Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:22:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081961.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_SRR3081961 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081961.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:22:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081961.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,672,757
Mapped reads	2,460,087 / 92.04%
Unmapped reads	212,670 / 7.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,363 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	103,863 / 3.89%
Duplication rate	3.14%
Clipped reads	768,757 / 28.76%

2.2. ACGT Content

Number/percentage of A's	49,960,203 / 29.12%
Number/percentage of C's	32,028,009 / 18.67%
Number/percentage of T's	54,204,664 / 31.6%
Number/percentage of G's	35,336,914 / 20.6%
Number/percentage of N's	22,245 / 0.01%
GC Percentage	39.27%

2.3. Coverage

Mean	0.0554

Standard Deviation	0.5024

2.4. Mapping Quality

Mean Mapping Quality	47.1

2.5. Mismatches and indels

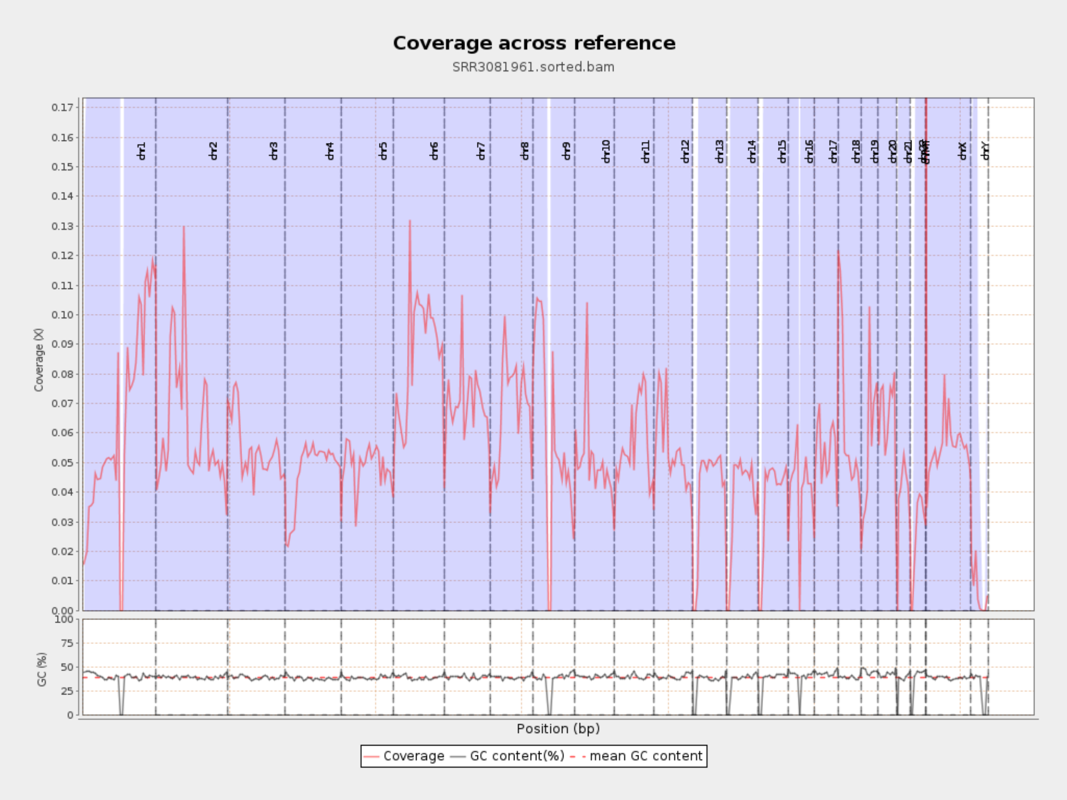
General error rate	0.79%
Mismatches	1,324,340
Insertions	12,696
Mapped reads with at least one insertion	0.51%
Deletions	37,554
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.19%

2.6. Chromosome stats

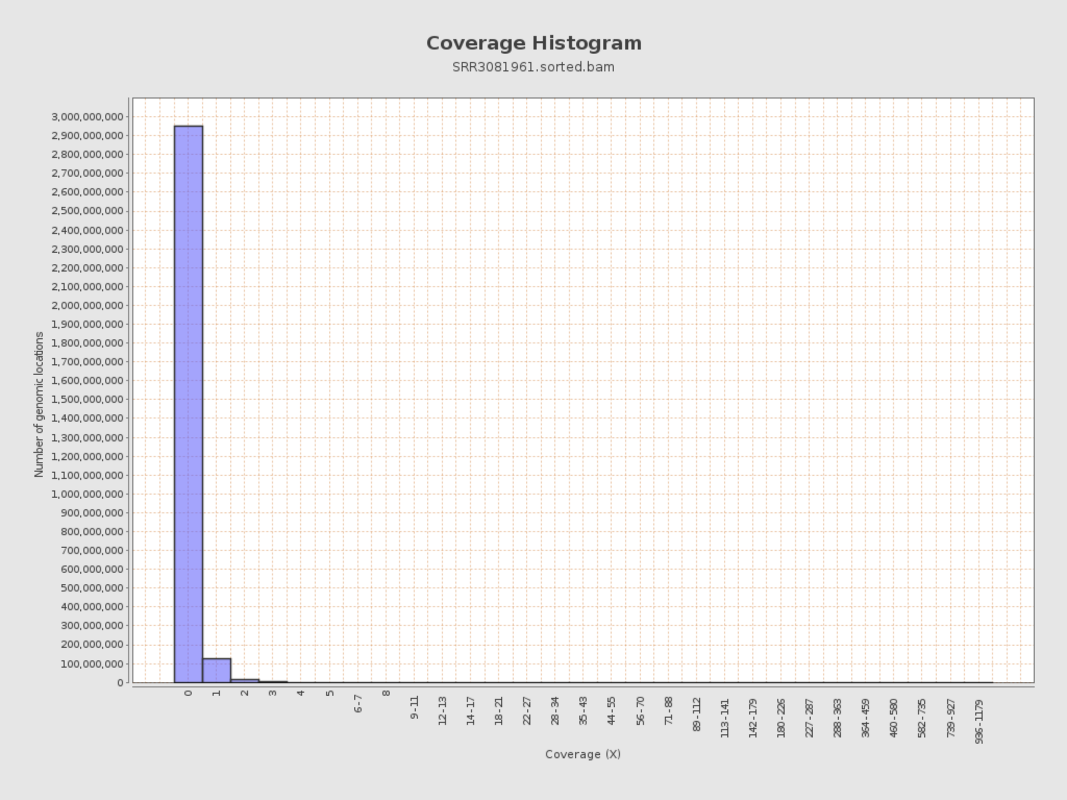
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15834619	0.0635	0.9245
chr2	243199373	15146872	0.0623	0.6113
chr3	198022430	10915270	0.0551	0.2679
chr4	191154276	8961739	0.0469	0.2621
chr5	180915260	8818562	0.0487	0.2523
chr6	171115067	15022386	0.0878	0.4699
chr7	159138663	11174523	0.0702	0.6645

chr8	146364022	10000607	0.0683	0.806
chr9	141213431	8444520	0.0598	0.5216
chr10	135534747	6903314	0.0509	0.4849
chr11	135006516	7683064	0.0569	0.3579
chr12	133851895	7328339	0.0547	0.2785
chr13	115169878	4645813	0.0403	0.2251
chr14	107349540	4119372	0.0384	0.2472
chr15	102531392	3800756	0.0371	0.2178
chr16	90354753	3648256	0.0404	0.2848
chr17	81195210	4445788	0.0548	0.2989
chr18	78077248	4939132	0.0633	0.8361
chr19	59128983	3384066	0.0572	0.6271
chr20	63025520	4230016	0.0671	0.299
chr21	48129895	1841813	0.0383	0.2566
chr22	51304566	1314859	0.0256	0.1779
chrMT	16571	10484	0.6327	0.8589
chrX	155270560	8628821	0.0556	0.3123
chrY	59373566	375106	0.0063	0.16

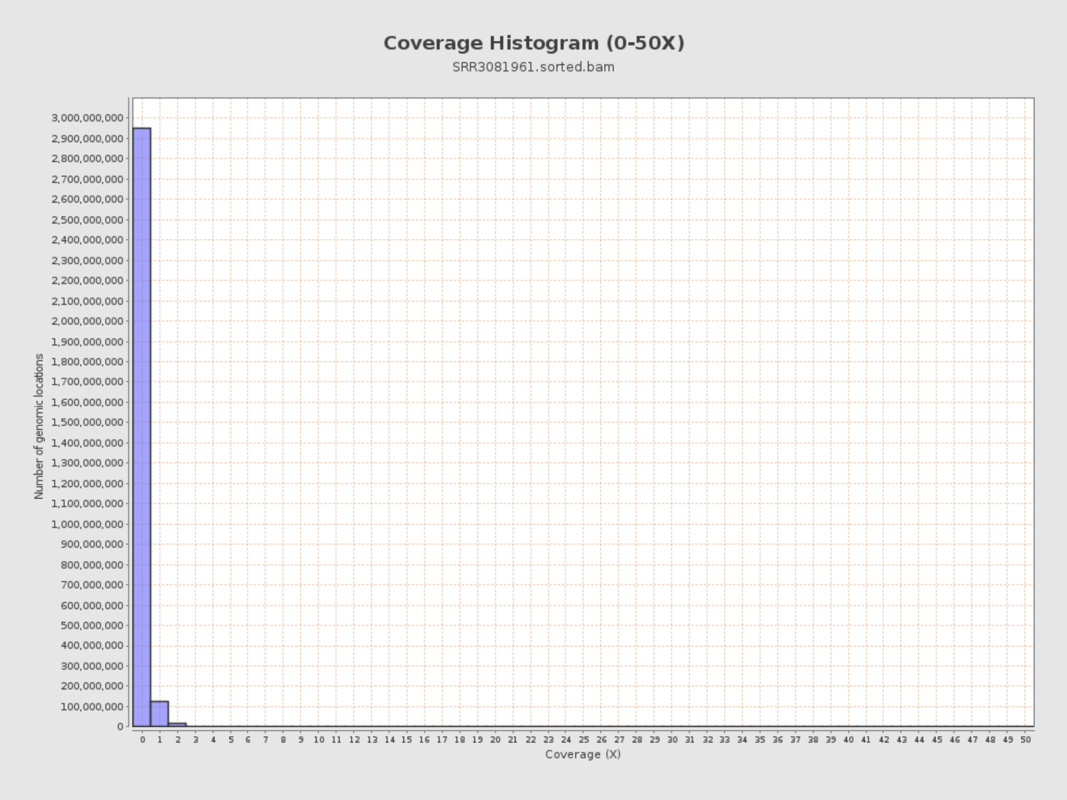
3. Results : Coverage across reference



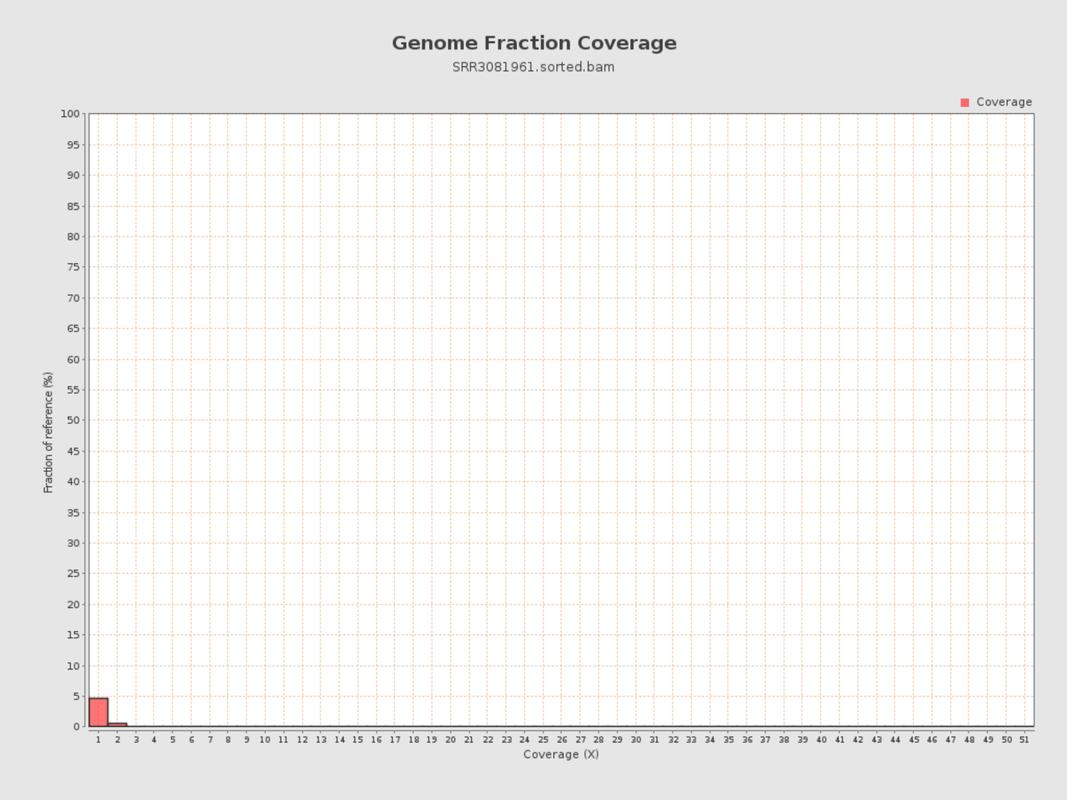
4. Results : Coverage Histogram



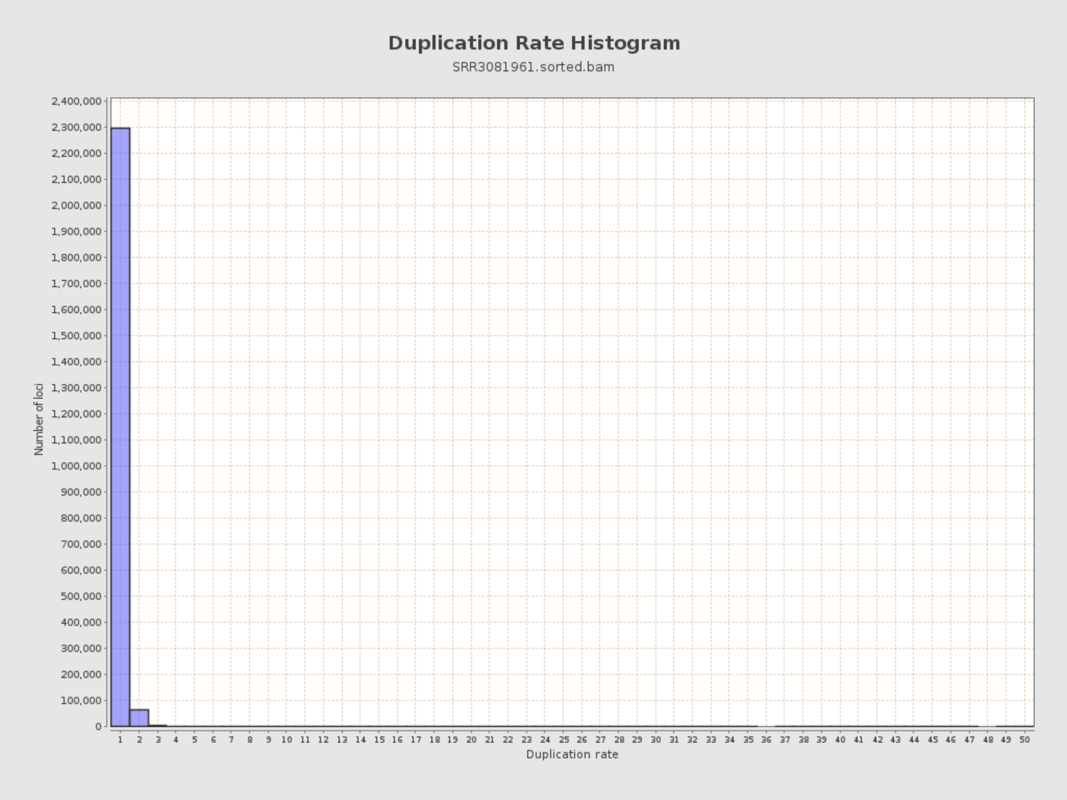
5. Results : Coverage Histogram (0-50X)



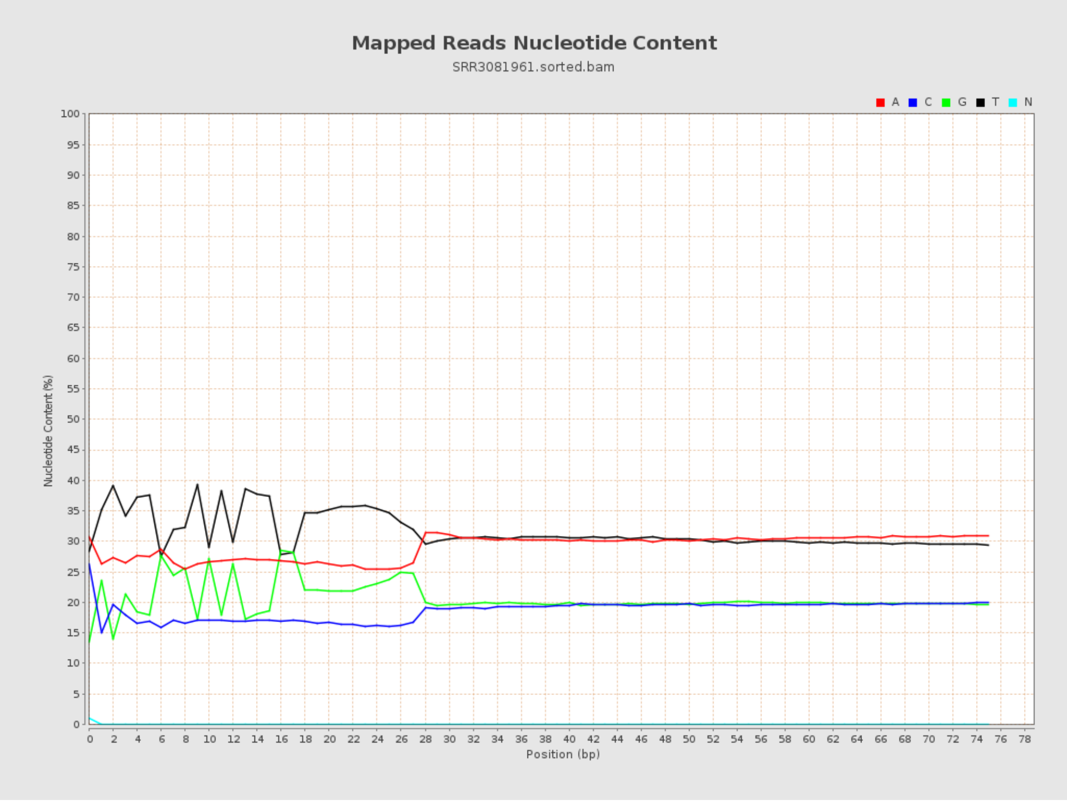
6. Results : Genome Fraction Coverage



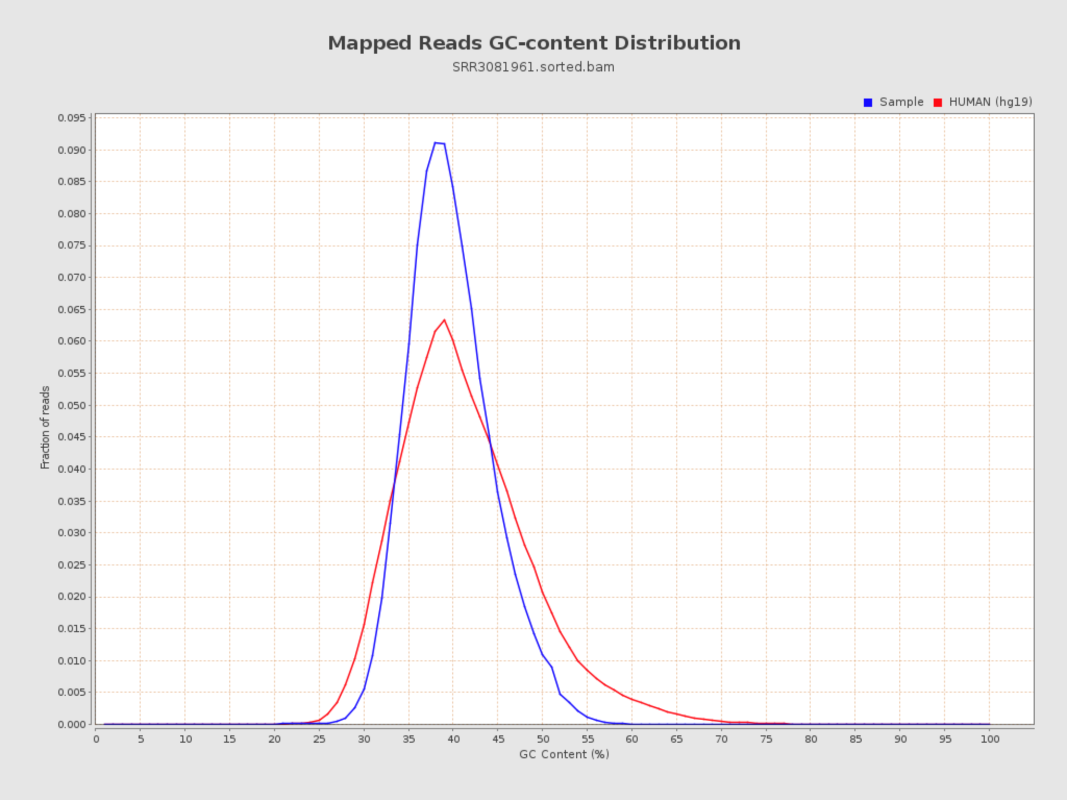
7. Results : Duplication Rate Histogram



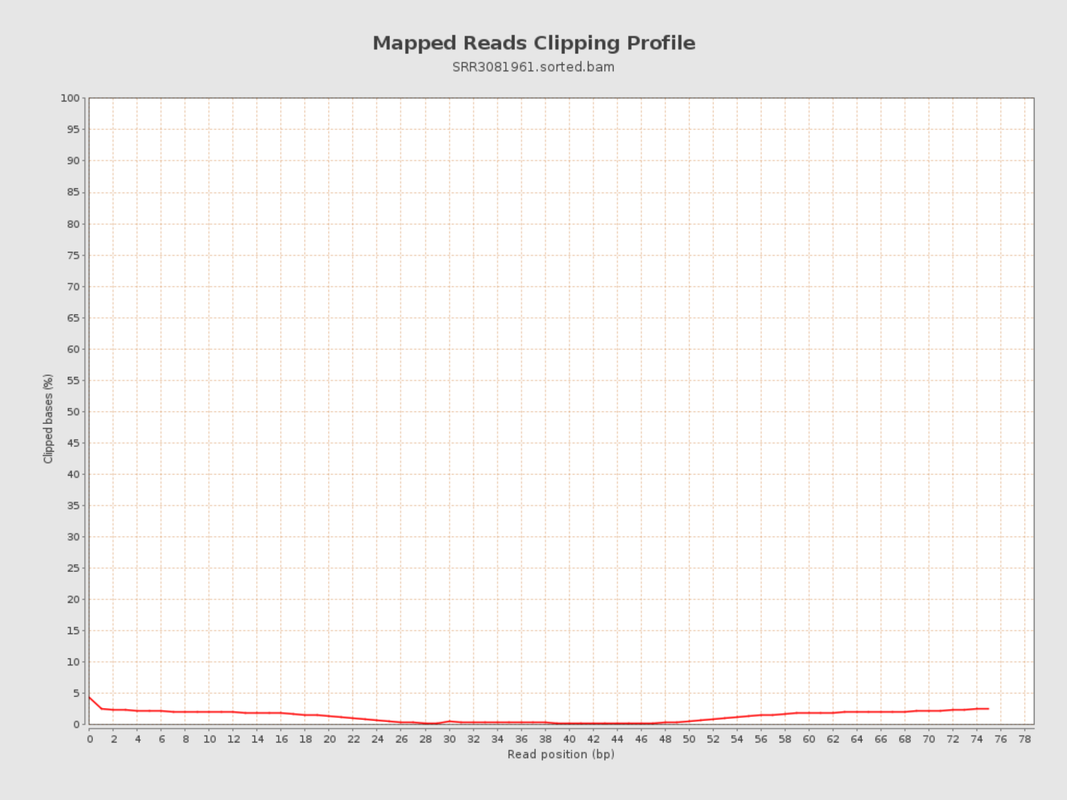
8. Results : Mapped Reads Nucleotide Content



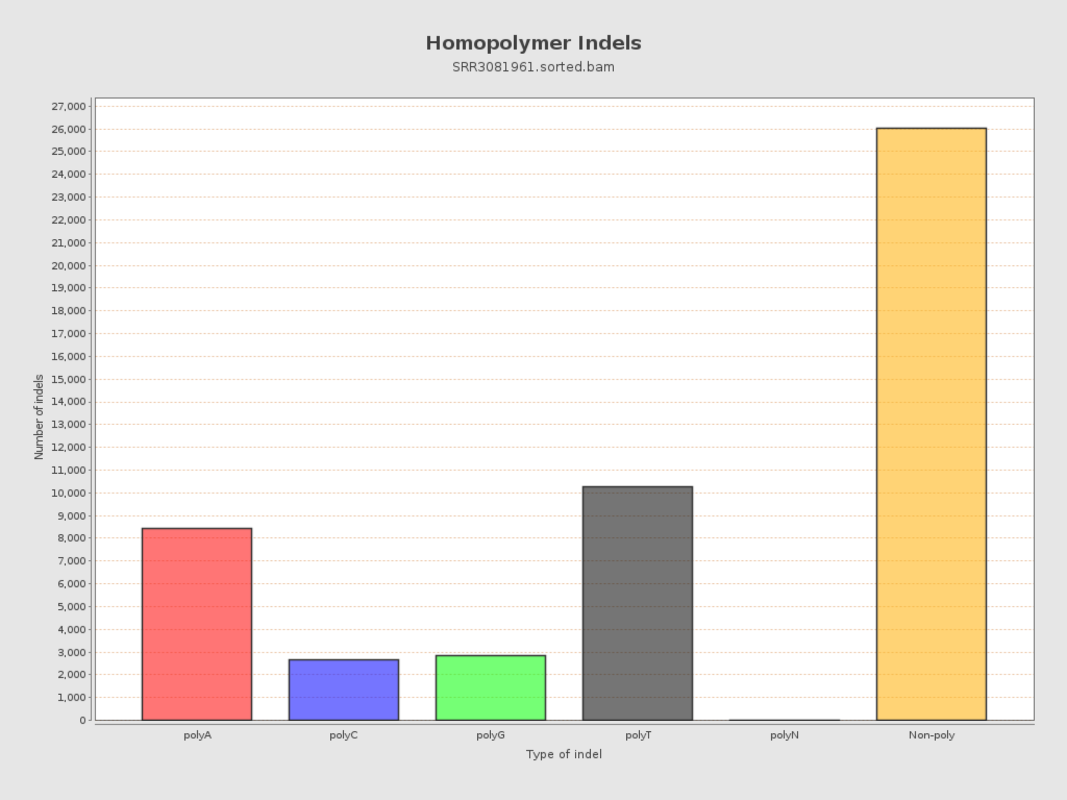
9. Results : Mapped Reads GC-content Distribution



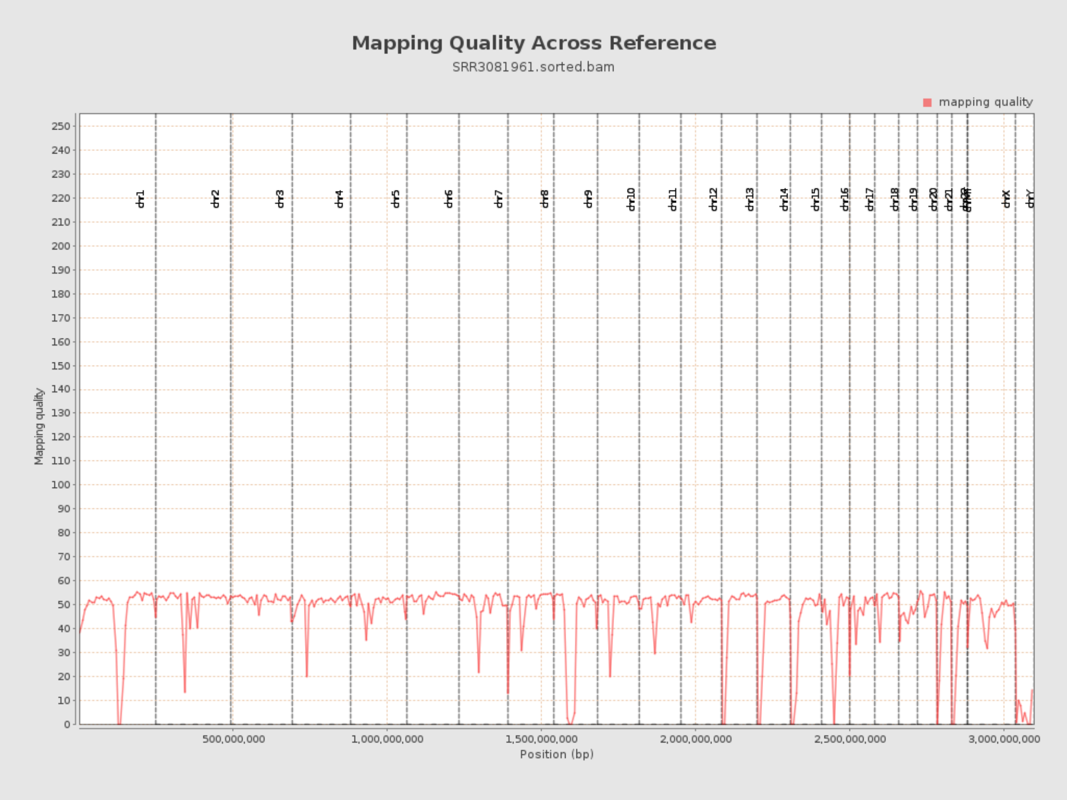
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram