Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:38:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003994.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_SRR6003994 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003994.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:38:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003994.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,102,995
Mapped reads	2,696,138 / 86.89%
Unmapped reads	406,857 / 13.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,513 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	140,944 / 4.54%
Duplication rate	4.08%
Clipped reads	1,104,156 / 35.58%

2.2. ACGT Content

Number/percentage of A's	50,541,123 / 27.64%
Number/percentage of C's	34,308,184 / 18.76%
Number/percentage of T's	58,368,876 / 31.92%
Number/percentage of G's	39,593,556 / 21.66%
Number/percentage of N's	24,891 / 0.01%
GC Percentage	40.42%

2.3. Coverage

Mean	0.0591

Standard Deviation	0.5099

2.4. Mapping Quality

Mean Mapping Quality	46.7

2.5. Mismatches and indels

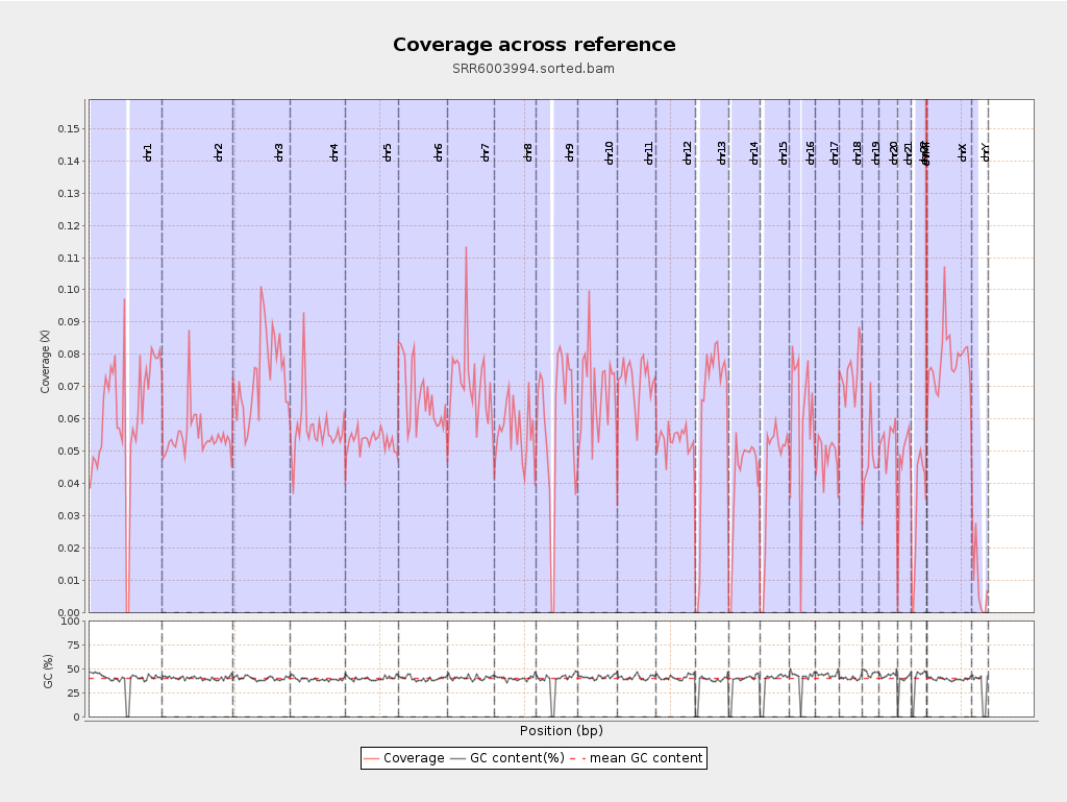
General error rate	0.95%
Mismatches	1,712,643
Insertions	14,831
Mapped reads with at least one insertion	0.54%
Deletions	43,199
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.1%

2.6. Chromosome stats

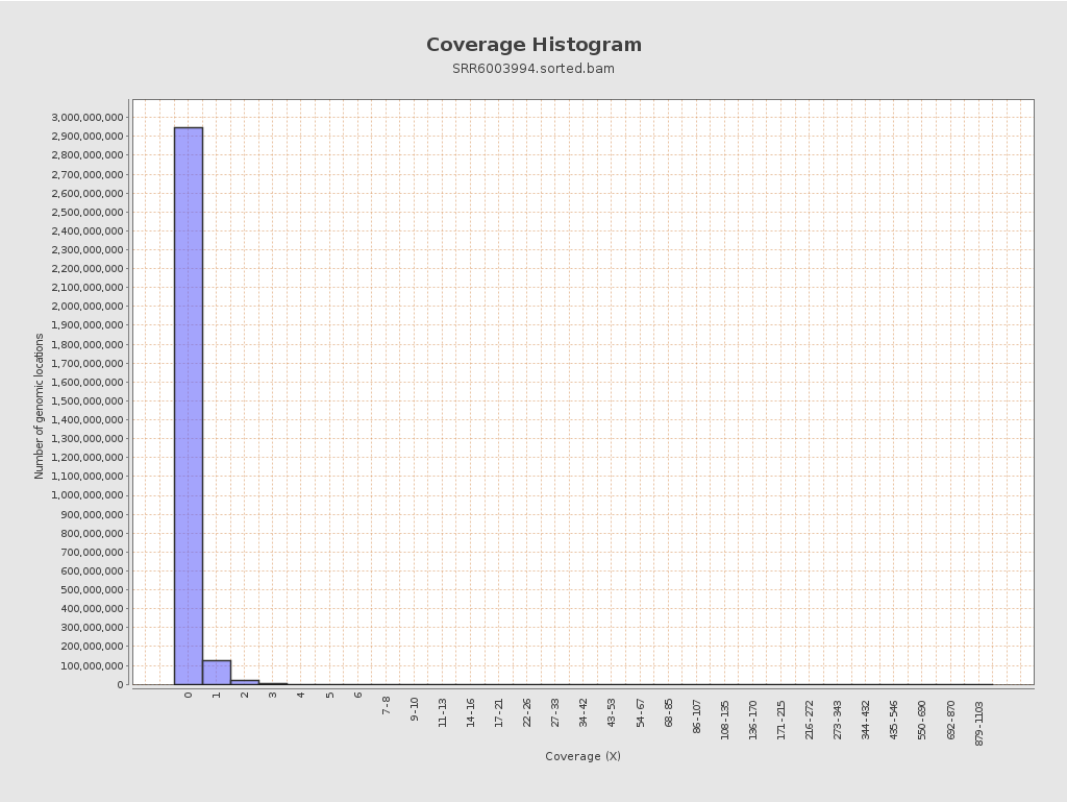
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15305531	0.0614	0.962
chr2	243199373	13326981	0.0548	0.5224
chr3	198022430	14533100	0.0734	0.3165
chr4	191154276	10836132	0.0567	0.3165
chr5	180915260	9640602	0.0533	0.2727
chr6	171115067	11416963	0.0667	0.3554
chr7	159138663	11371858	0.0715	0.7236

chr8	146364022	8205619	0.0561	0.7087
chr9	141213431	8290875	0.0587	0.4666
chr10	135534747	9302331	0.0686	0.4916
chr11	135006516	9639735	0.0714	0.5153
chr12	133851895	7131074	0.0533	0.2822
chr13	115169878	7162276	0.0622	0.2911
chr14	107349540	4362115	0.0406	0.2752
chr15	102531392	4415694	0.0431	0.2429
chr16	90354753	5571739	0.0617	0.3318
chr17	81195210	3903768	0.0481	0.3046
chr18	78077248	5773338	0.0739	0.9056
chr19	59128983	2794001	0.0473	0.6362
chr20	63025520	3314350	0.0526	0.2802
chr21	48129895	2197642	0.0457	0.309
chr22	51304566	1634393	0.0319	0.205
chrMT	16571	107696	6.4991	4.2901
chrX	155270560	12144556	0.0782	0.3756
chrY	59373566	526564	0.0089	0.2067

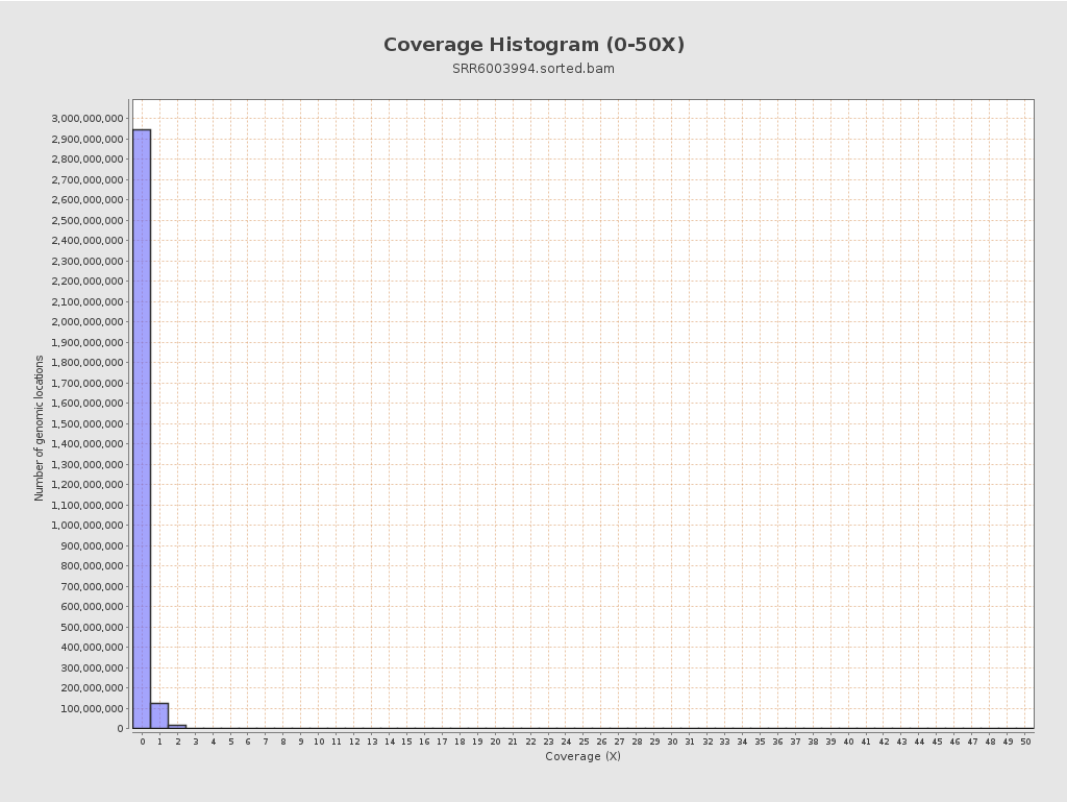
3. Results : Coverage across reference



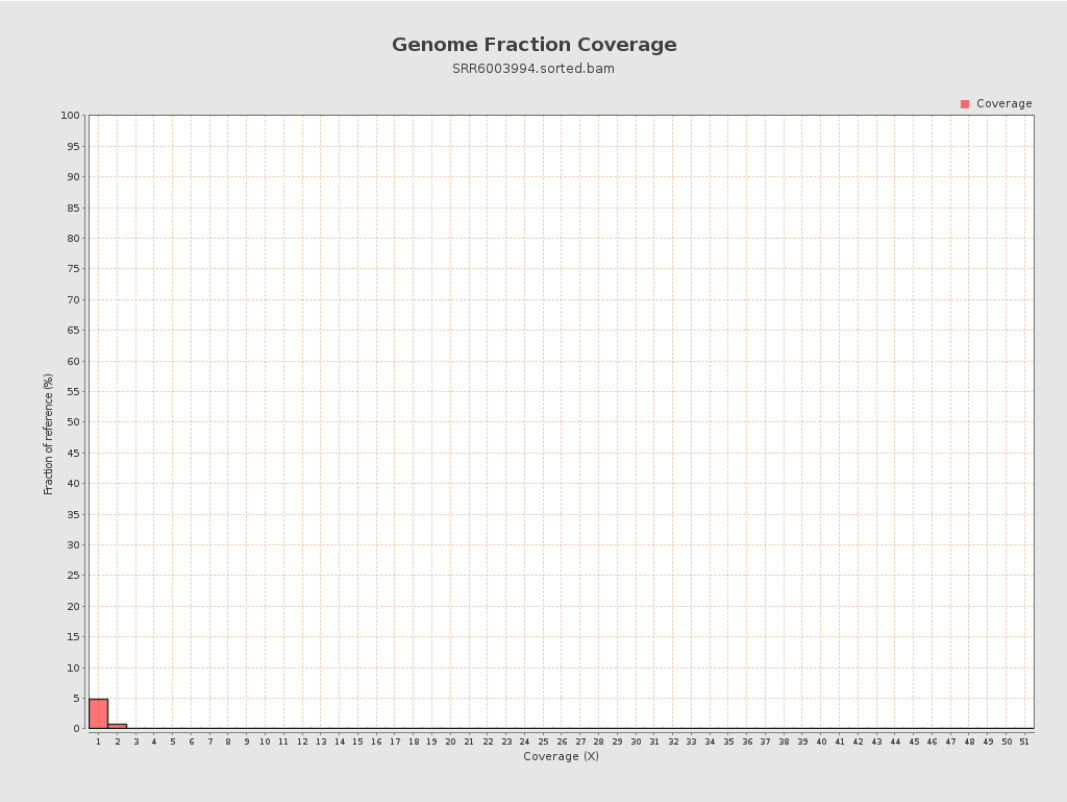
4. Results : Coverage Histogram



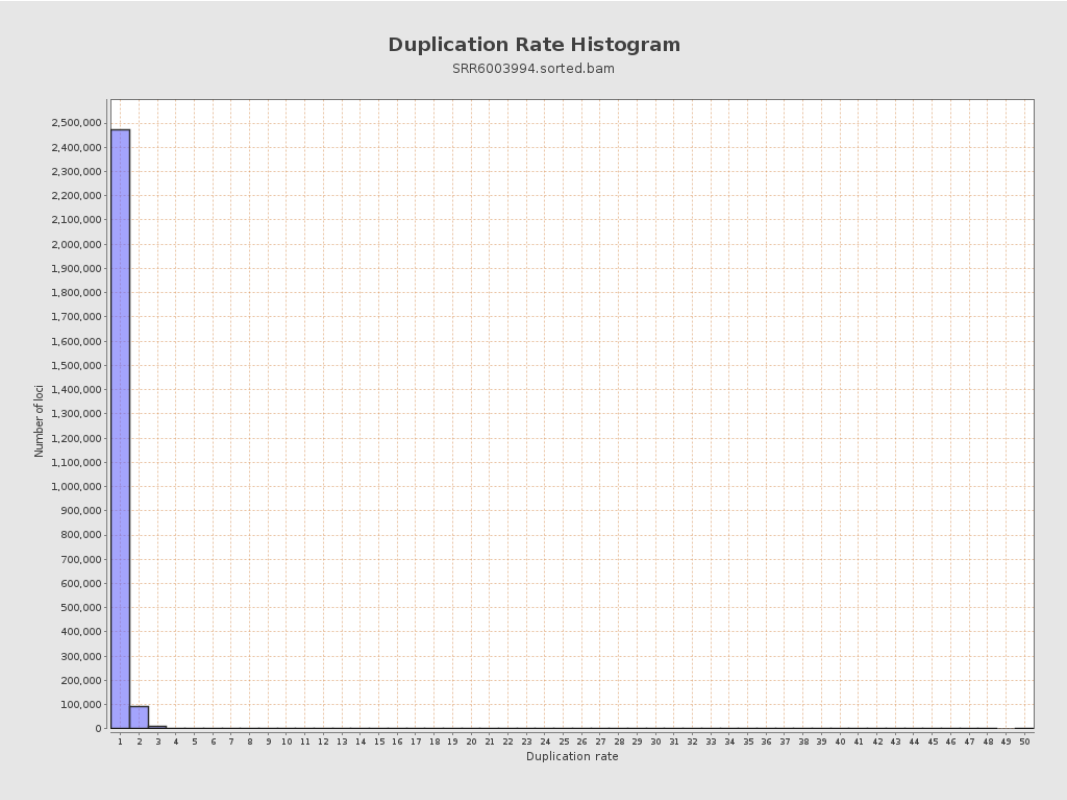
5. Results : Coverage Histogram (0-50X)



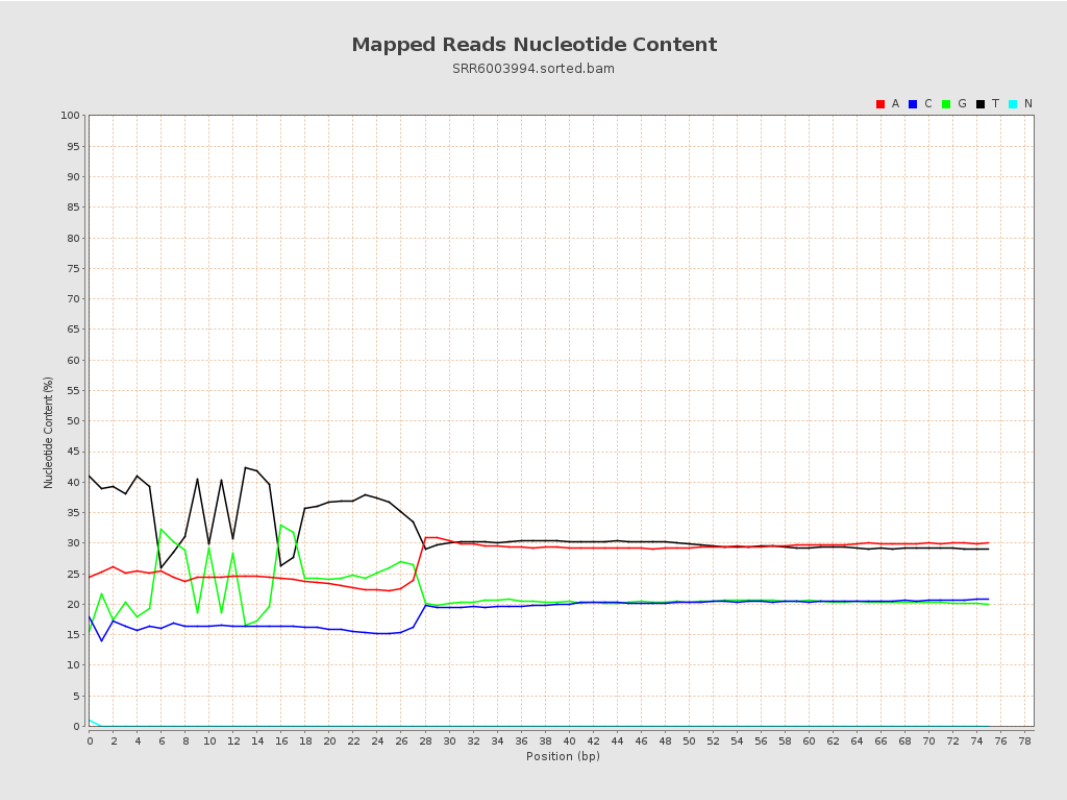
6. Results : Genome Fraction Coverage



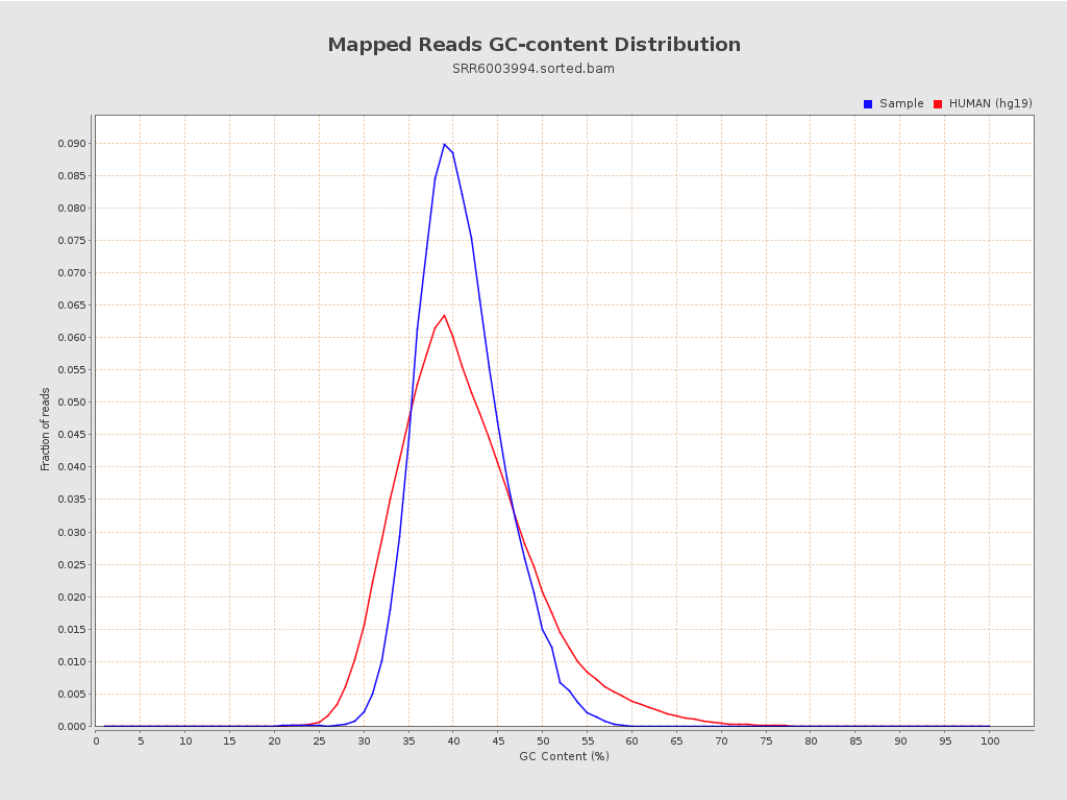
7. Results : Duplication Rate Histogram



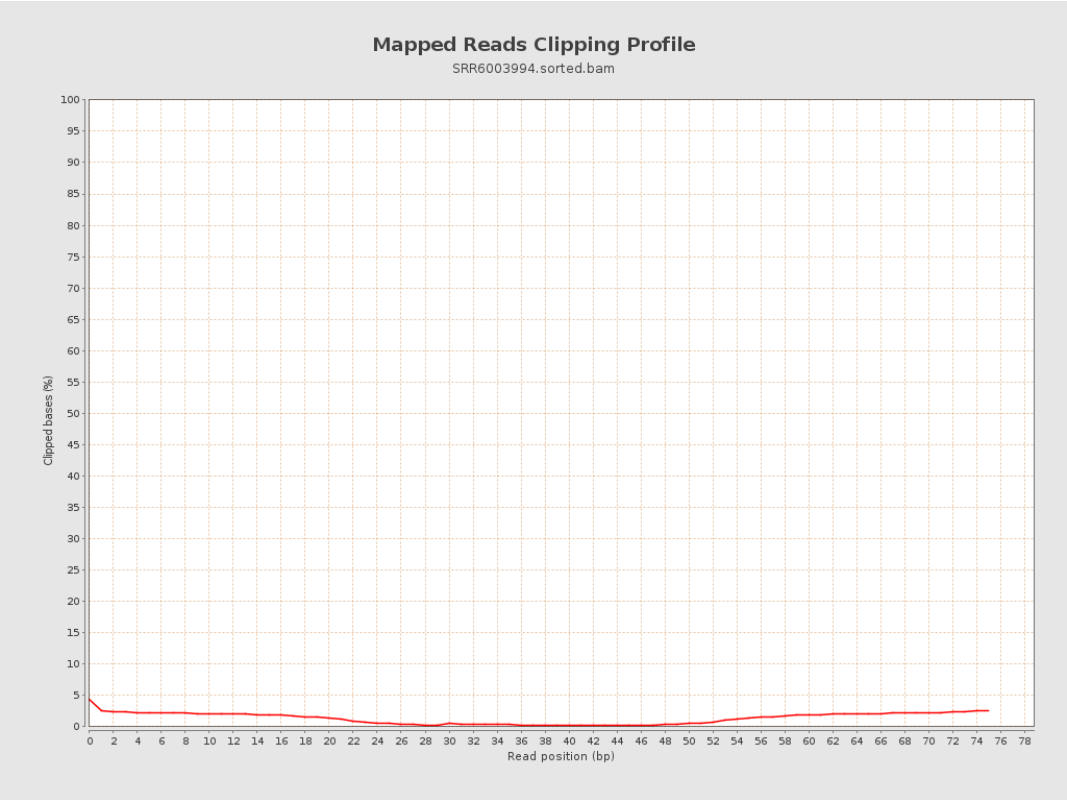
8. Results : Mapped Reads Nucleotide Content



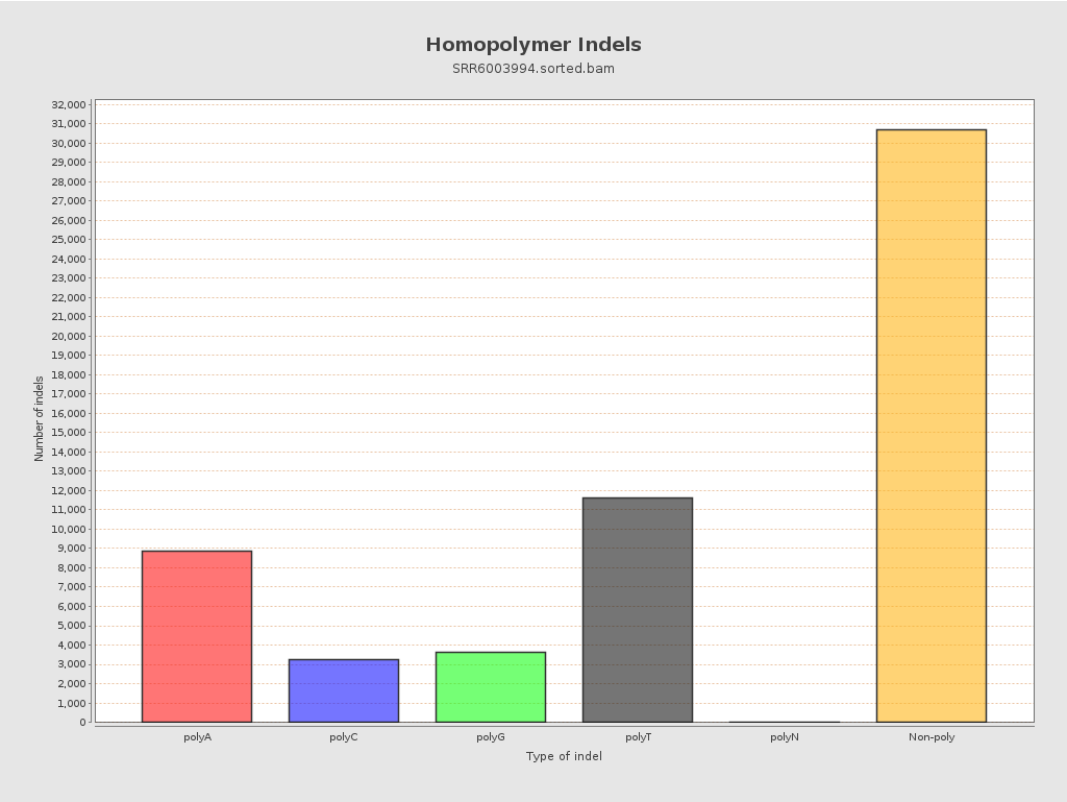
9. Results : Mapped Reads GC-content Distribution



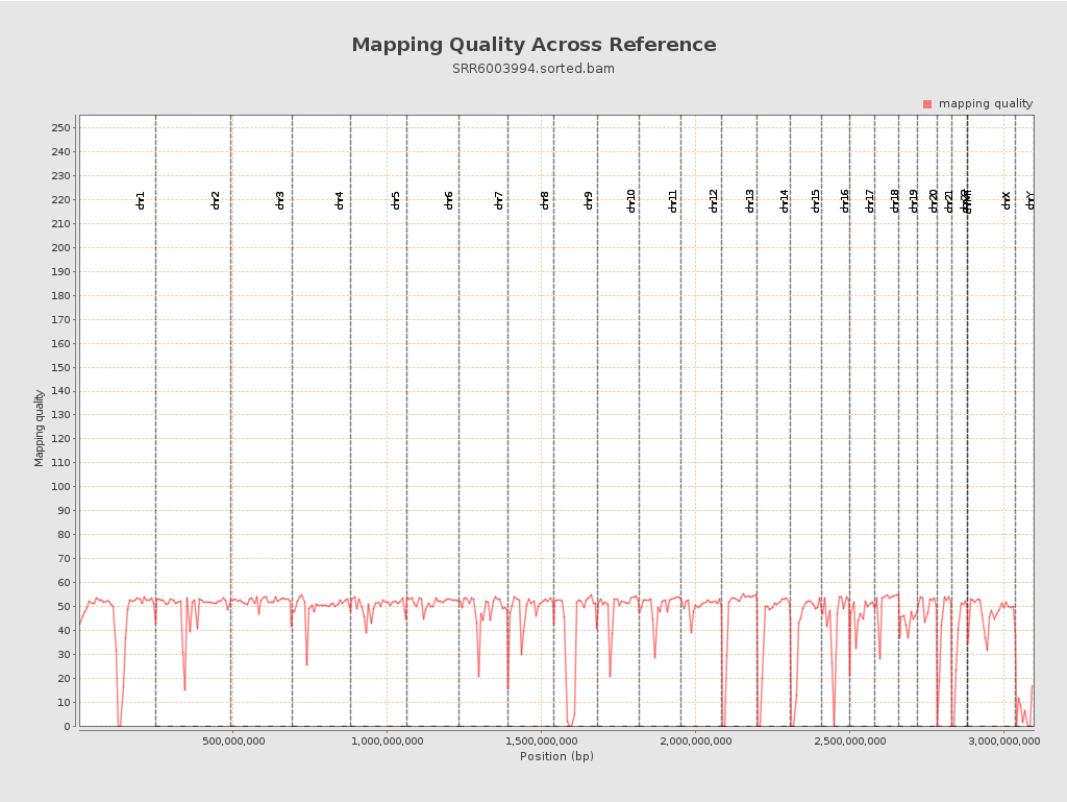
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram