Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:13:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081944.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_SRR3081944 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081944.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:13:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081944.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,083,169
Mapped reads	2,826,708 / 91.68%
Unmapped reads	256,461 / 8.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,746 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	146,310 / 4.75%
Duplication rate	3.76%
Clipped reads	1,101,293 / 35.72%

2.2. ACGT Content

Number/percentage of A's	54,009,570 / 28.16%
Number/percentage of C's	35,437,457 / 18.48%
Number/percentage of T's	60,367,067 / 31.48%
Number/percentage of G's	41,936,957 / 21.87%
Number/percentage of N's	24,358 / 0.01%
GC Percentage	40.35%

2.3. Coverage

Mean	0.062

Standard Deviation	0.5923

2.4. Mapping Quality

Mean Mapping Quality	45.11

2.5. Mismatches and indels

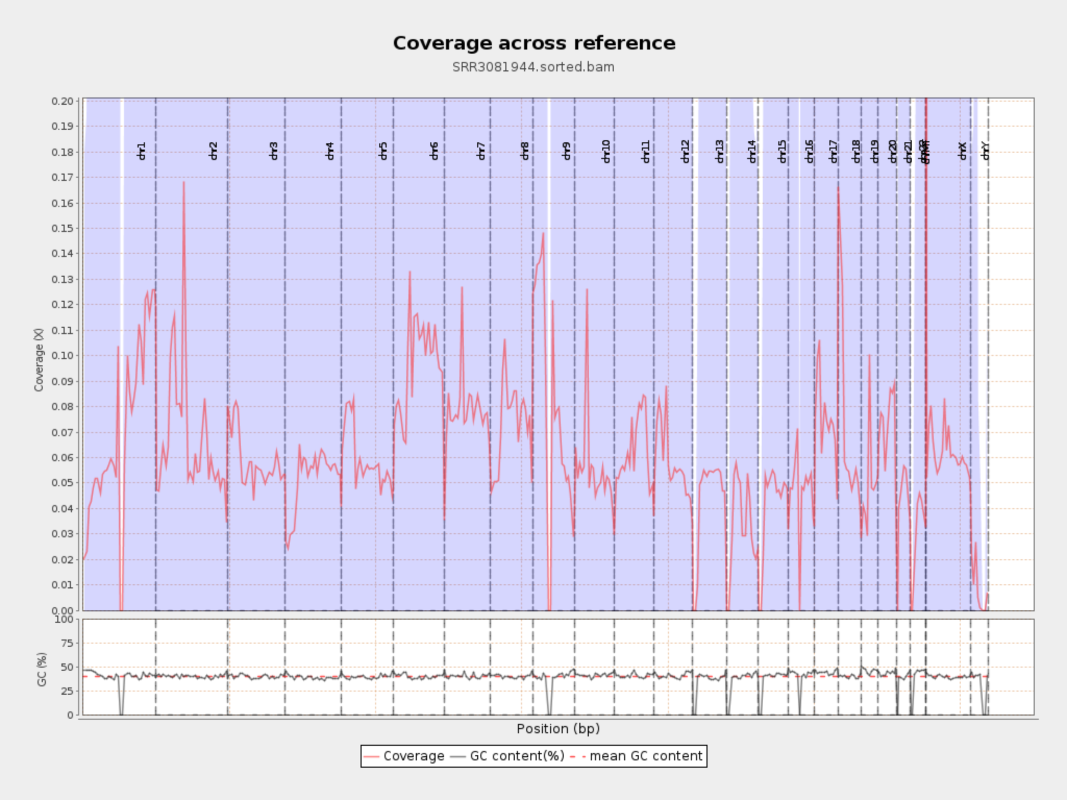
General error rate	0.79%
Mismatches	1,490,125
Insertions	14,416
Mapped reads with at least one insertion	0.51%
Deletions	40,682
Mapped reads with at least one deletion	1.43%
Homopolymer indels	47.84%

2.6. Chromosome stats

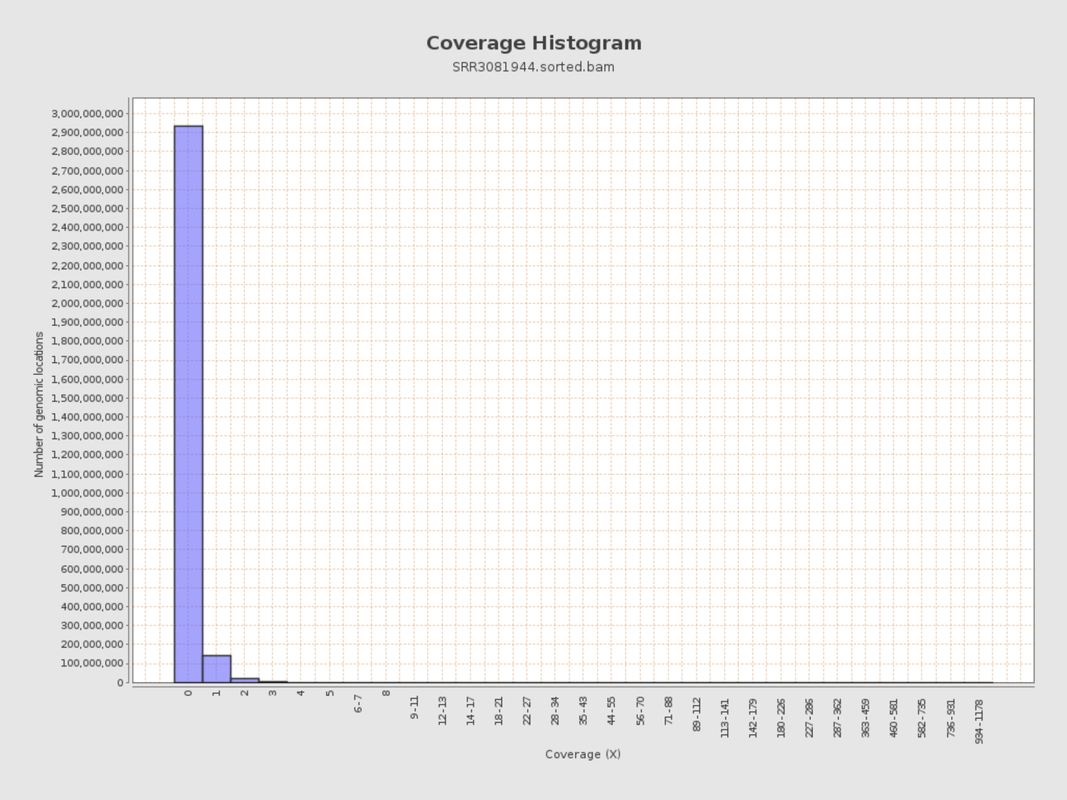
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17466119	0.0701	1.0133
chr2	243199373	16665372	0.0685	0.8983
chr3	198022430	11735936	0.0593	0.2797
chr4	191154276	9867637	0.0516	0.3053
chr5	180915260	10718144	0.0592	0.2802
chr6	171115067	16658730	0.0974	0.4658
chr7	159138663	12500084	0.0785	0.802

chr8	146364022	10694354	0.0731	0.8238
chr9	141213431	11278439	0.0799	0.6734
chr10	135534747	7618310	0.0562	0.5876
chr11	135006516	8436018	0.0625	0.4305
chr12	133851895	7834116	0.0585	0.3005
chr13	115169878	5017492	0.0436	0.2367
chr14	107349540	3661499	0.0341	0.2846
chr15	102531392	4157536	0.0405	0.2309
chr16	90354753	4125327	0.0457	0.3315
chr17	81195210	6228661	0.0767	0.3749
chr18	78077248	5803680	0.0743	1.017
chr19	59128983	2943103	0.0498	0.8143
chr20	63025520	4700673	0.0746	0.3256
chr21	48129895	2053468	0.0427	0.2978
chr22	51304566	1502365	0.0293	0.191
chrMT	16571	21818	1.3166	1.3728
chrX	155270560	9654740	0.0622	0.3668
chrY	59373566	504323	0.0085	0.2256

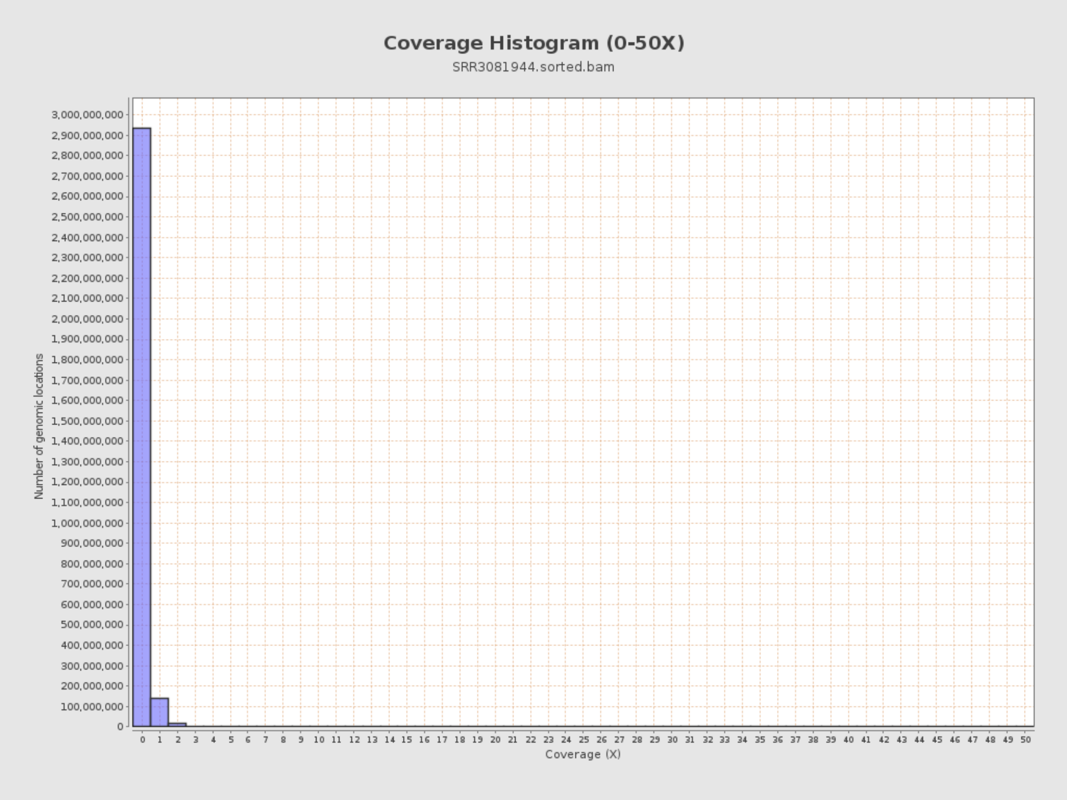
3. Results : Coverage across reference



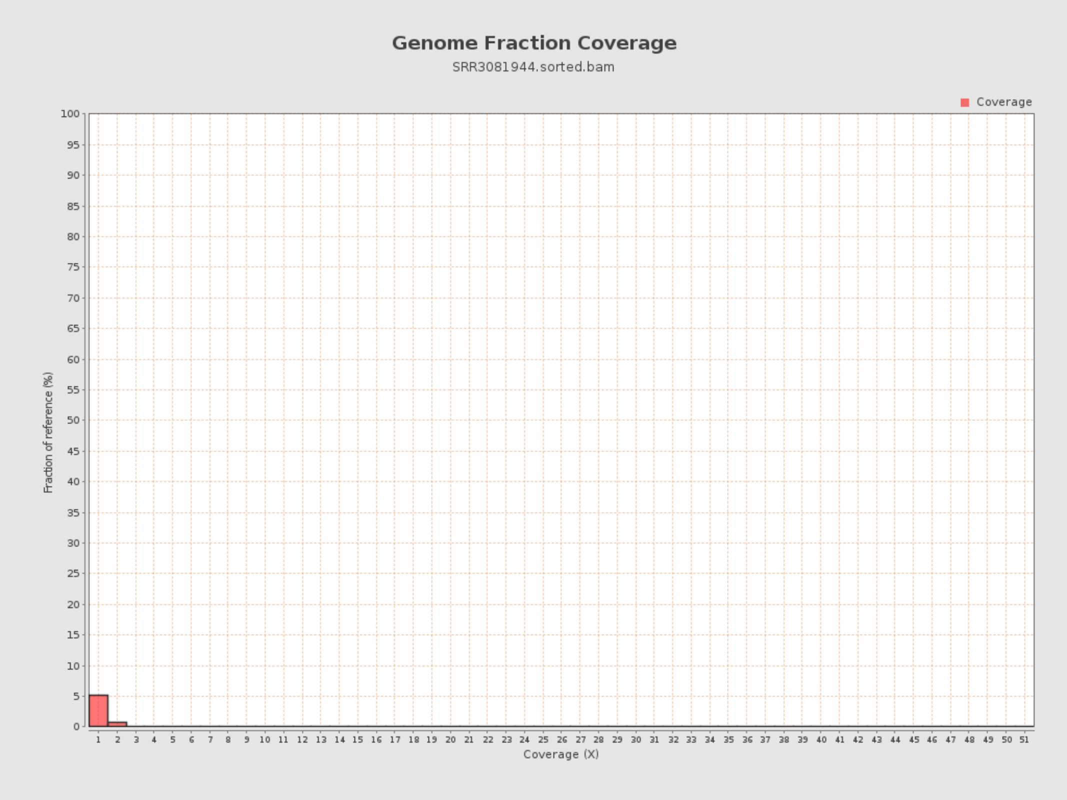
4. Results : Coverage Histogram



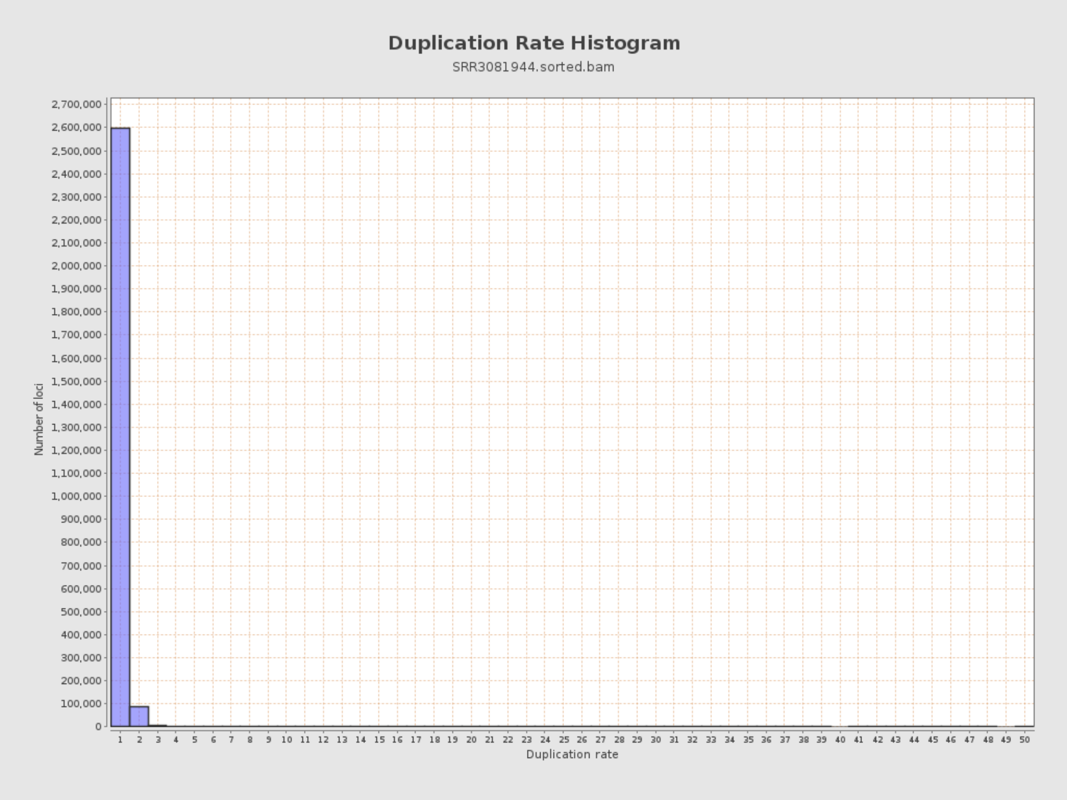
5. Results : Coverage Histogram (0-50X)



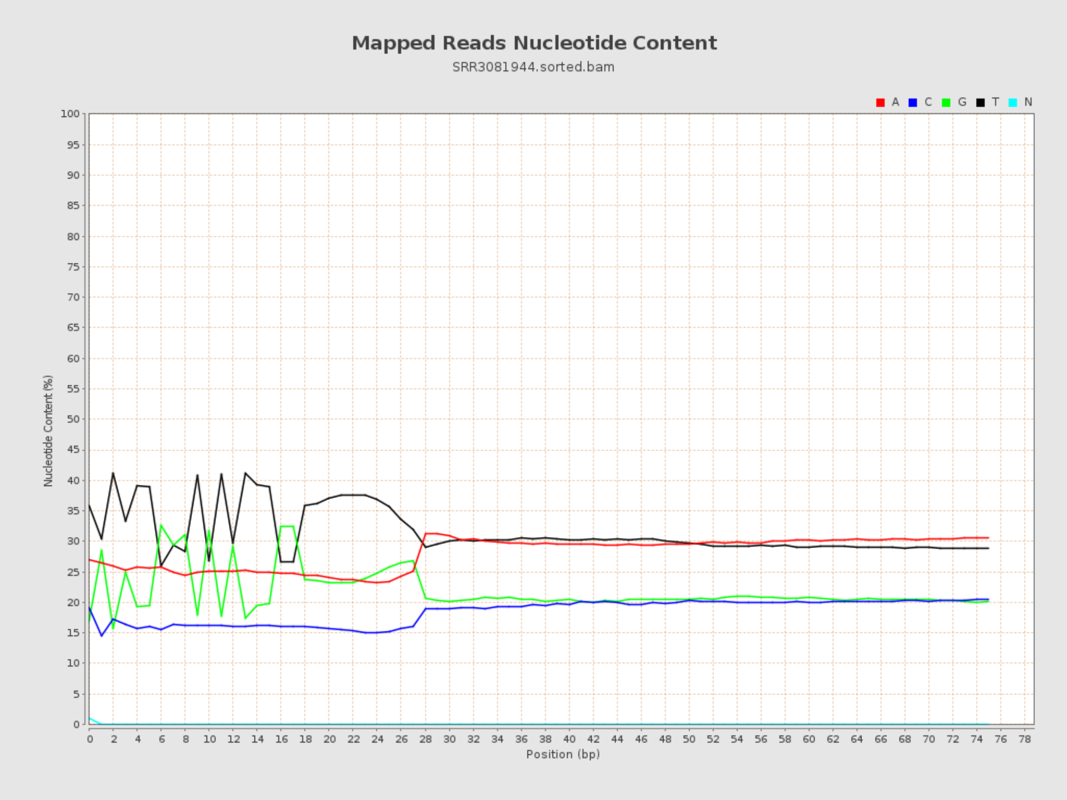
6. Results : Genome Fraction Coverage



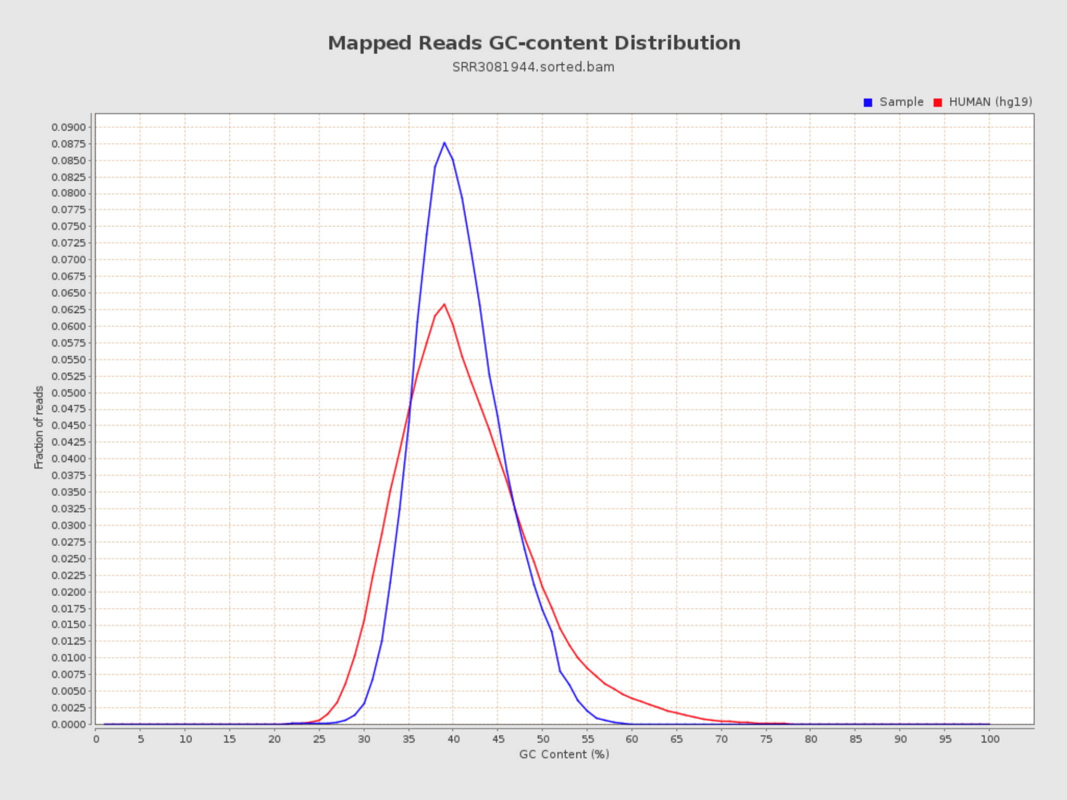
7. Results : Duplication Rate Histogram



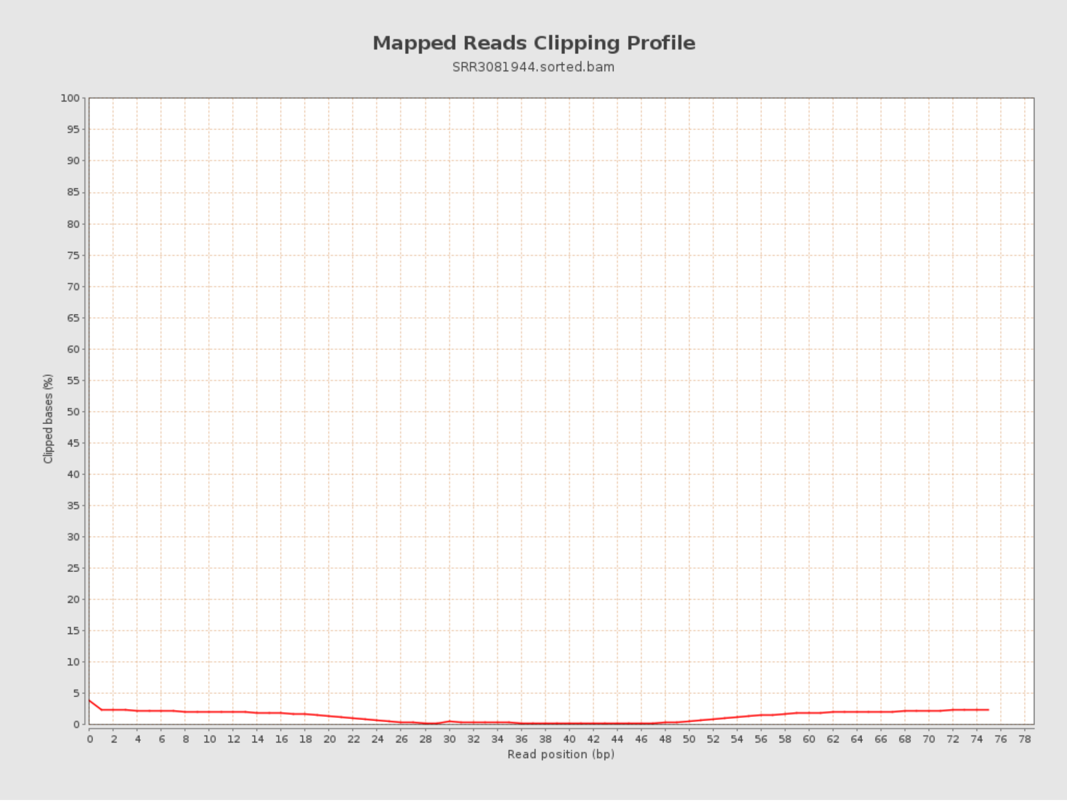
8. Results : Mapped Reads Nucleotide Content



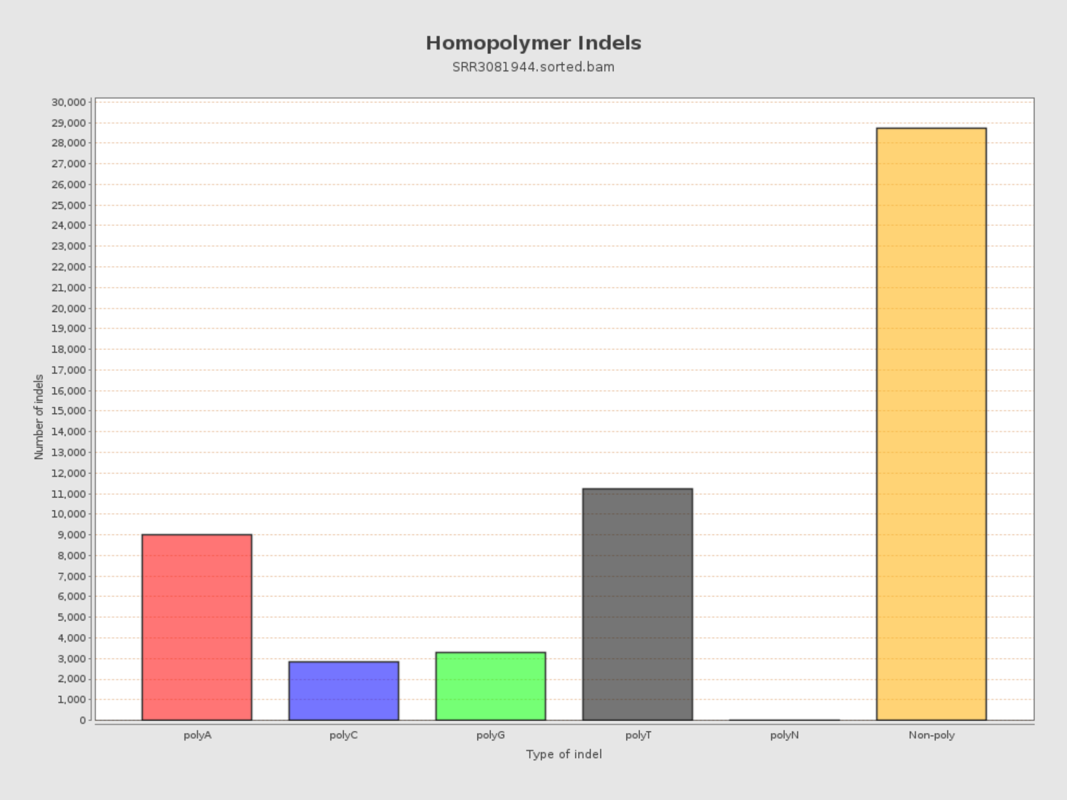
9. Results : Mapped Reads GC-content Distribution



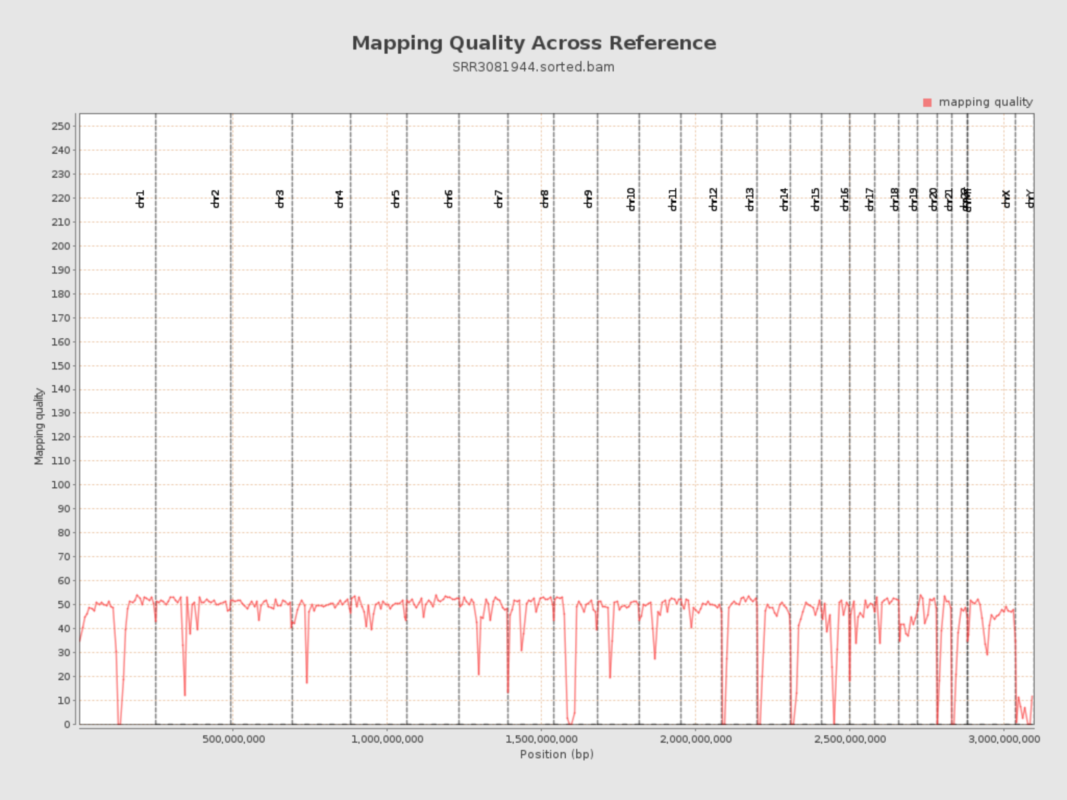
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram