Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:22:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004044.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_SRR6004044 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004044.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:22:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004044.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,984,118
Mapped reads	2,517,462 / 84.36%
Unmapped reads	466,656 / 15.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,729 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	179,566 / 6.02%
Duplication rate	5.65%
Clipped reads	1,251,779 / 41.95%

2.2. ACGT Content

Number/percentage of A's	45,698,553 / 27.62%
Number/percentage of C's	31,051,532 / 18.77%
Number/percentage of T's	51,692,806 / 31.24%
Number/percentage of G's	36,986,954 / 22.36%
Number/percentage of N's	18,456 / 0.01%
GC Percentage	41.12%

2.3. Coverage

Mean	0.0535

Standard Deviation	0.4918

2.4. Mapping Quality

Mean Mapping Quality	45.52

2.5. Mismatches and indels

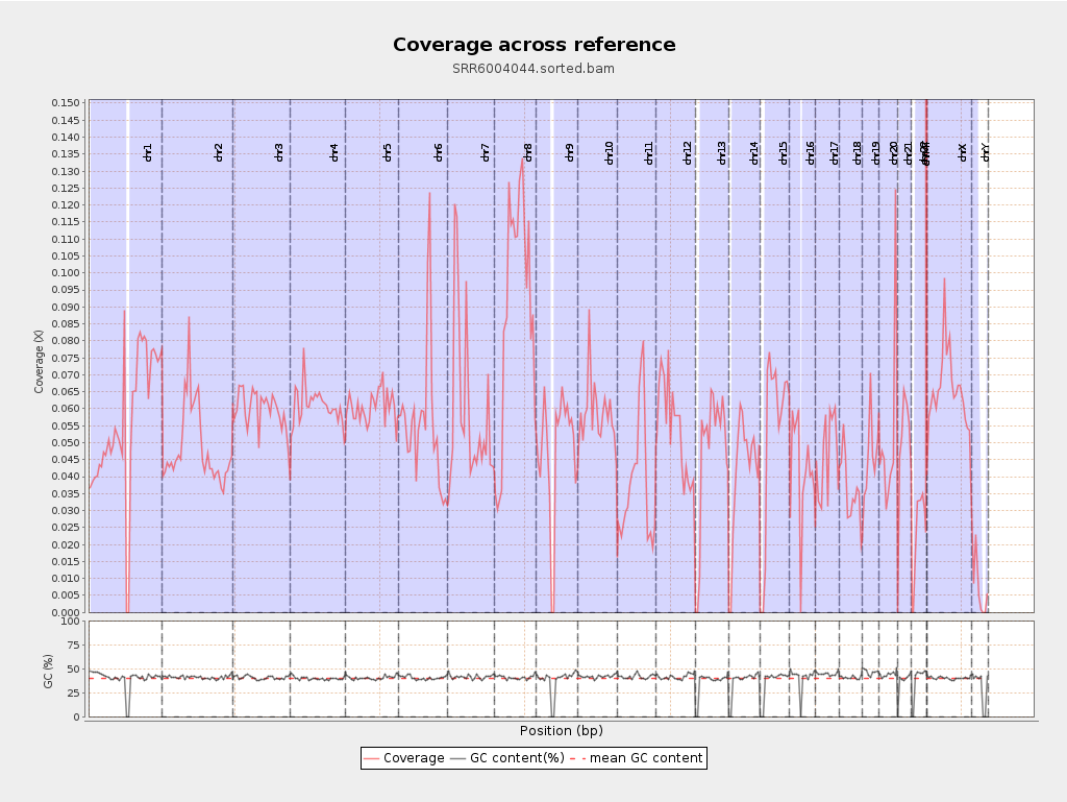
General error rate	0.76%
Mismatches	1,244,065
Insertions	11,550
Mapped reads with at least one insertion	0.46%
Deletions	40,696
Mapped reads with at least one deletion	1.6%
Homopolymer indels	45.39%

2.6. Chromosome stats

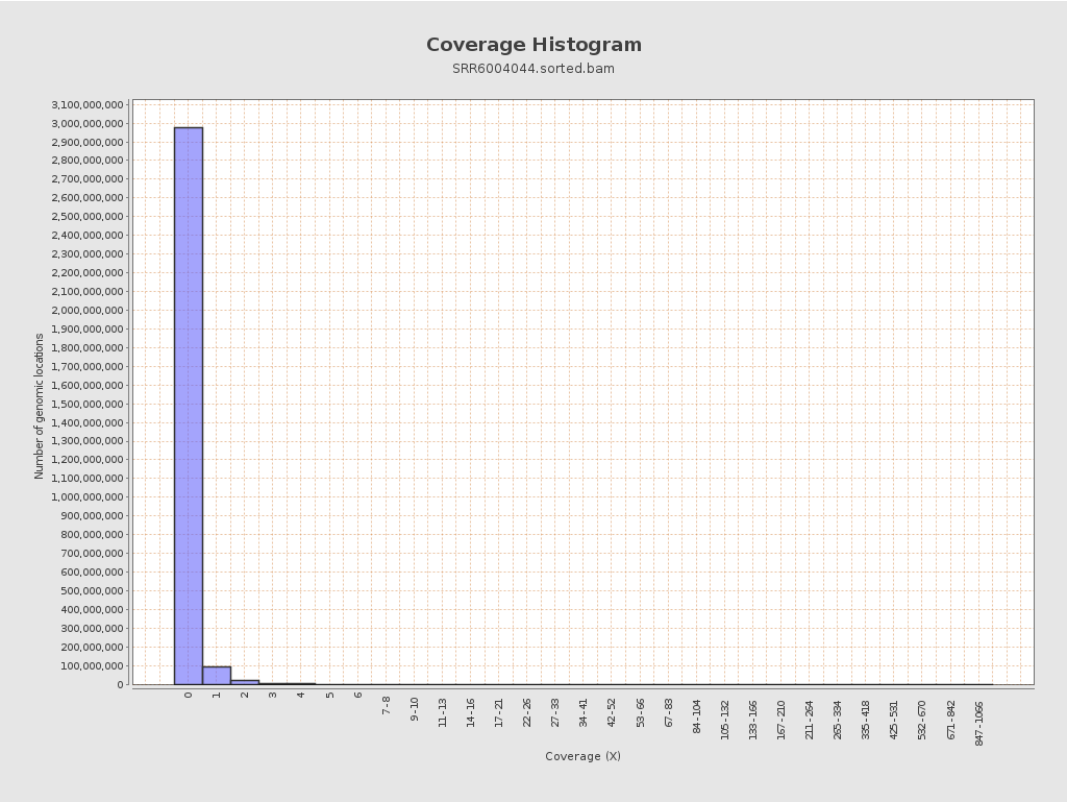
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14061084	0.0564	0.9452
chr2	243199373	11858759	0.0488	0.4651
chr3	198022430	11859569	0.0599	0.316
chr4	191154276	11609601	0.0607	0.3434
chr5	180915260	10948931	0.0605	0.3229
chr6	171115067	9548797	0.0558	0.3514
chr7	159138663	9507276	0.0597	0.7139

chr8	146364022	13047621	0.0891	0.7167
chr9	141213431	6696723	0.0474	0.4191
chr10	135534747	7939270	0.0586	0.4712
chr11	135006516	5194278	0.0385	0.3821
chr12	133851895	7151838	0.0534	0.3107
chr13	115169878	5412031	0.047	0.2829
chr14	107349540	4441804	0.0414	0.314
chr15	102531392	5451156	0.0532	0.307
chr16	90354753	3808968	0.0422	0.2998
chr17	81195210	3789032	0.0467	0.3082
chr18	78077248	2880247	0.0369	0.6988
chr19	59128983	2730202	0.0462	0.6642
chr20	63025520	3357684	0.0533	0.3176
chr21	48129895	2379932	0.0494	0.3131
chr22	51304566	1189784	0.0232	0.1911
chrMT	16571	113041	6.8216	5.5475
chrX	155270560	10106359	0.0651	0.3733
chrY	59373566	435134	0.0073	0.1573

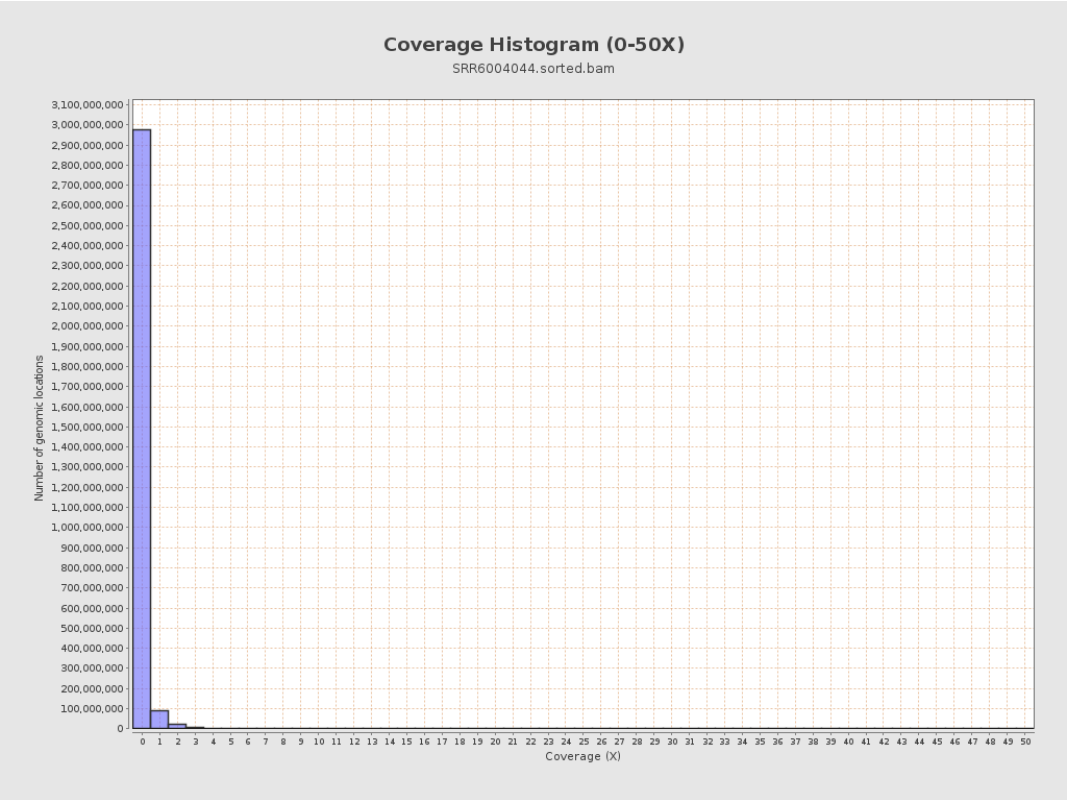
3. Results : Coverage across reference



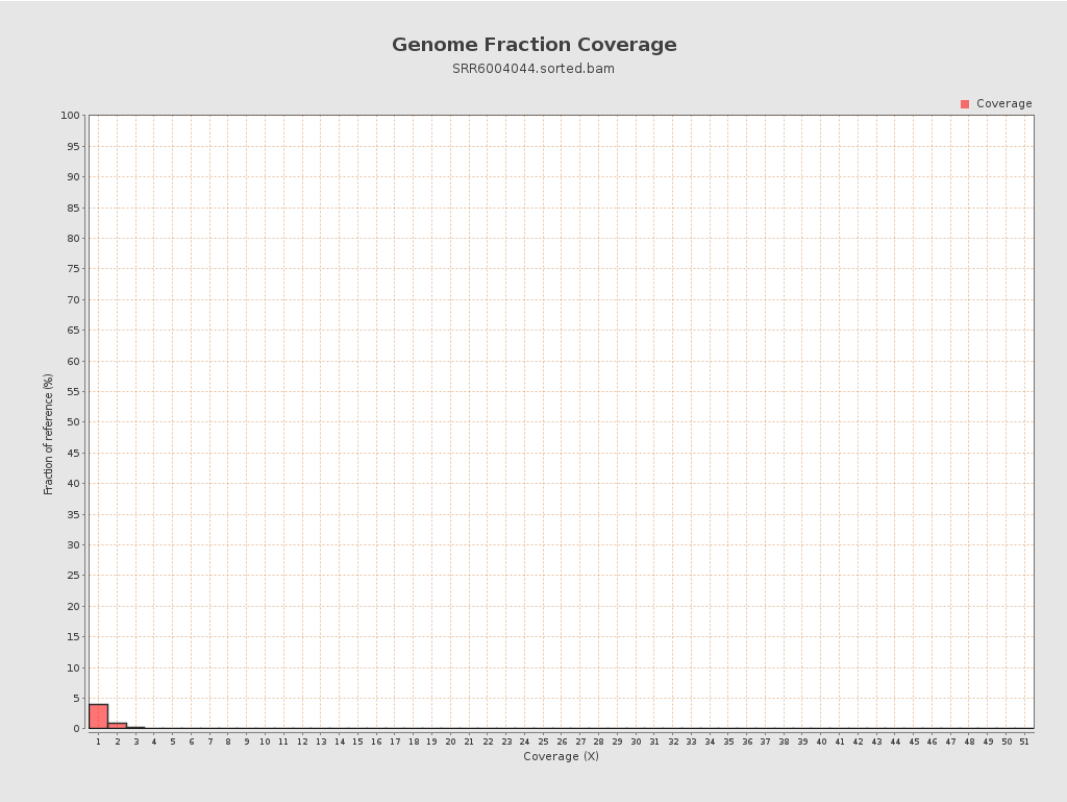
4. Results : Coverage Histogram



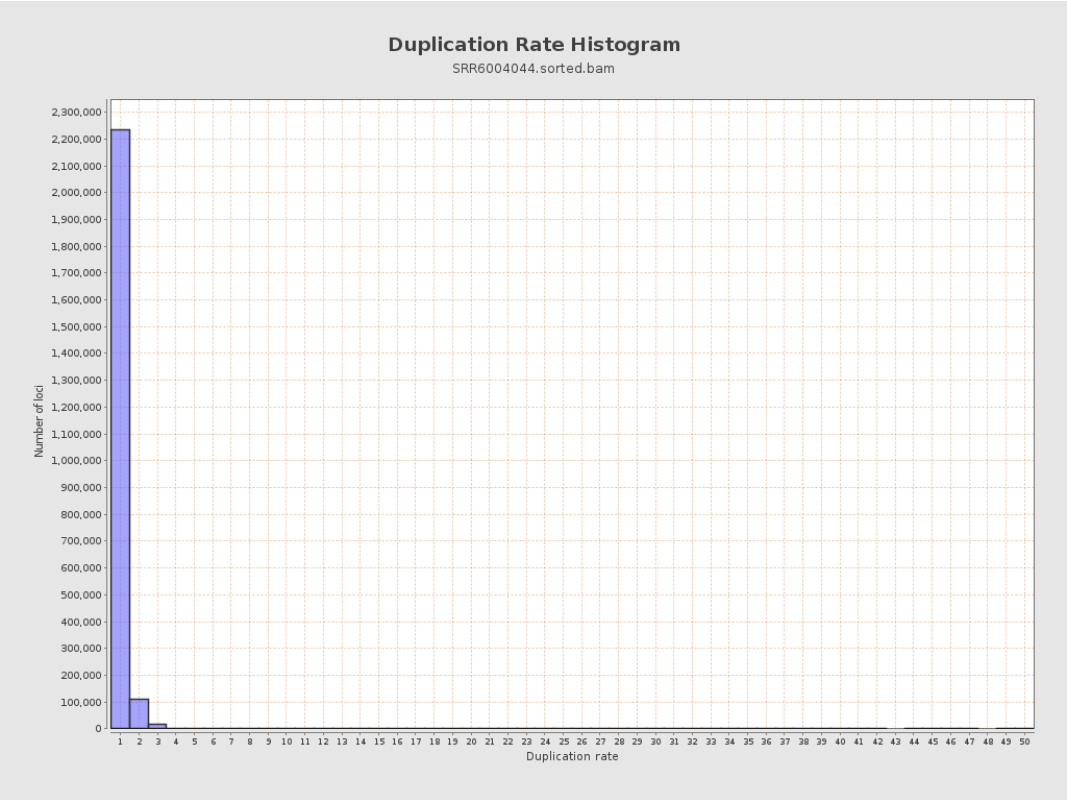
5. Results : Coverage Histogram (0-50X)



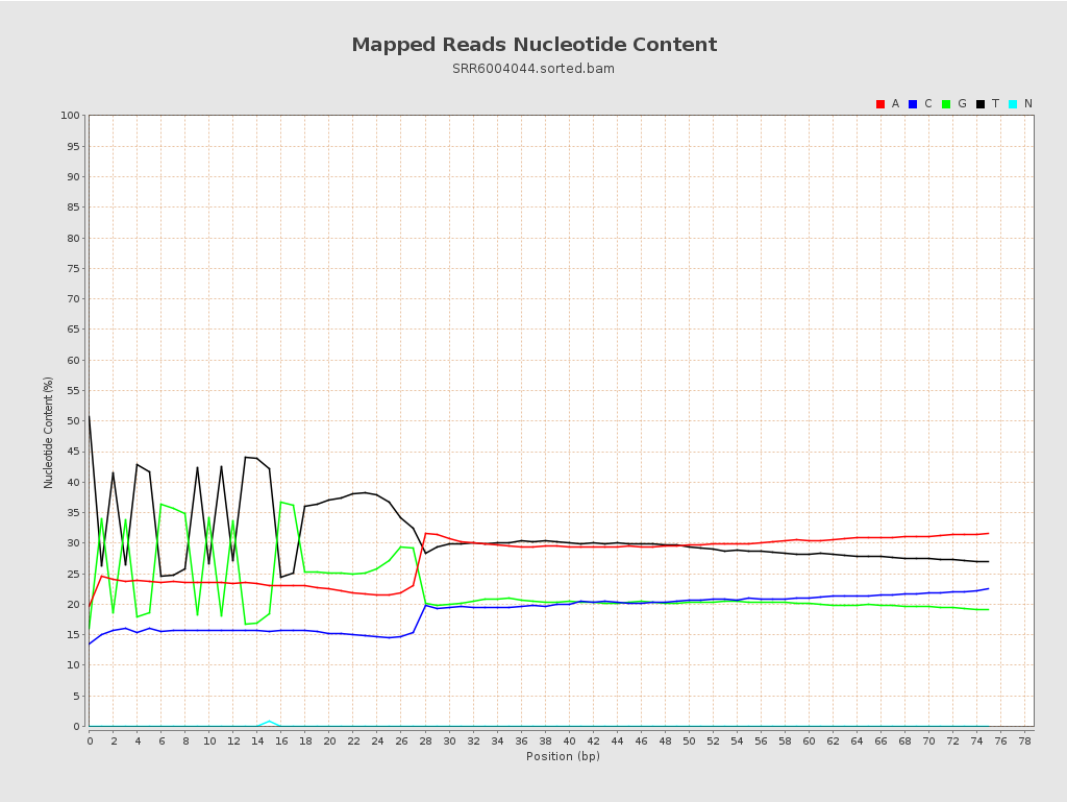
6. Results : Genome Fraction Coverage



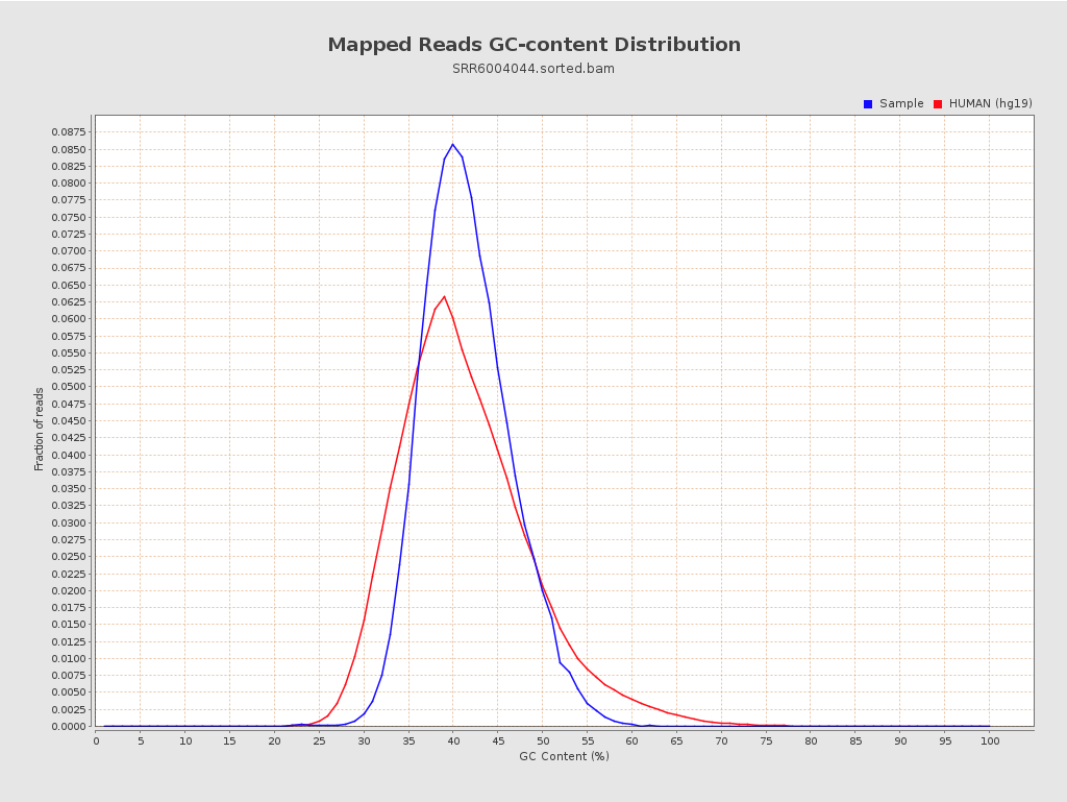
7. Results : Duplication Rate Histogram



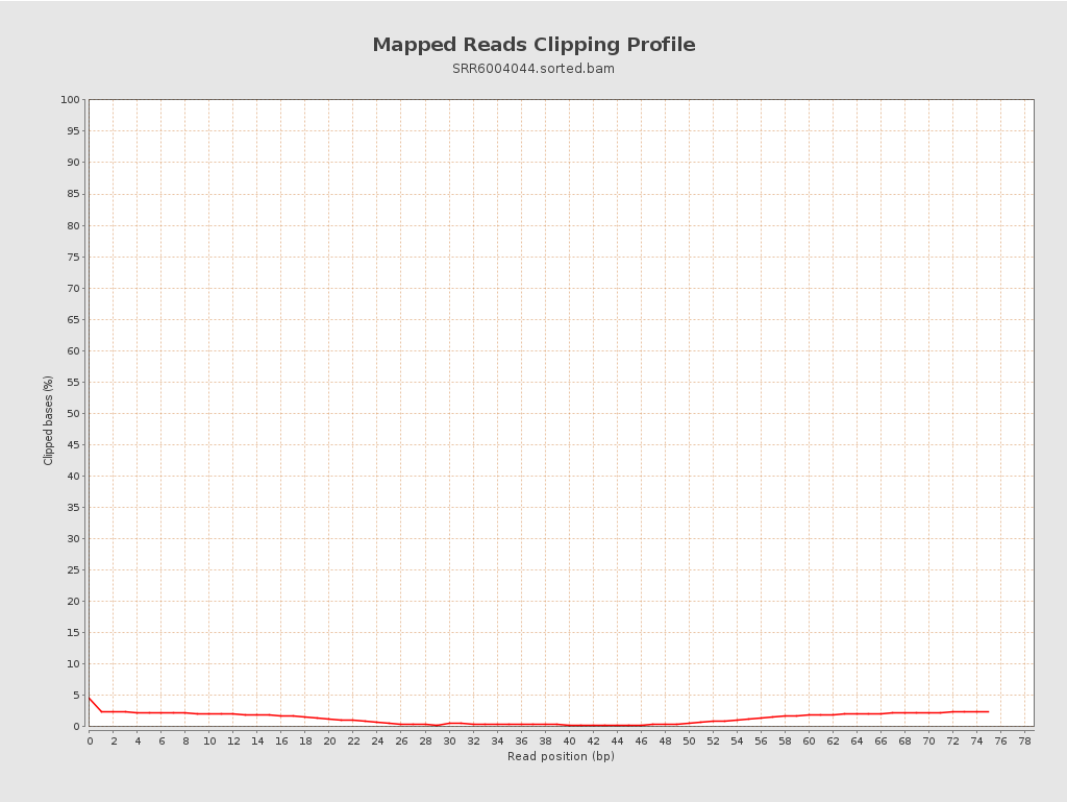
8. Results : Mapped Reads Nucleotide Content



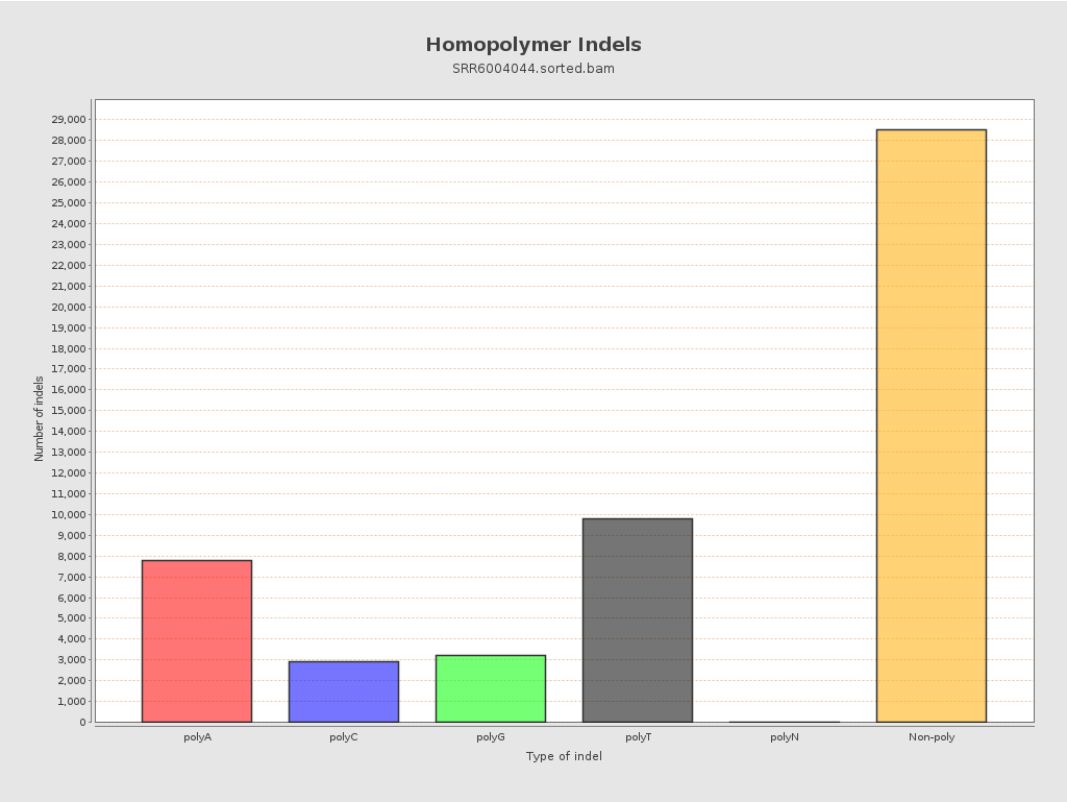
9. Results : Mapped Reads GC-content Distribution



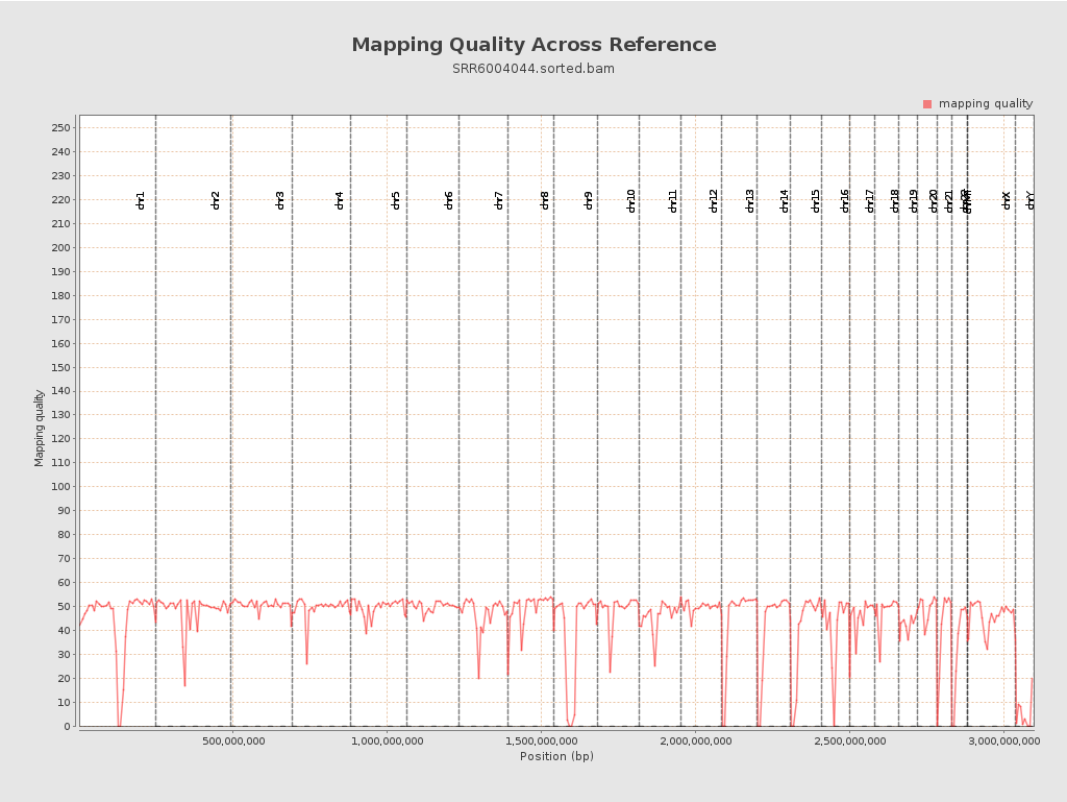
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram