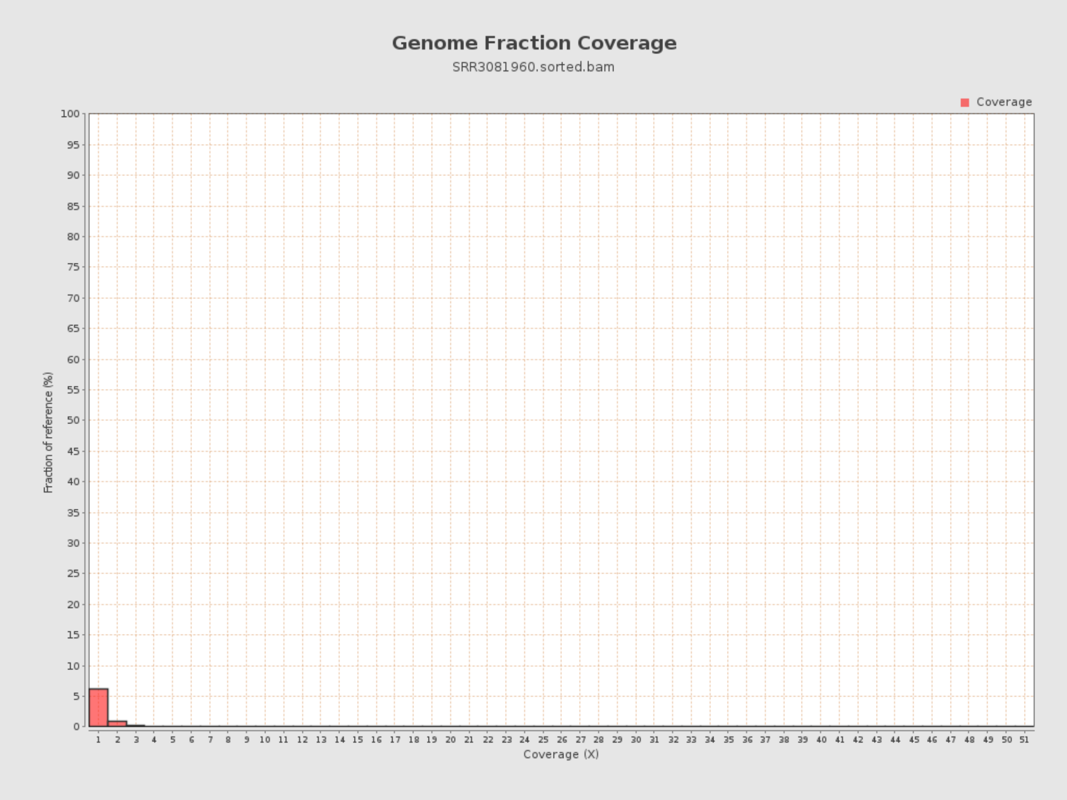
4. Results : Coverage Histogram



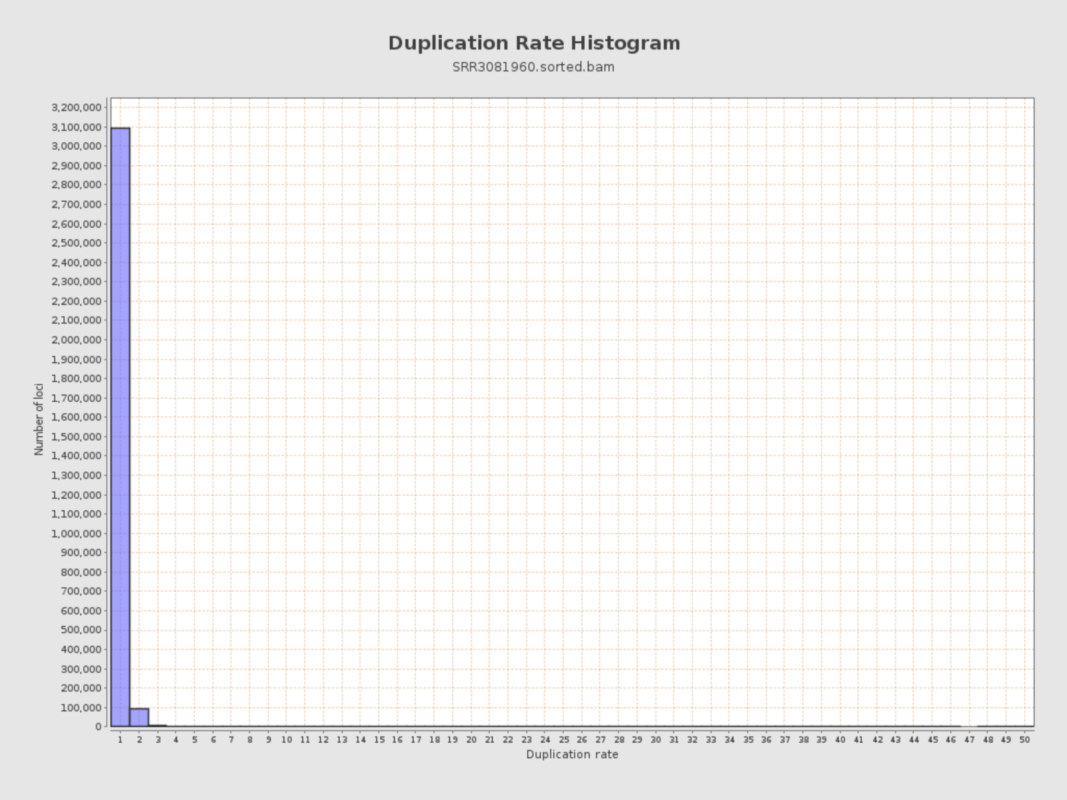
5. Results : Coverage Histogram (0-50X)



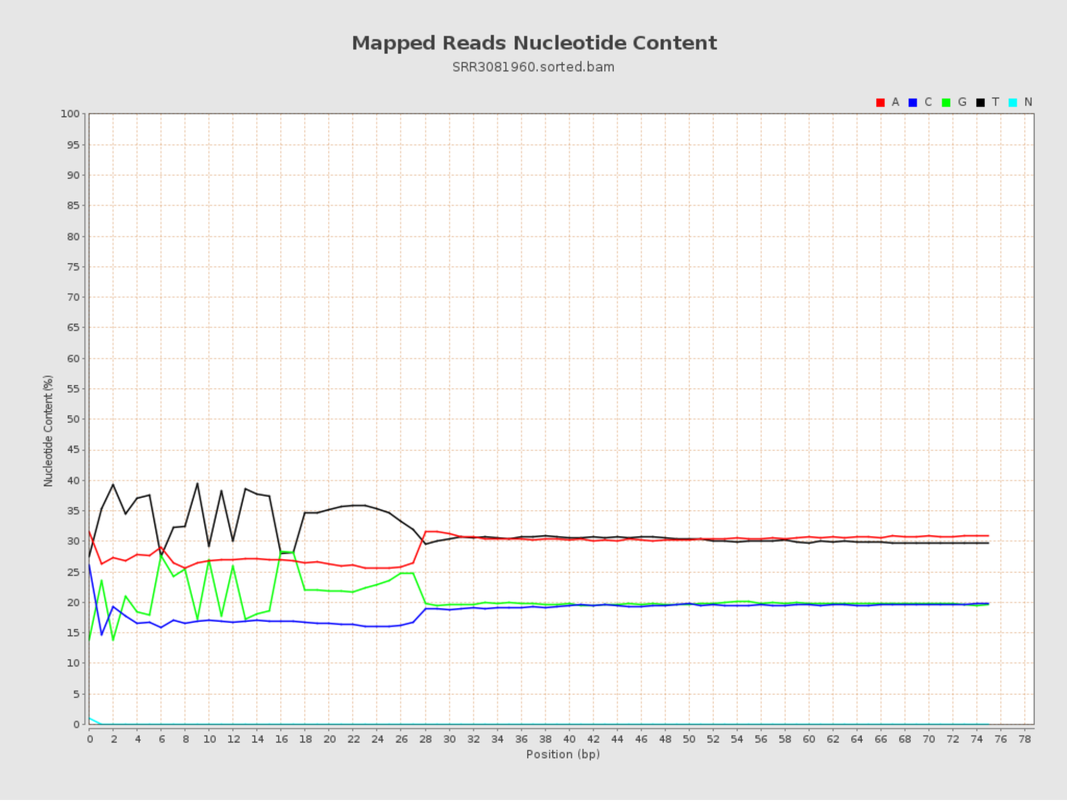
6. Results : Genome Fraction Coverage



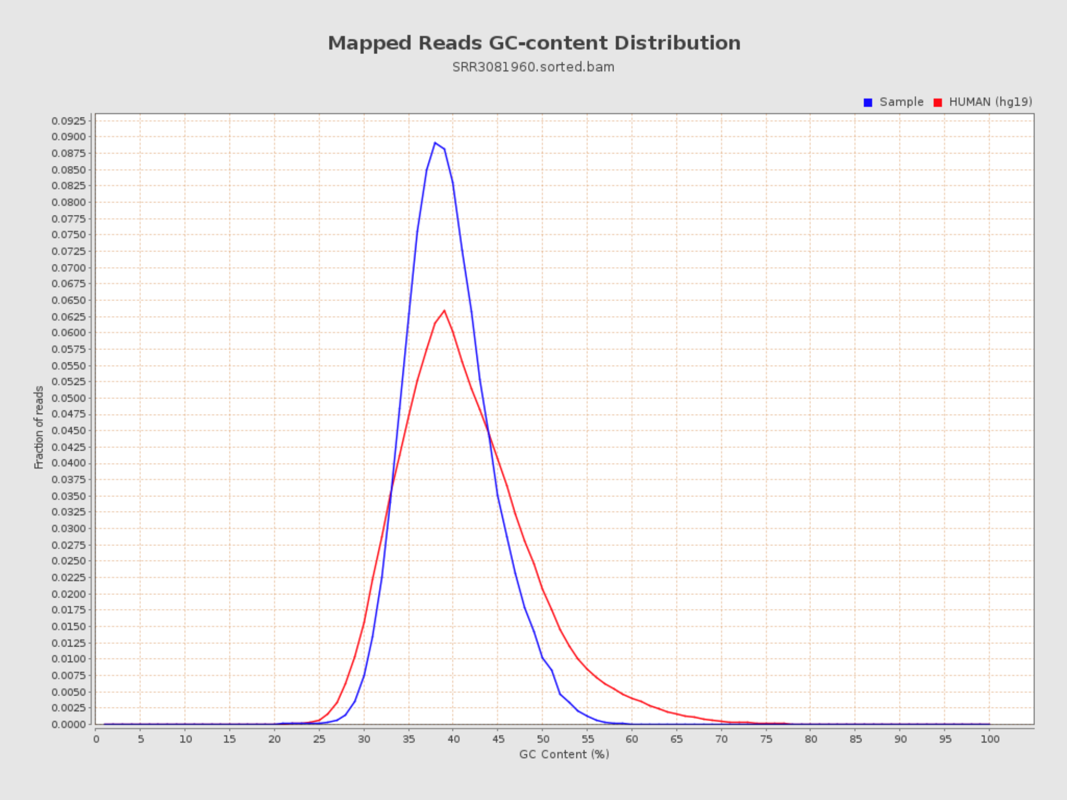
7. Results : Duplication Rate Histogram



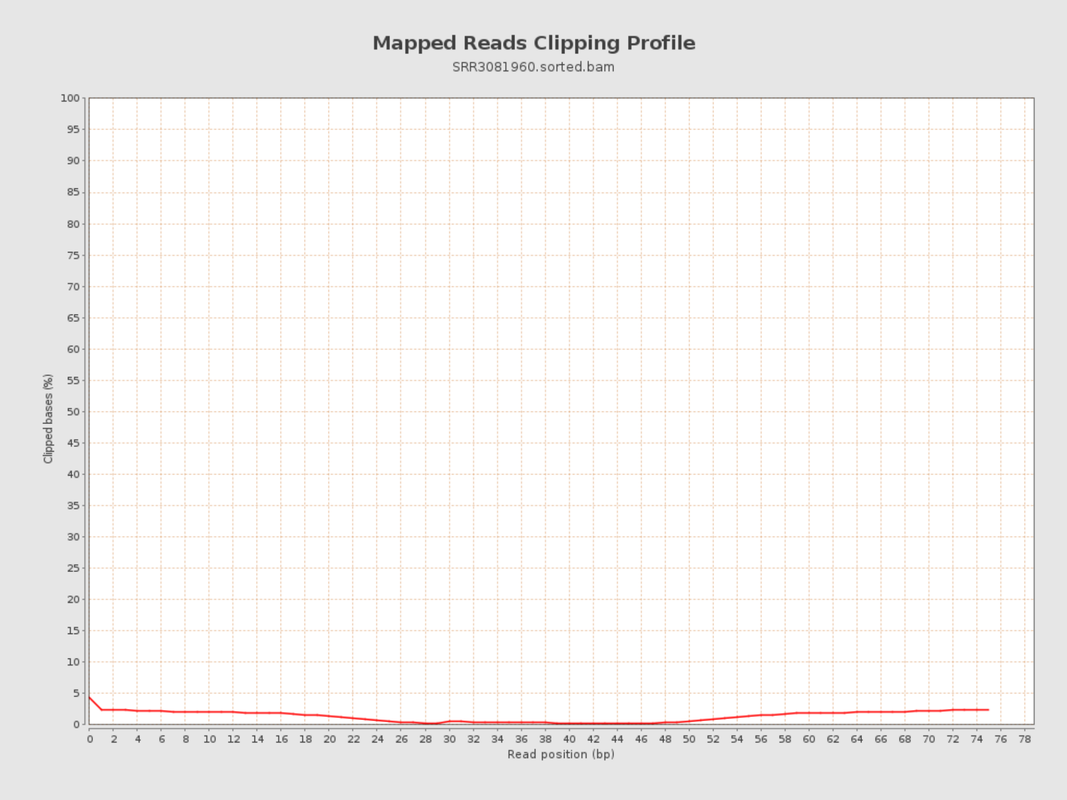
8. Results : Mapped Reads Nucleotide Content



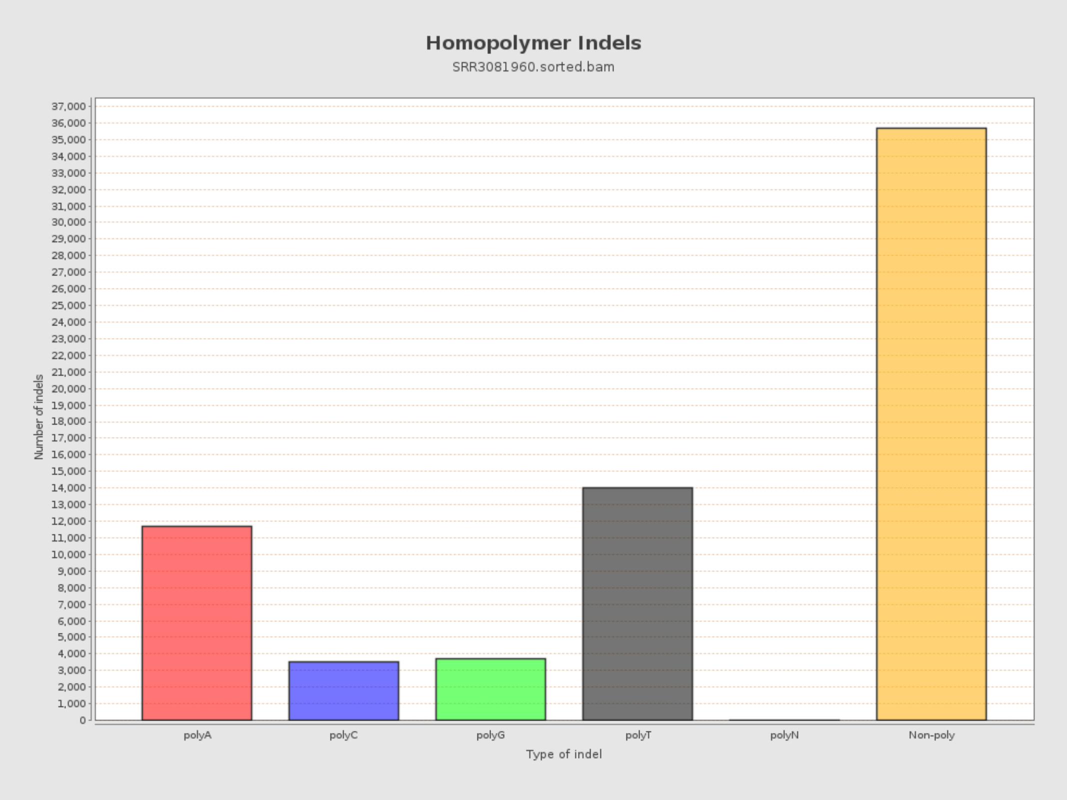
9. Results : Mapped Reads GC-content Distribution



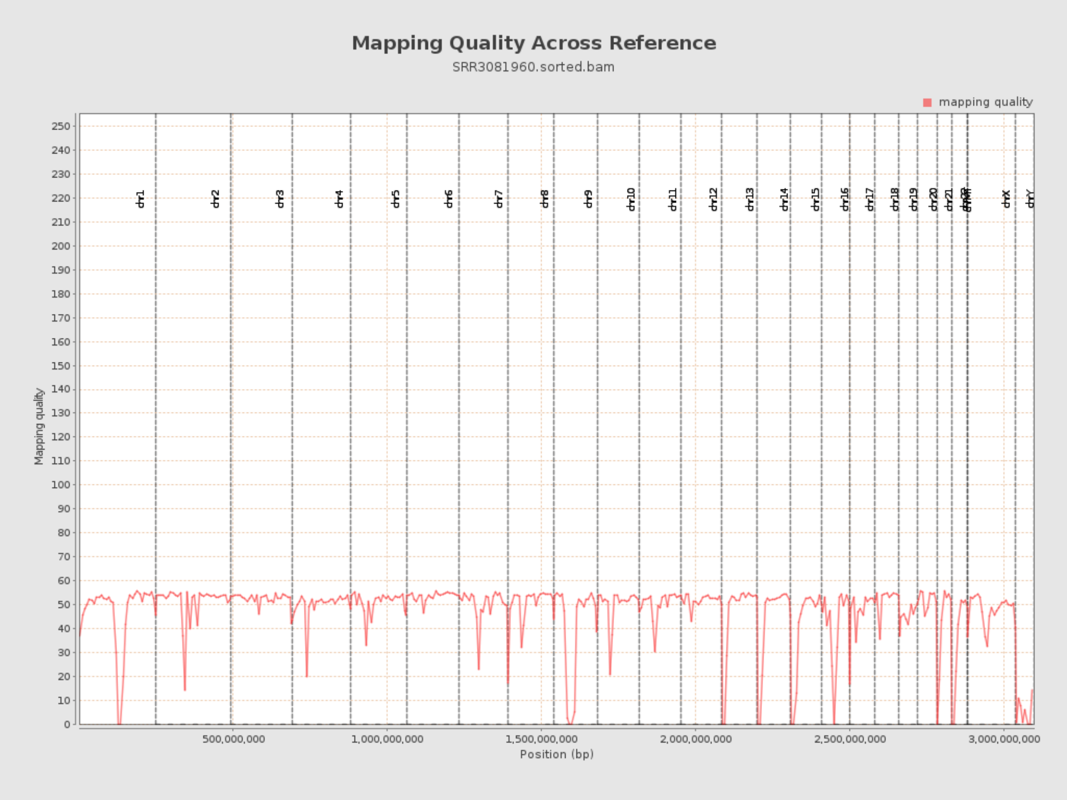
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram