Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:41:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080709.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_SRR3080709 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080709.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:41:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080709.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,196,302
Mapped reads	2,001,336 / 91.12%
Unmapped reads	194,966 / 8.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,841 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	99,036 / 4.51%
Duplication rate	4.17%
Clipped reads	770,338 / 35.07%

2.2. ACGT Content

Number/percentage of A's	38,240,558 / 28.11%
Number/percentage of C's	25,224,829 / 18.54%
Number/percentage of T's	43,173,653 / 31.73%
Number/percentage of G's	29,414,707 / 21.62%
Number/percentage of N's	2,092 / 0%
GC Percentage	40.16%

2.3. Coverage

Mean	0.044

Standard Deviation	0.3675

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Mismatches and indels

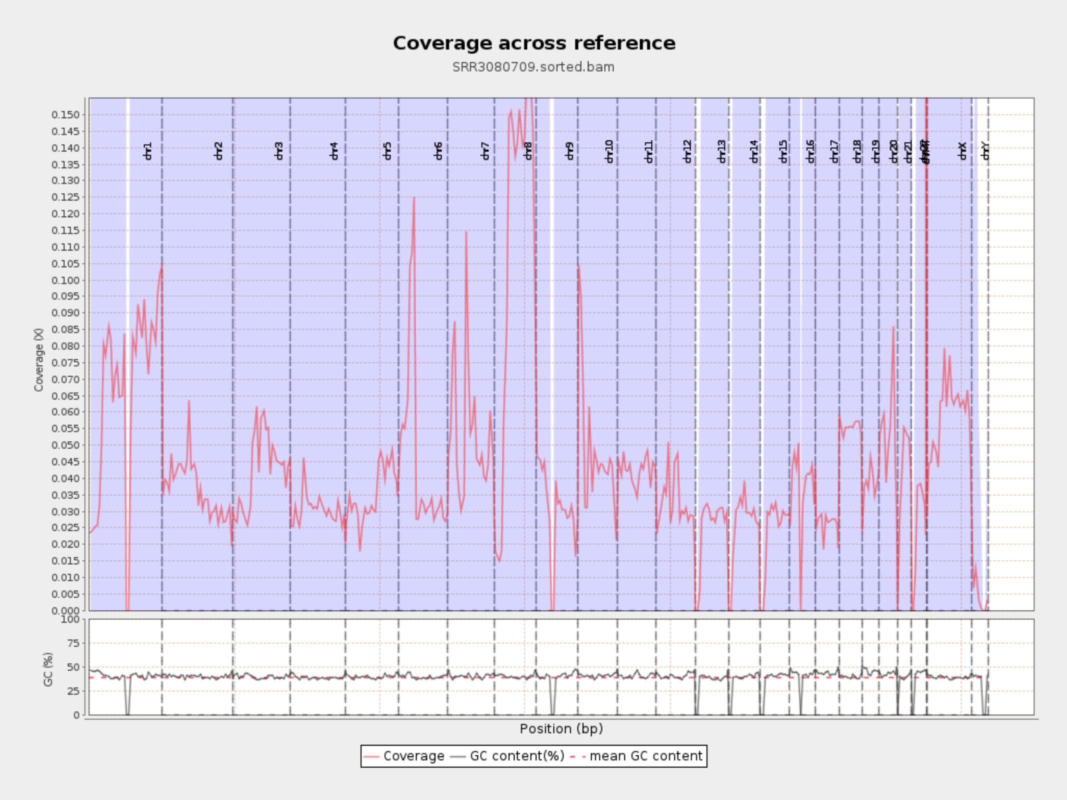
General error rate	0.82%
Mismatches	1,101,828
Insertions	9,644
Mapped reads with at least one insertion	0.48%
Deletions	29,080
Mapped reads with at least one deletion	1.44%
Homopolymer indels	48.15%

2.6. Chromosome stats

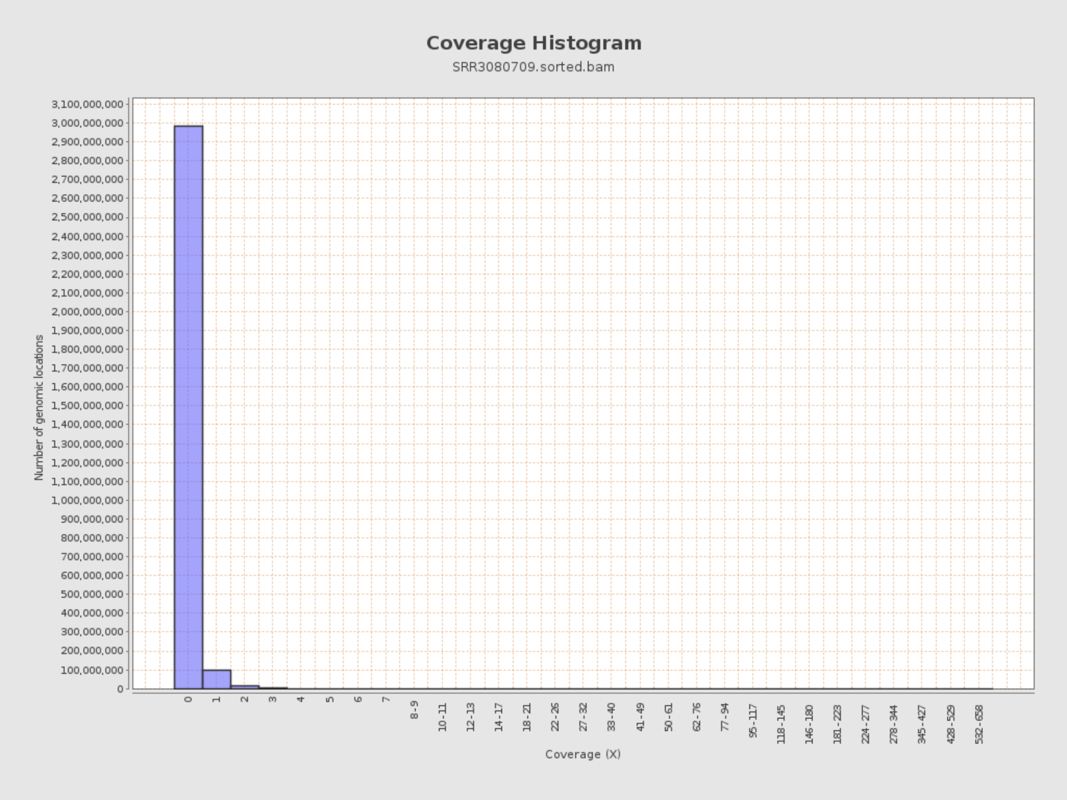
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16451990	0.066	0.5313
chr2	243199373	8903712	0.0366	0.3606
chr3	198022430	8467081	0.0428	0.2359
chr4	191154276	5833234	0.0305	0.2093
chr5	180915260	6358052	0.0351	0.2132
chr6	171115067	7991124	0.0467	0.3326
chr7	159138663	8694307	0.0546	0.8864

chr8	146364022	16130154	0.1102	0.4963
chr9	141213431	4263387	0.0302	0.2672
chr10	135534747	6672696	0.0492	0.3442
chr11	135006516	5708744	0.0423	0.2669
chr12	133851895	4354640	0.0325	0.207
chr13	115169878	2810652	0.0244	0.1782
chr14	107349540	2772500	0.0258	0.1897
chr15	102531392	2430737	0.0237	0.1765
chr16	90354753	3370292	0.0373	0.2399
chr17	81195210	2116953	0.0261	0.1922
chr18	78077248	4348288	0.0557	0.4465
chr19	59128983	2294433	0.0388	0.3497
chr20	63025520	3405954	0.054	0.2715
chr21	48129895	1969301	0.0409	0.2395
chr22	51304566	1248707	0.0243	0.1759
chrMT	16571	86854	5.2413	3.4024
chrX	155270560	9130858	0.0588	0.2971
chrY	59373566	292090	0.0049	0.1046

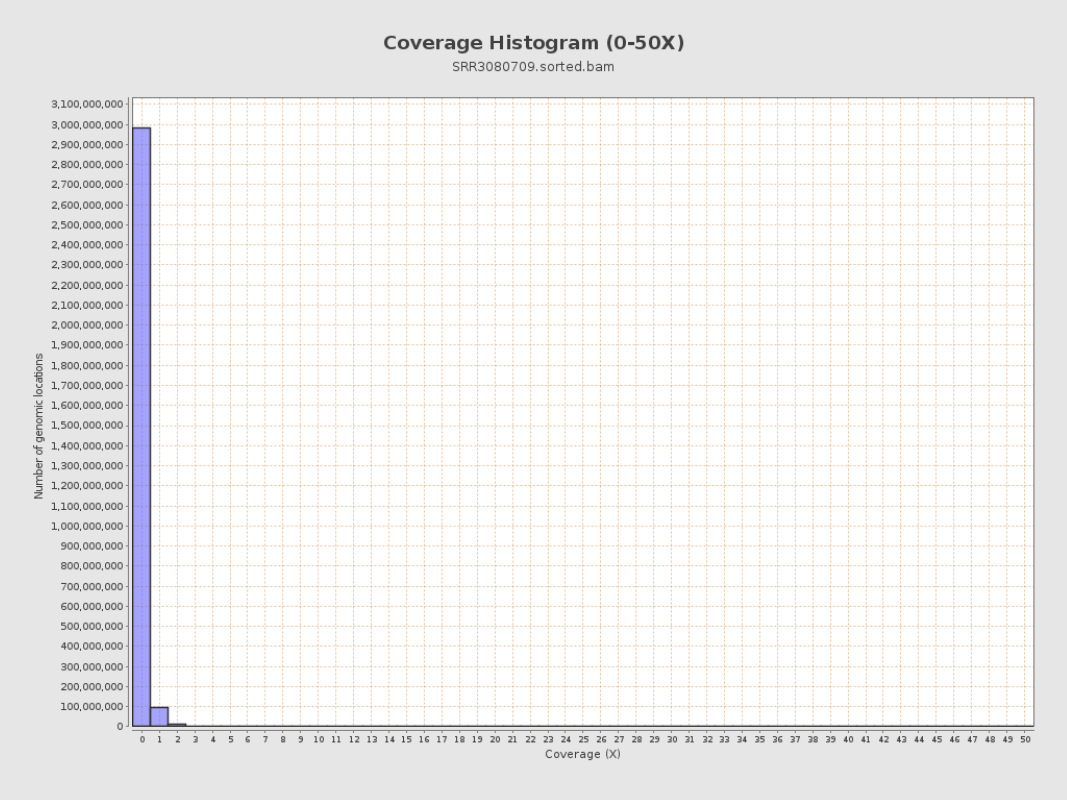
3. Results : Coverage across reference



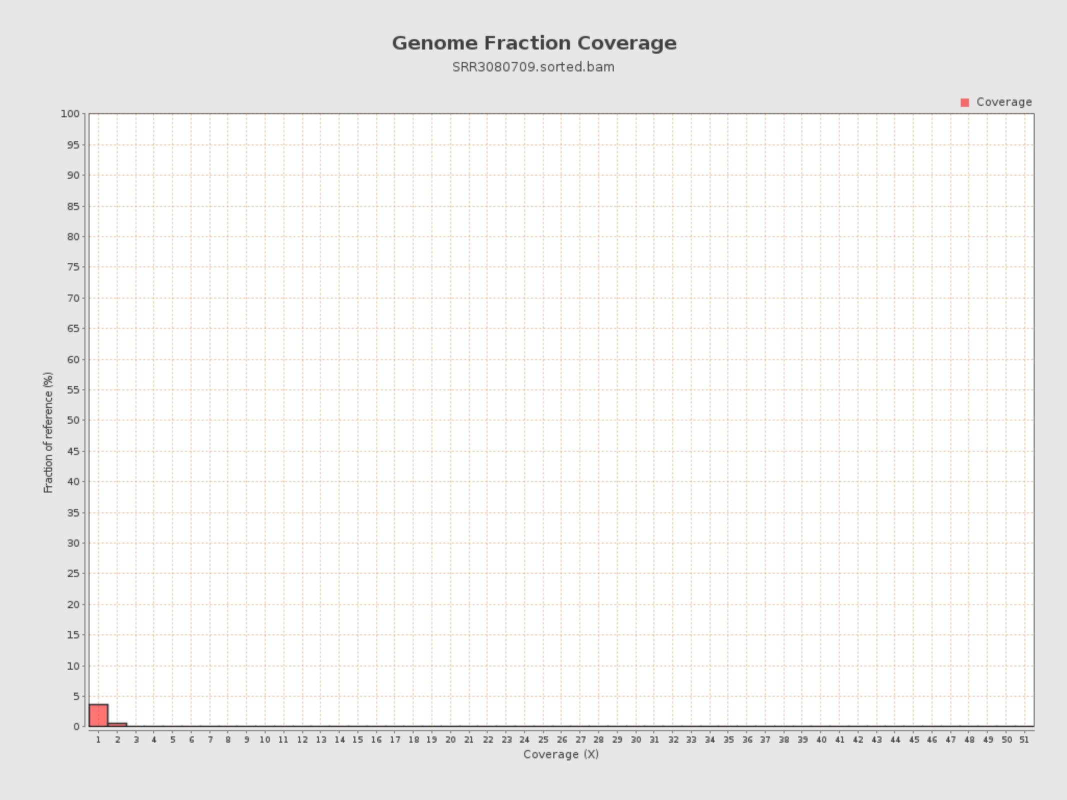
4. Results : Coverage Histogram



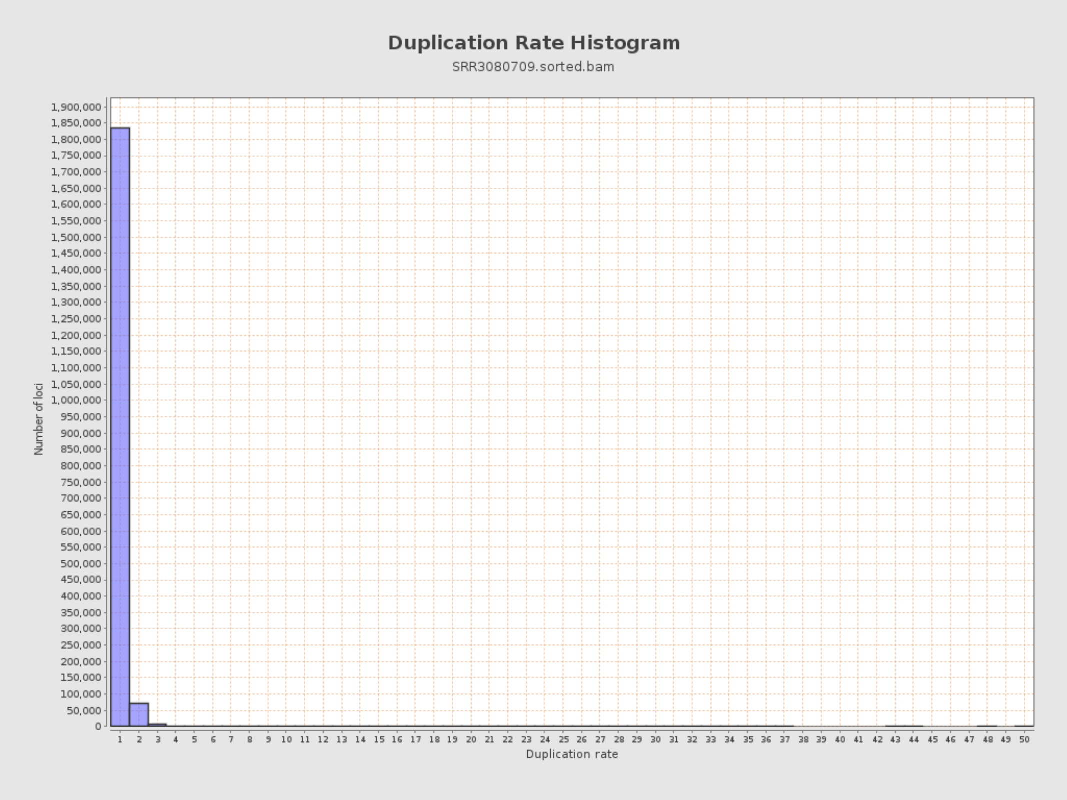
5. Results : Coverage Histogram (0-50X)



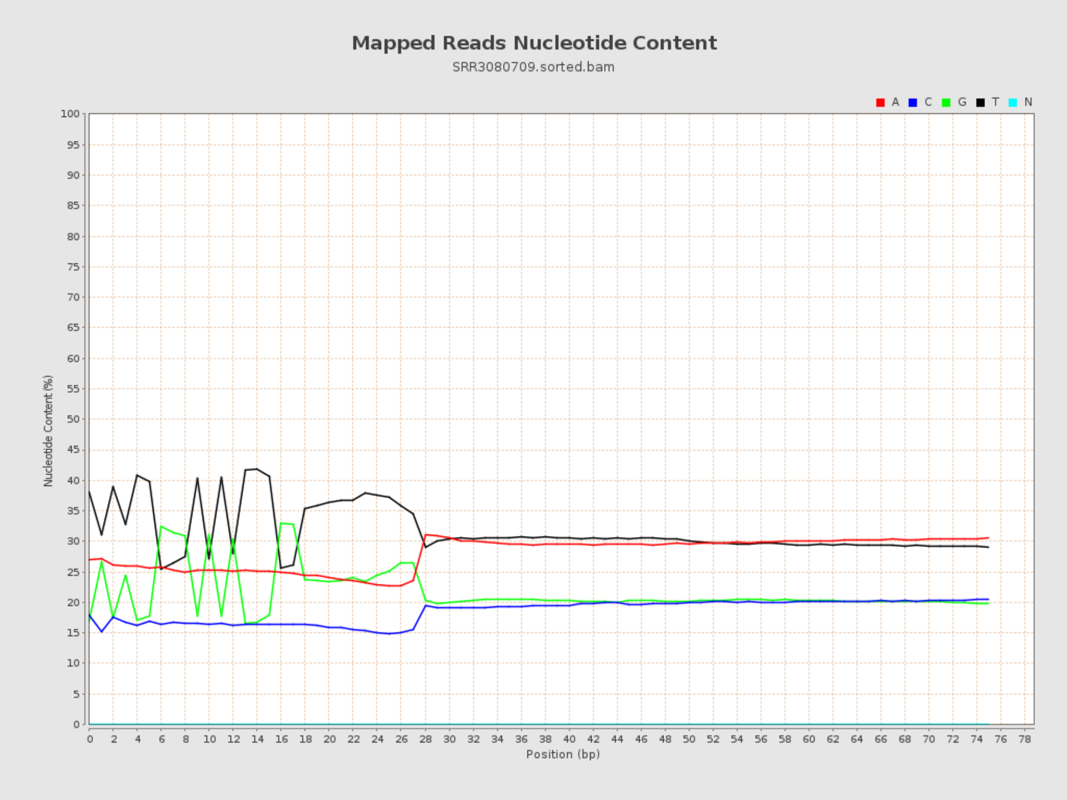
6. Results : Genome Fraction Coverage



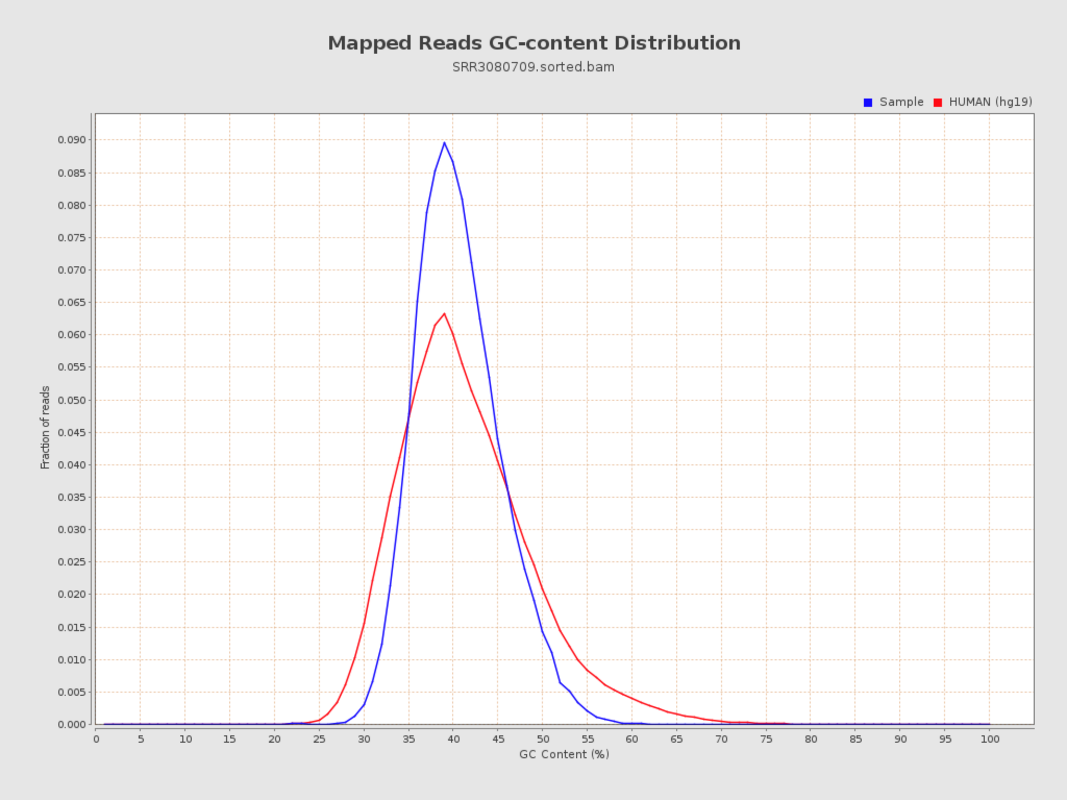
7. Results : Duplication Rate Histogram



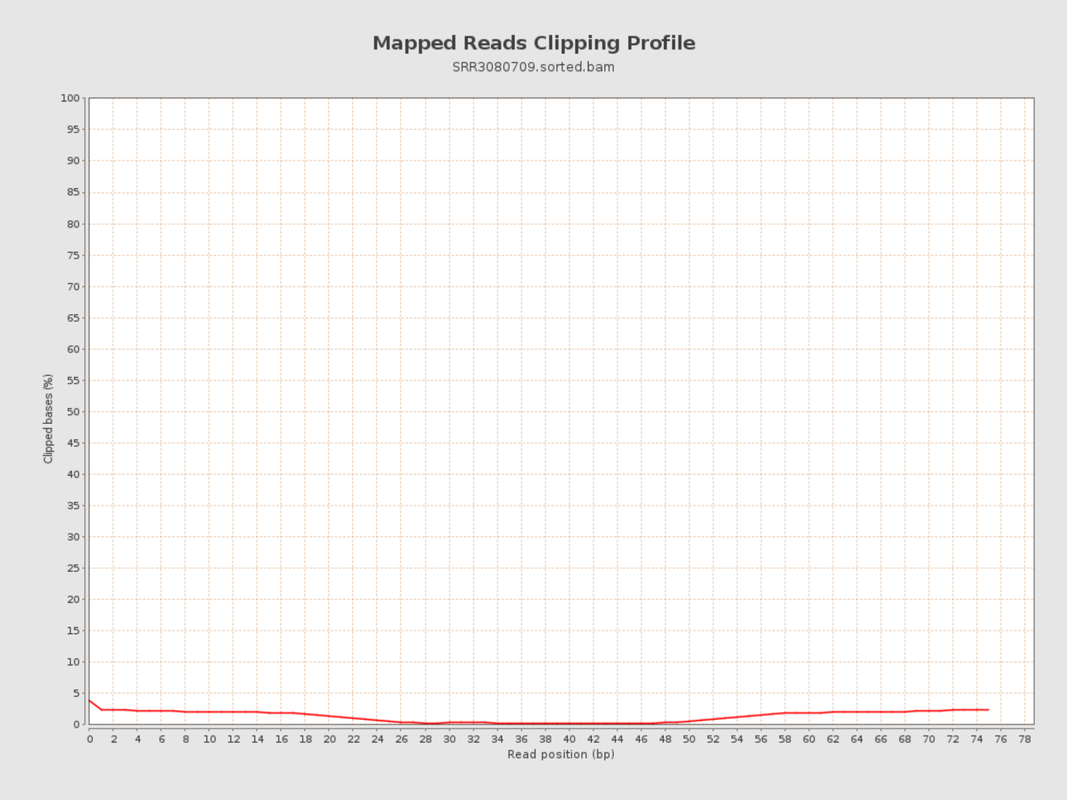
8. Results : Mapped Reads Nucleotide Content



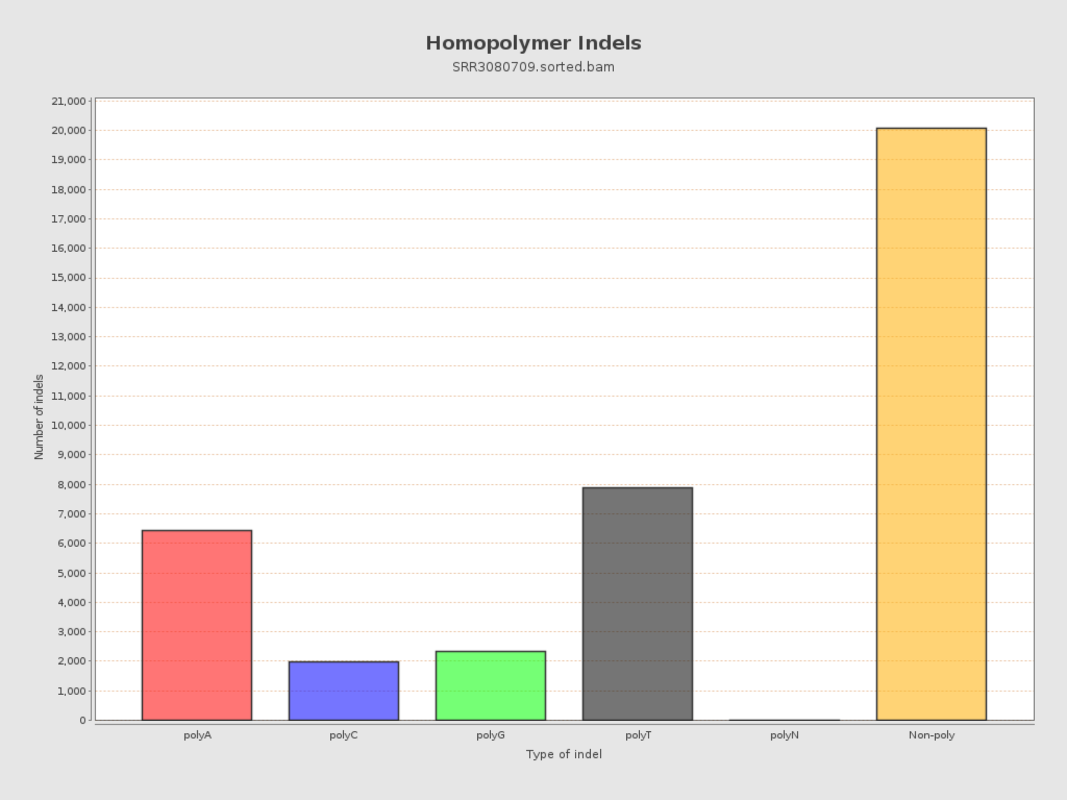
9. Results : Mapped Reads GC-content Distribution



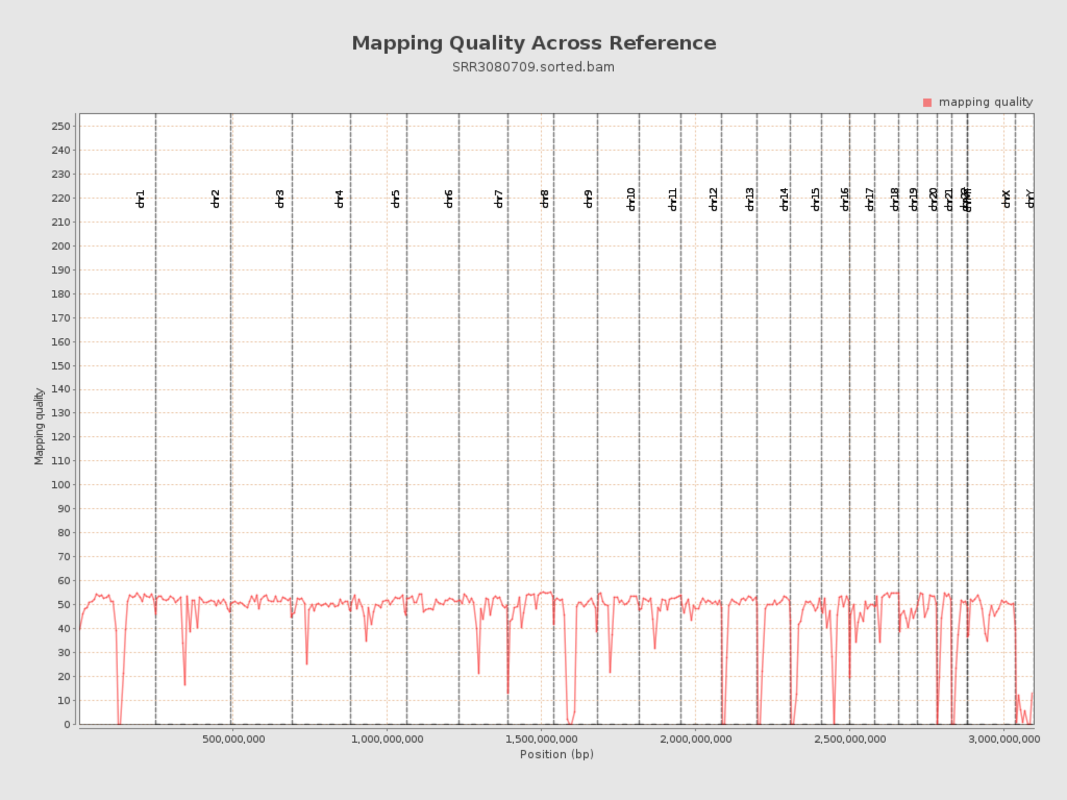
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram