Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:58:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084844.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_SRR3084844 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084844.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:58:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084844.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,809,109
Mapped reads	2,509,142 / 89.32%
Unmapped reads	299,967 / 10.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,813 / 0.81%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	133,226 / 4.74%
Duplication rate	4.49%
Clipped reads	847,300 / 30.16%

2.2. ACGT Content

Number/percentage of A's	50,771,691 / 29.18%
Number/percentage of C's	31,819,990 / 18.29%
Number/percentage of T's	55,971,050 / 32.17%
Number/percentage of G's	35,406,515 / 20.35%
Number/percentage of N's	27,352 / 0.02%
GC Percentage	38.64%

2.3. Coverage

Mean	0.0562

Standard Deviation	0.4567

2.4. Mapping Quality

Mean Mapping Quality	48.28

2.5. Mismatches and indels

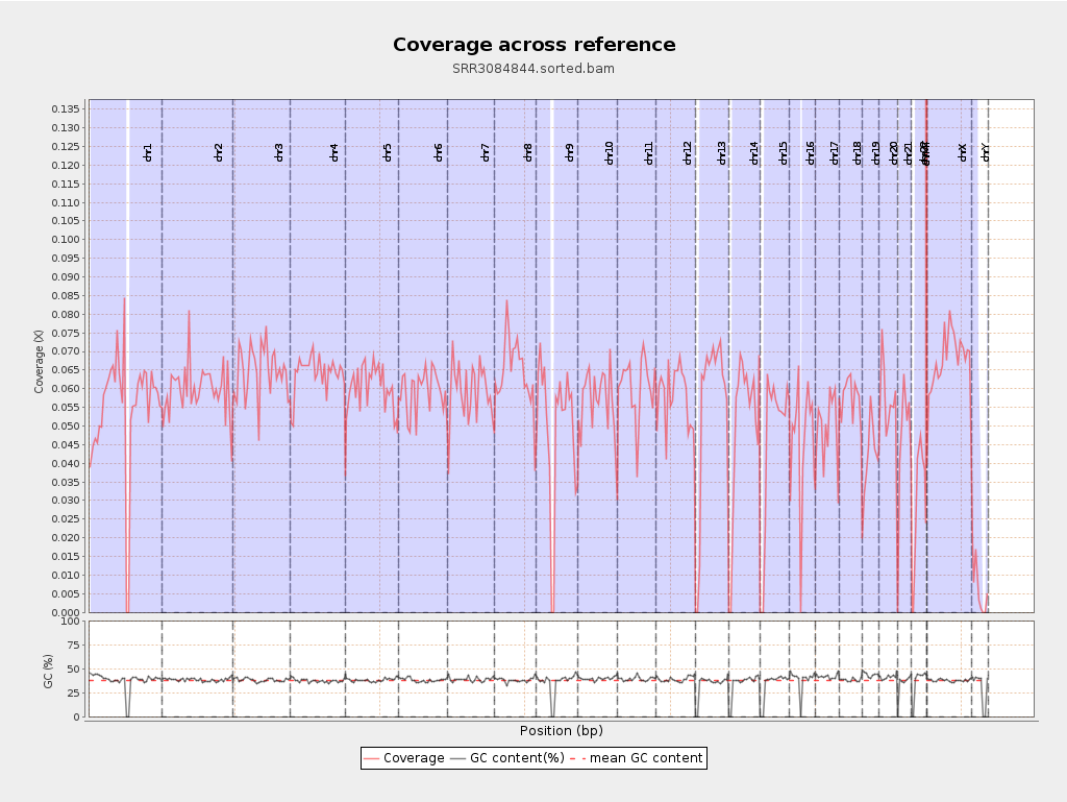
General error rate	0.82%
Mismatches	1,396,145
Insertions	13,615
Mapped reads with at least one insertion	0.54%
Deletions	36,911
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.78%

2.6. Chromosome stats

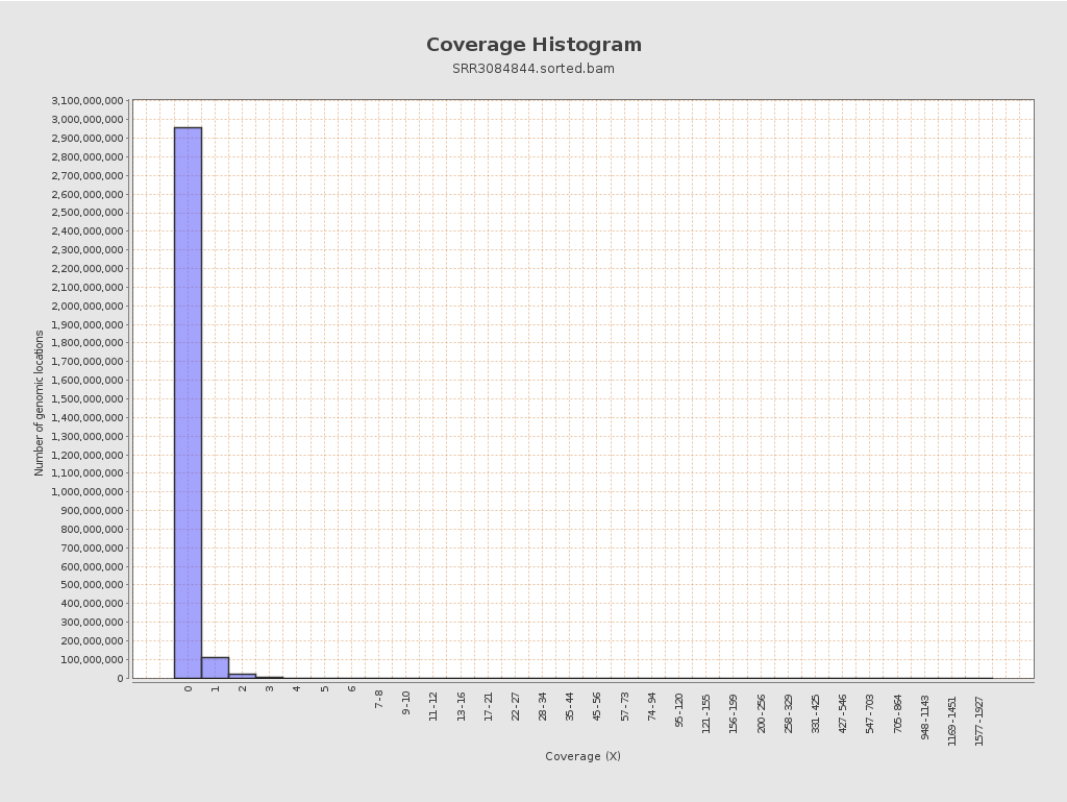
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13702657	0.055	0.6777
chr2	243199373	14571234	0.0599	0.3967
chr3	198022430	12802661	0.0647	0.3057
chr4	191154276	12273758	0.0642	0.312
chr5	180915260	10898995	0.0602	0.2974
chr6	171115067	10149790	0.0593	0.2979
chr7	159138663	9515004	0.0598	0.3714

chr8	146364022	9399657	0.0642	1.2331
chr9	141213431	7031165	0.0498	0.3547
chr10	135534747	7778883	0.0574	0.3478
chr11	135006516	8147858	0.0604	0.3498
chr12	133851895	7725423	0.0577	0.2924
chr13	115169878	6295219	0.0547	0.2831
chr14	107349540	5328561	0.0496	0.2818
chr15	102531392	4781336	0.0466	0.259
chr16	90354753	4188693	0.0464	0.2761
chr17	81195210	3967490	0.0489	0.2889
chr18	78077248	4512532	0.0578	0.5931
chr19	59128983	2524622	0.0427	0.4892
chr20	63025520	3569524	0.0566	0.2975
chr21	48129895	2225227	0.0462	0.2719
chr22	51304566	1494165	0.0291	0.2025
chrMT	16571	336380	20.2993	10.4915
chrX	155270560	10479042	0.0675	0.331
chrY	59373566	361602	0.0061	0.1174

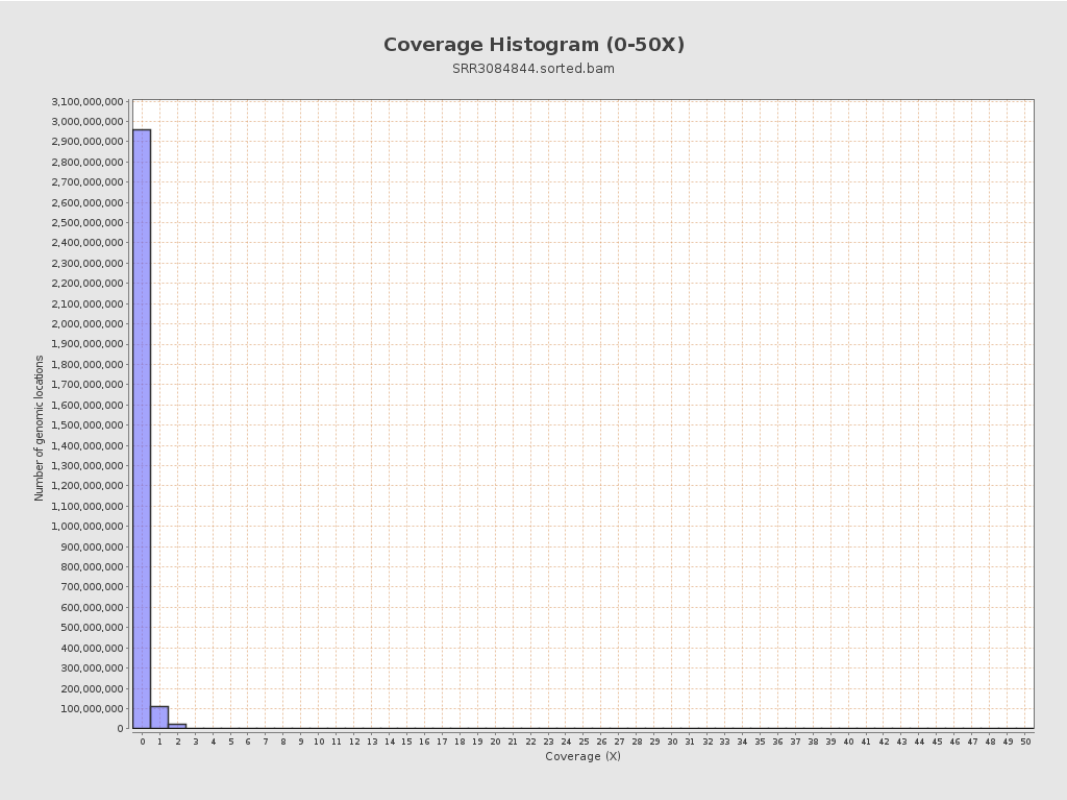
3. Results : Coverage across reference



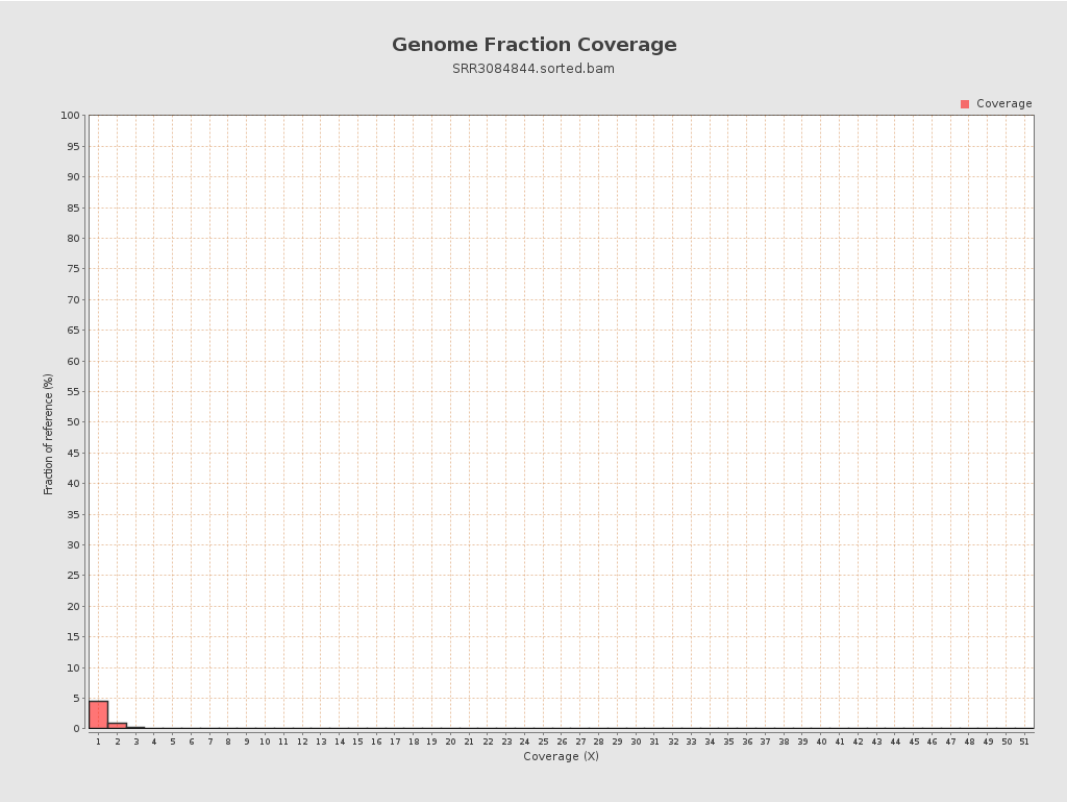
4. Results : Coverage Histogram



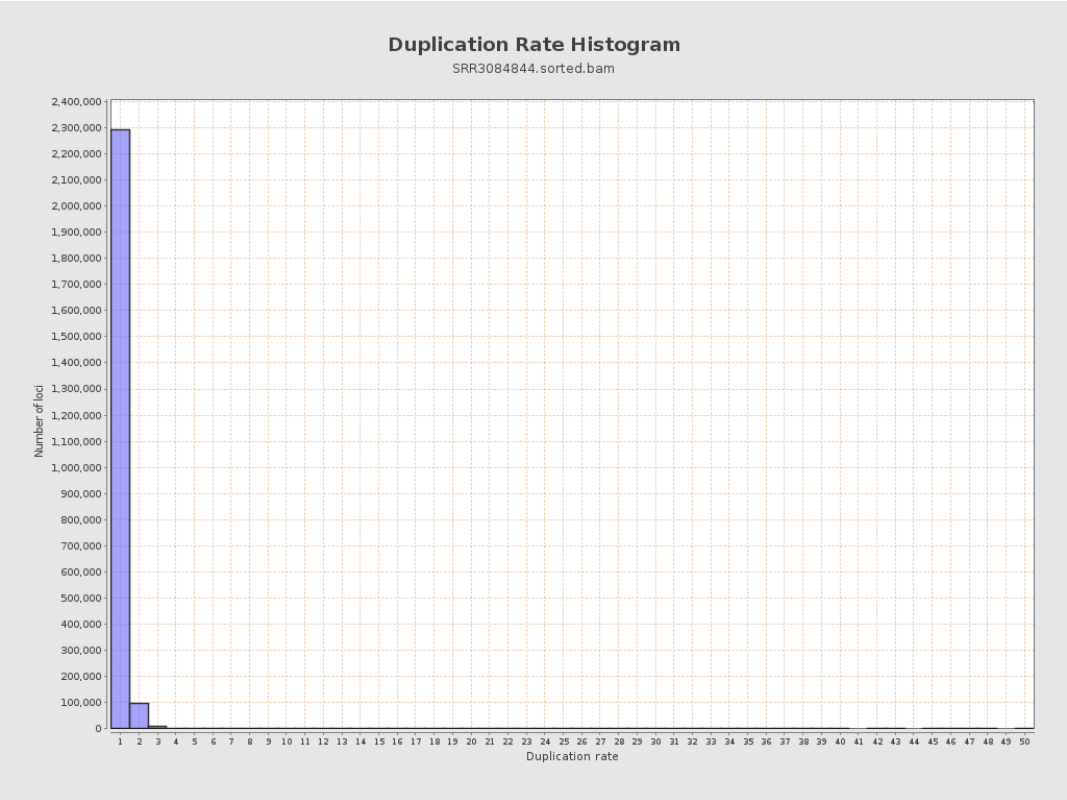
5. Results : Coverage Histogram (0-50X)



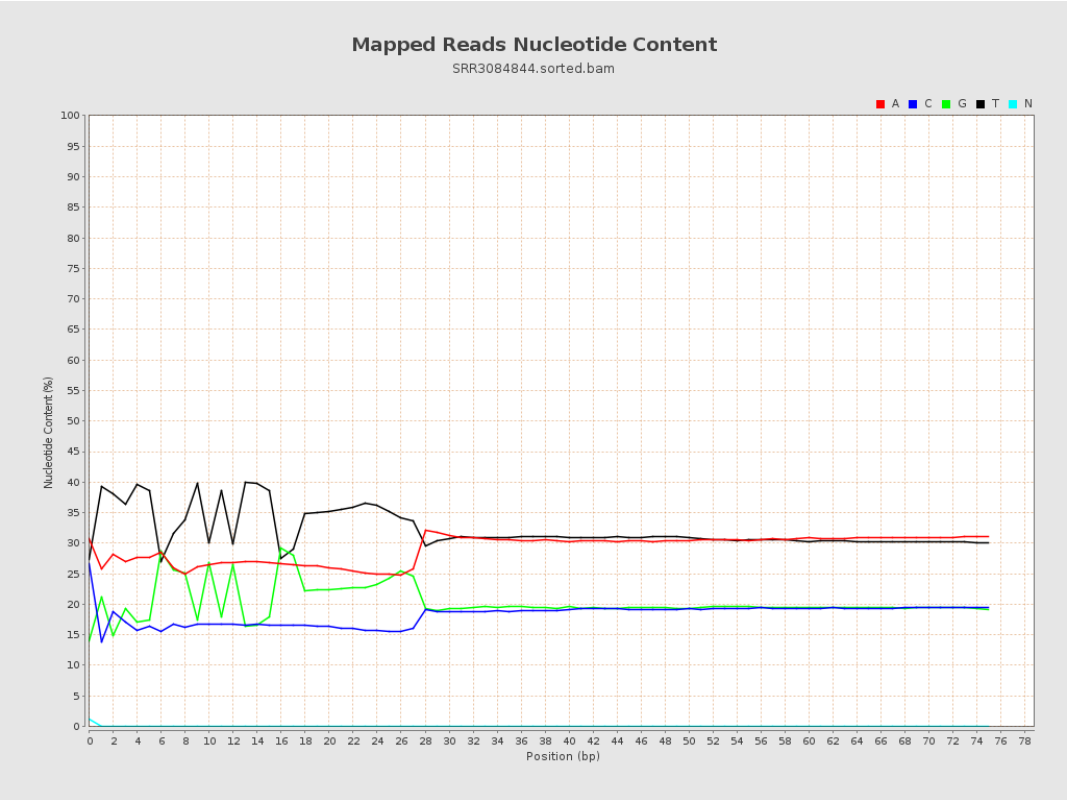
6. Results : Genome Fraction Coverage



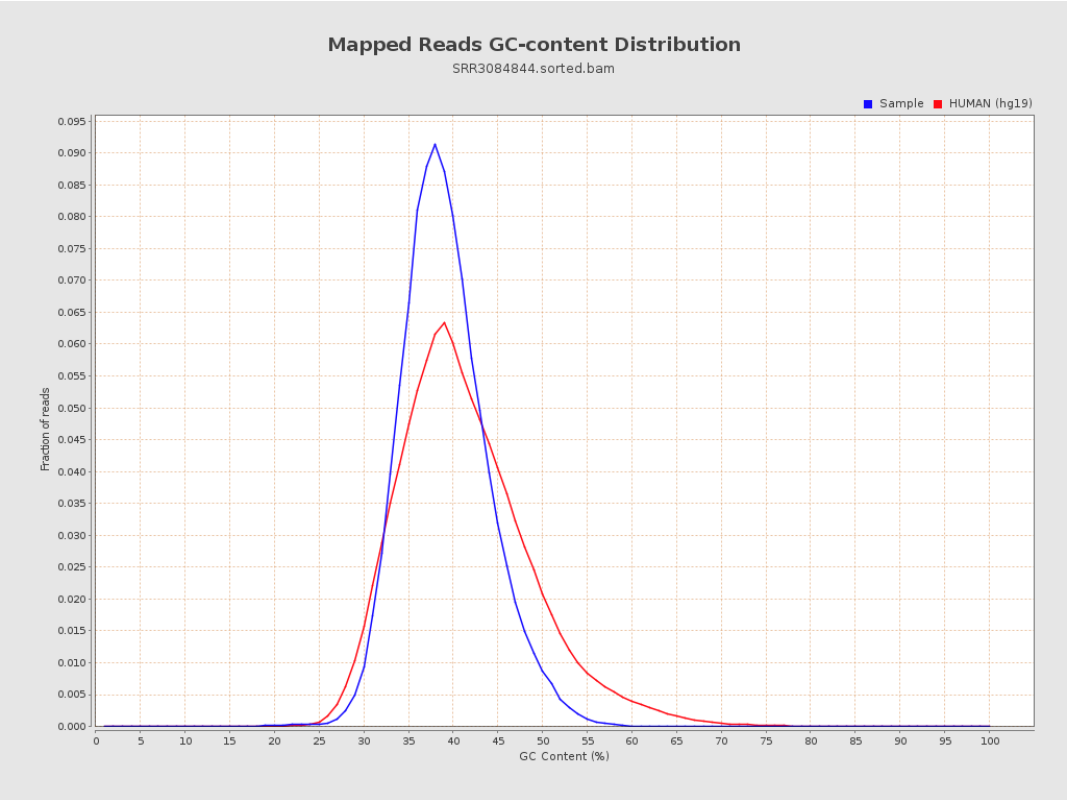
7. Results : Duplication Rate Histogram



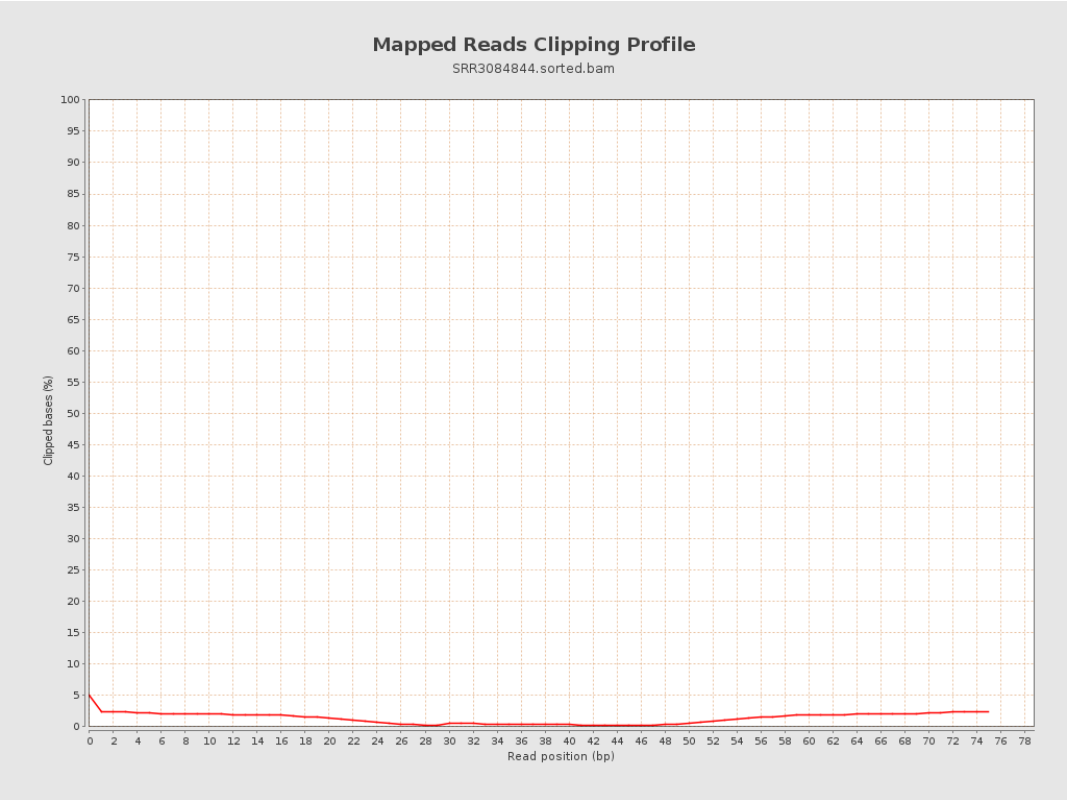
8. Results : Mapped Reads Nucleotide Content



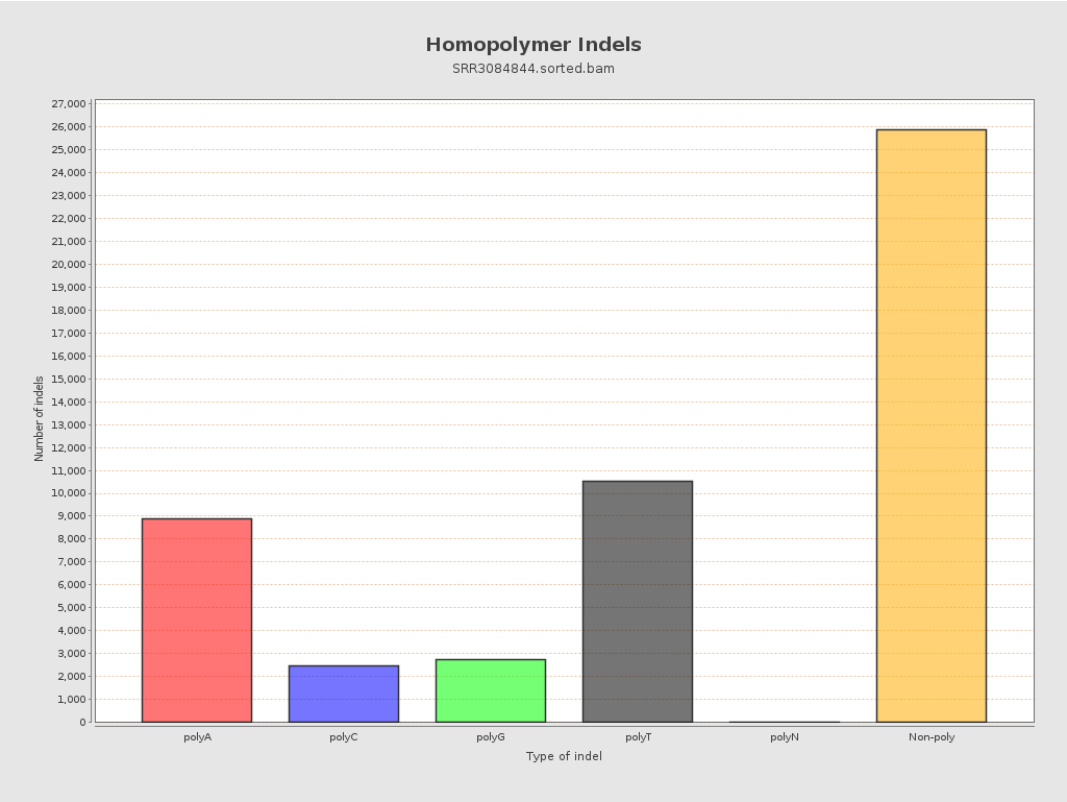
9. Results : Mapped Reads GC-content Distribution



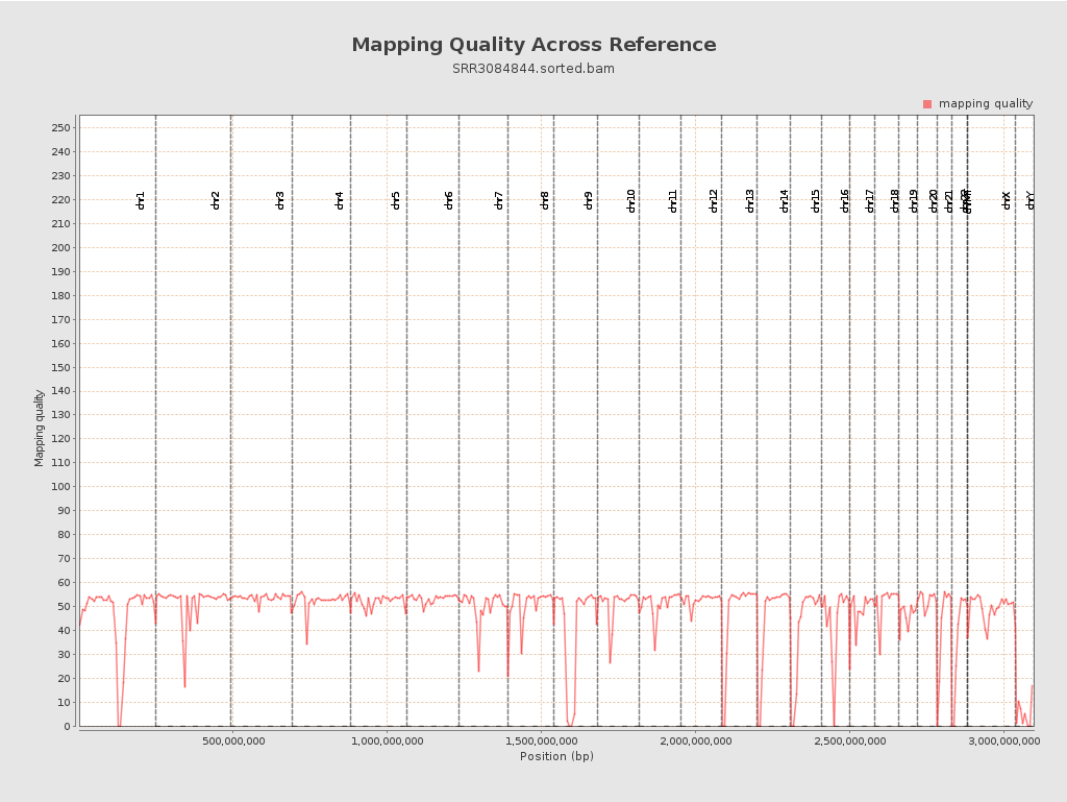
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram