Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:52:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084902.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_SRR3084902 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084902.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:52:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084902.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,209,491
Mapped reads	1,997,726 / 90.42%
Unmapped reads	211,765 / 9.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,535 / 0.93%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	98,792 / 4.47%
Duplication rate	4.21%
Clipped reads	934,327 / 42.29%

2.2. ACGT Content

Number/percentage of A's	35,770,224 / 27.01%
Number/percentage of C's	24,671,122 / 18.63%
Number/percentage of T's	41,657,747 / 31.45%
Number/percentage of G's	30,328,406 / 22.9%
Number/percentage of N's	18,453 / 0.01%
GC Percentage	41.53%

2.3. Coverage

Mean	0.0428

Standard Deviation	0.3151

2.4. Mapping Quality

Mean Mapping Quality	45.05

2.5. Mismatches and indels

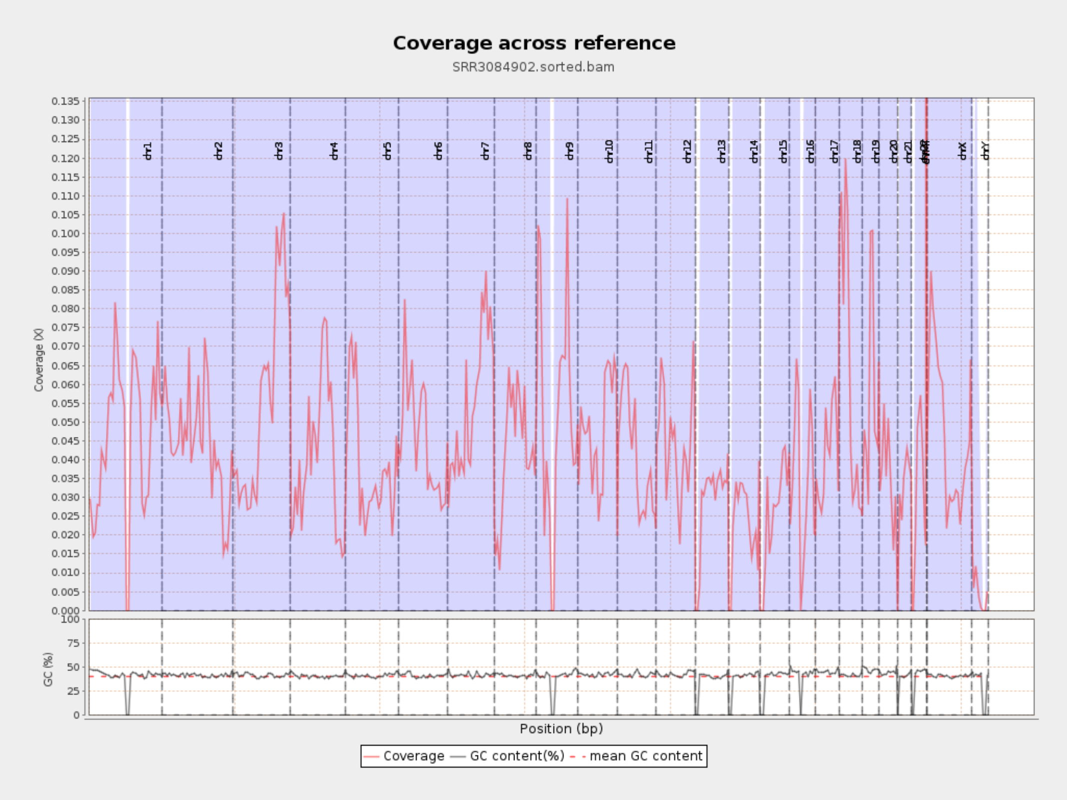
General error rate	0.77%
Mismatches	1,005,146
Insertions	10,412
Mapped reads with at least one insertion	0.52%
Deletions	31,031
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.44%

2.6. Chromosome stats

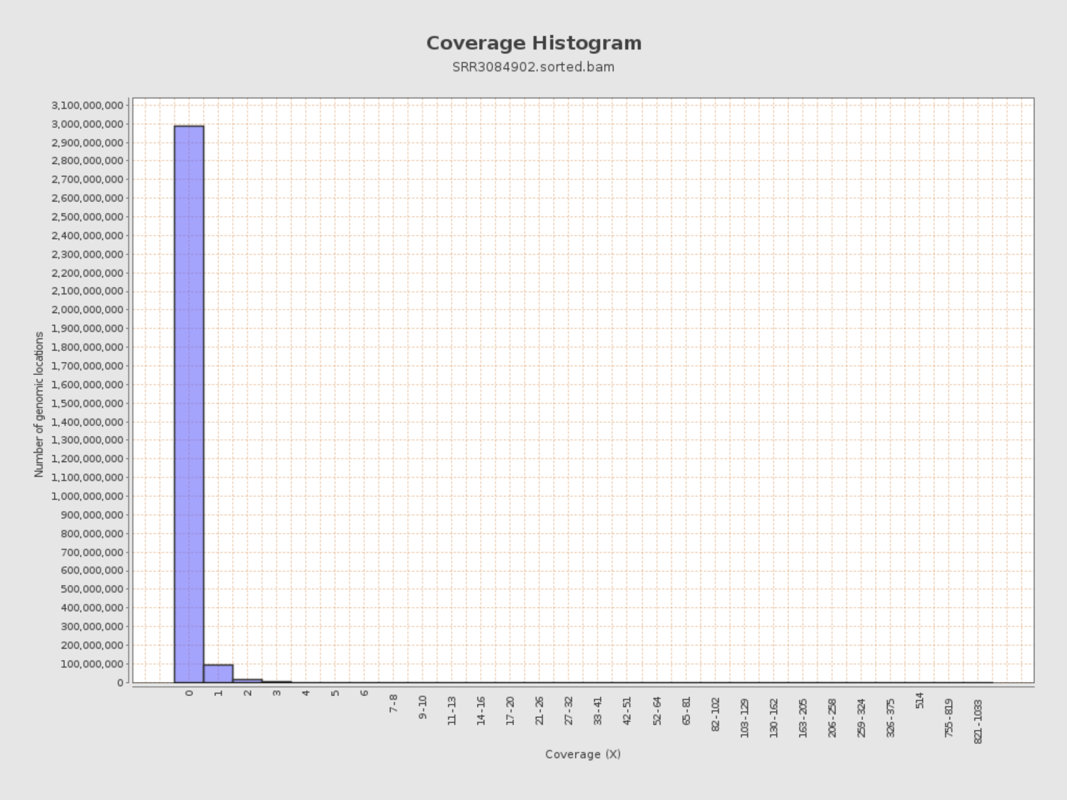
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11470418	0.046	0.398
chr2	243199373	10866483	0.0447	0.5226
chr3	198022430	11030846	0.0557	0.2799
chr4	191154276	7630727	0.0399	0.2435
chr5	180915260	7016676	0.0388	0.2346
chr6	171115067	7715794	0.0451	0.2687
chr7	159138663	8797434	0.0553	0.3378

chr8	146364022	6159546	0.0421	0.2994
chr9	141213431	7375606	0.0522	0.3162
chr10	135534747	6487969	0.0479	0.2979
chr11	135006516	5487120	0.0406	0.2783
chr12	133851895	5899574	0.0441	0.2493
chr13	115169878	3254725	0.0283	0.2003
chr14	107349540	2366579	0.022	0.1758
chr15	102531392	2603417	0.0254	0.2044
chr16	90354753	3235187	0.0358	0.2293
chr17	81195210	3403596	0.0419	0.2474
chr18	78077248	5044981	0.0646	0.4347
chr19	59128983	3390908	0.0573	0.3531
chr20	63025520	2266731	0.036	0.2258
chr21	48129895	1508023	0.0313	0.2132
chr22	51304566	1493031	0.0291	0.2007
chrMT	16571	405405	24.4647	12.6361
chrX	155270560	7306591	0.0471	0.2675
chrY	59373566	280211	0.0047	0.0912

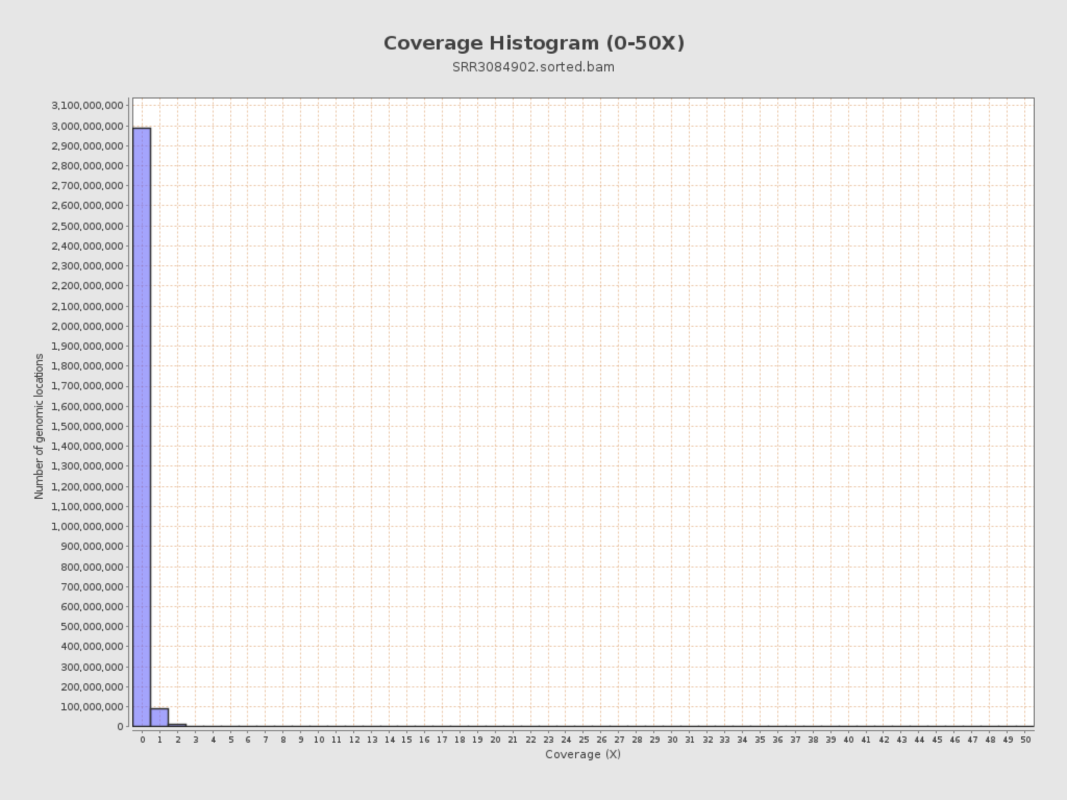
3. Results : Coverage across reference



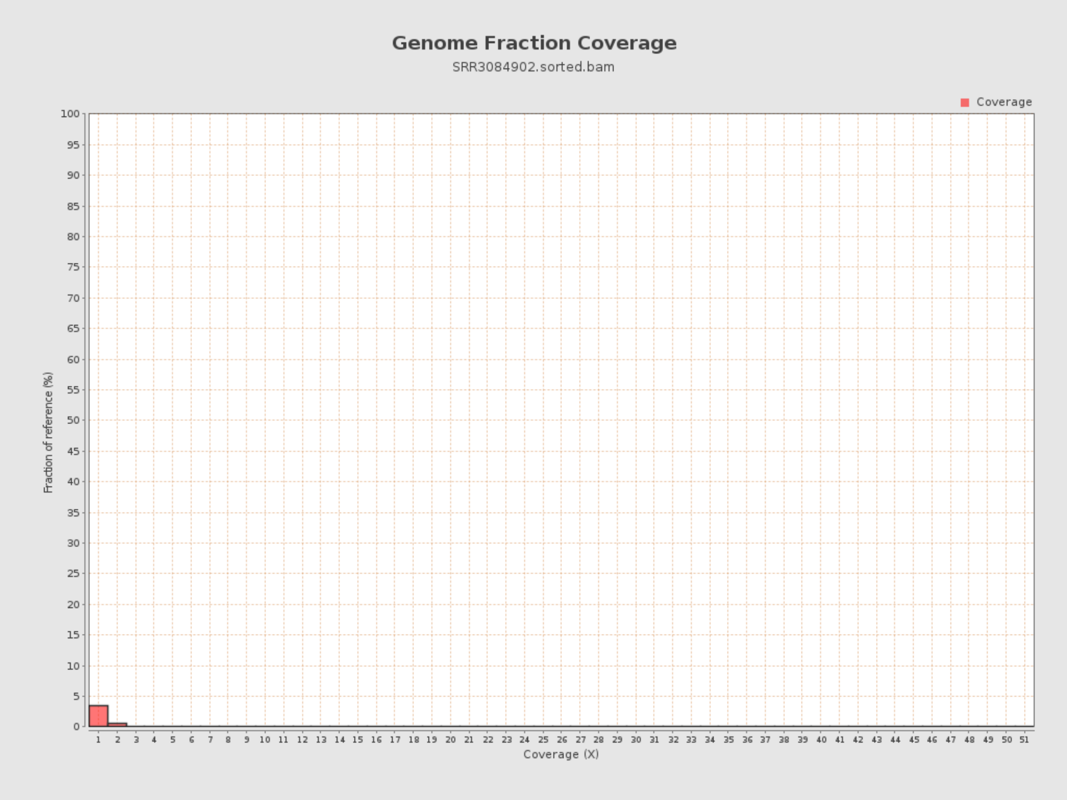
4. Results : Coverage Histogram



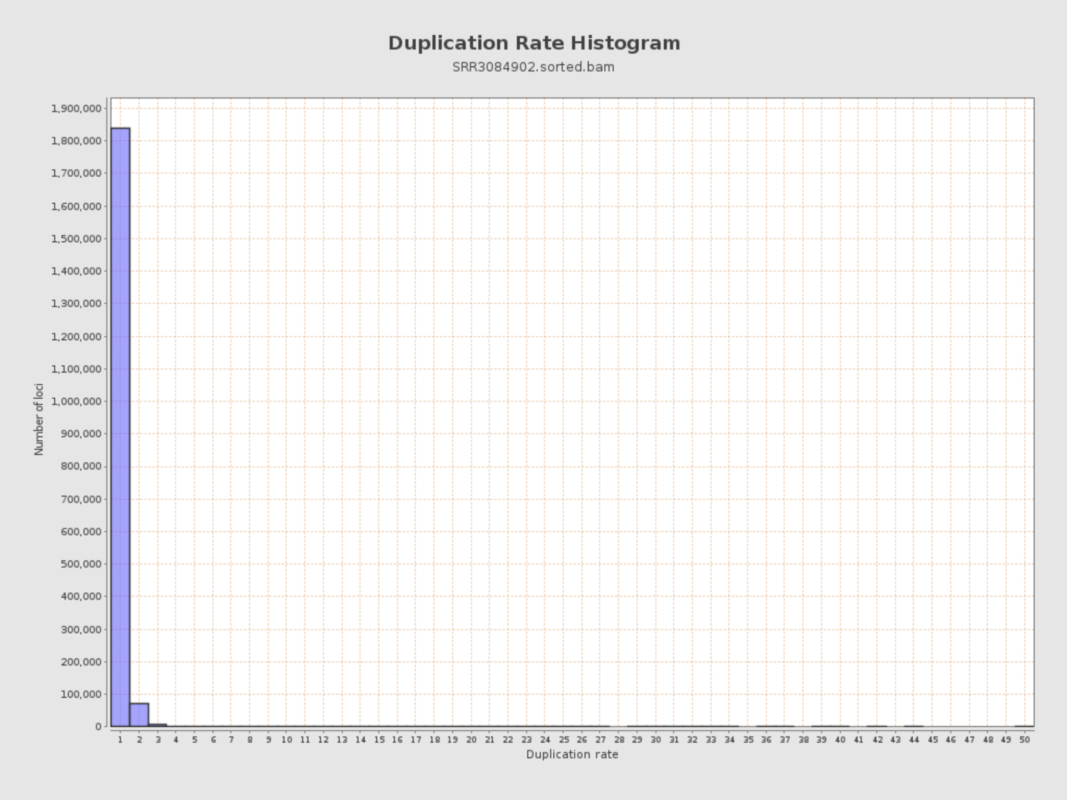
5. Results : Coverage Histogram (0-50X)



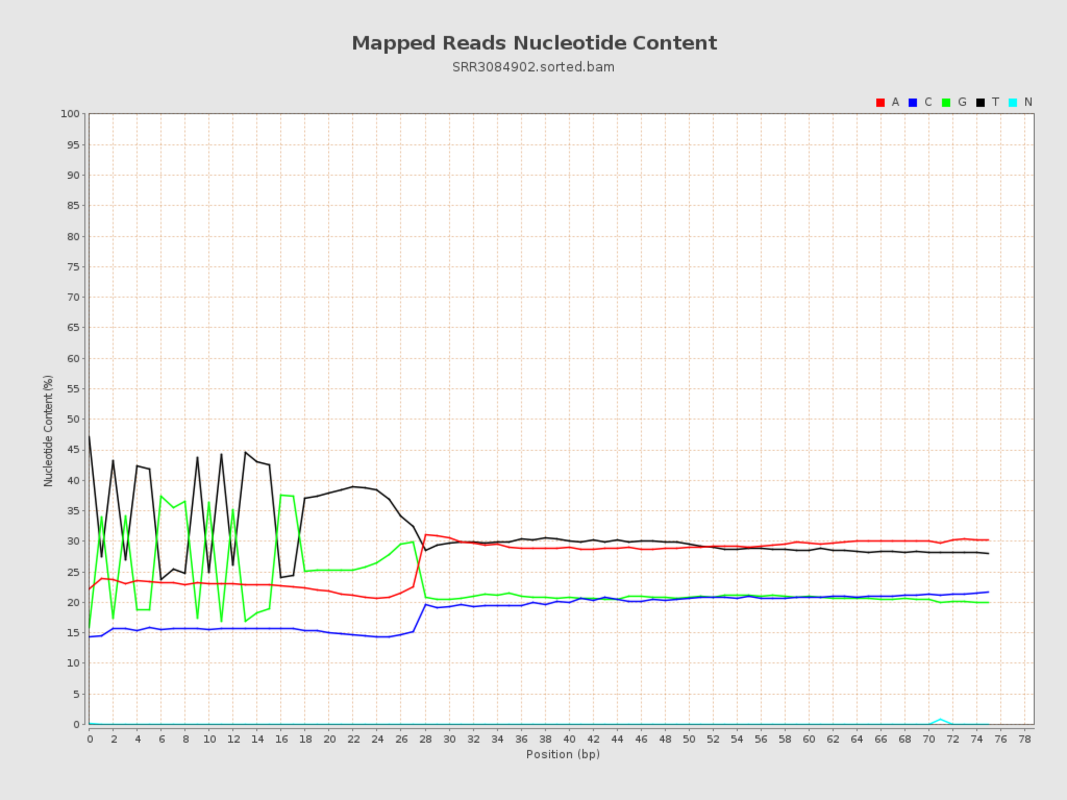
6. Results : Genome Fraction Coverage



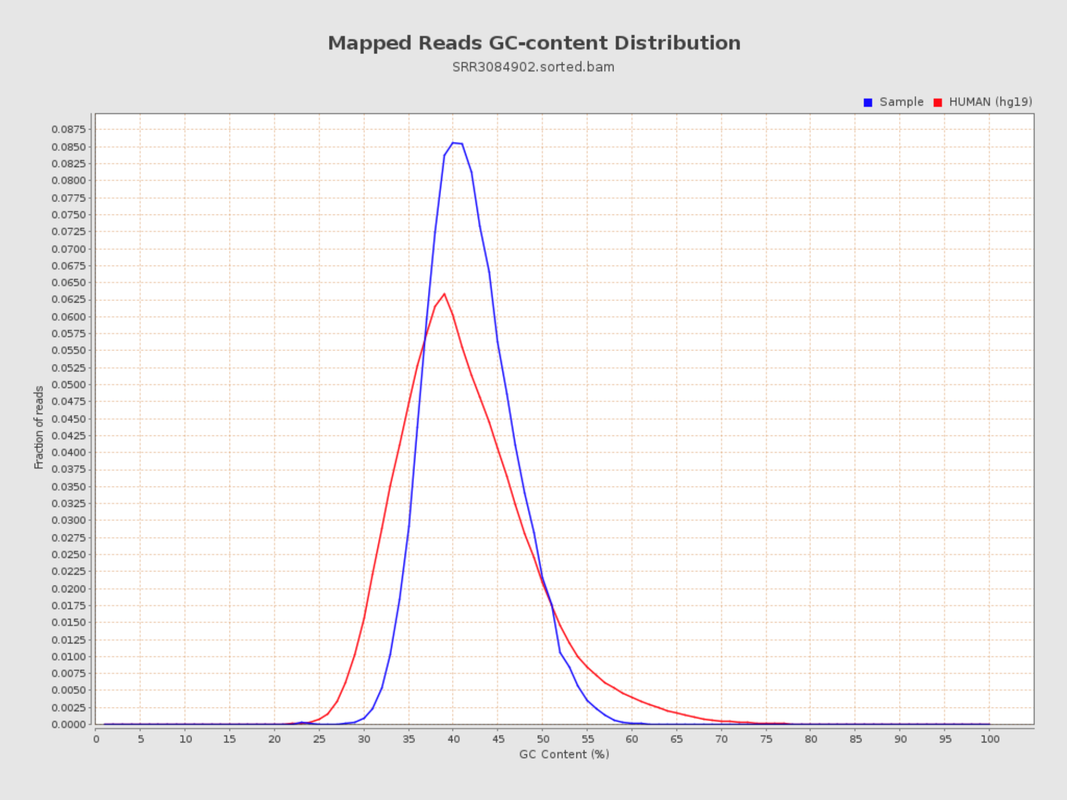
7. Results : Duplication Rate Histogram



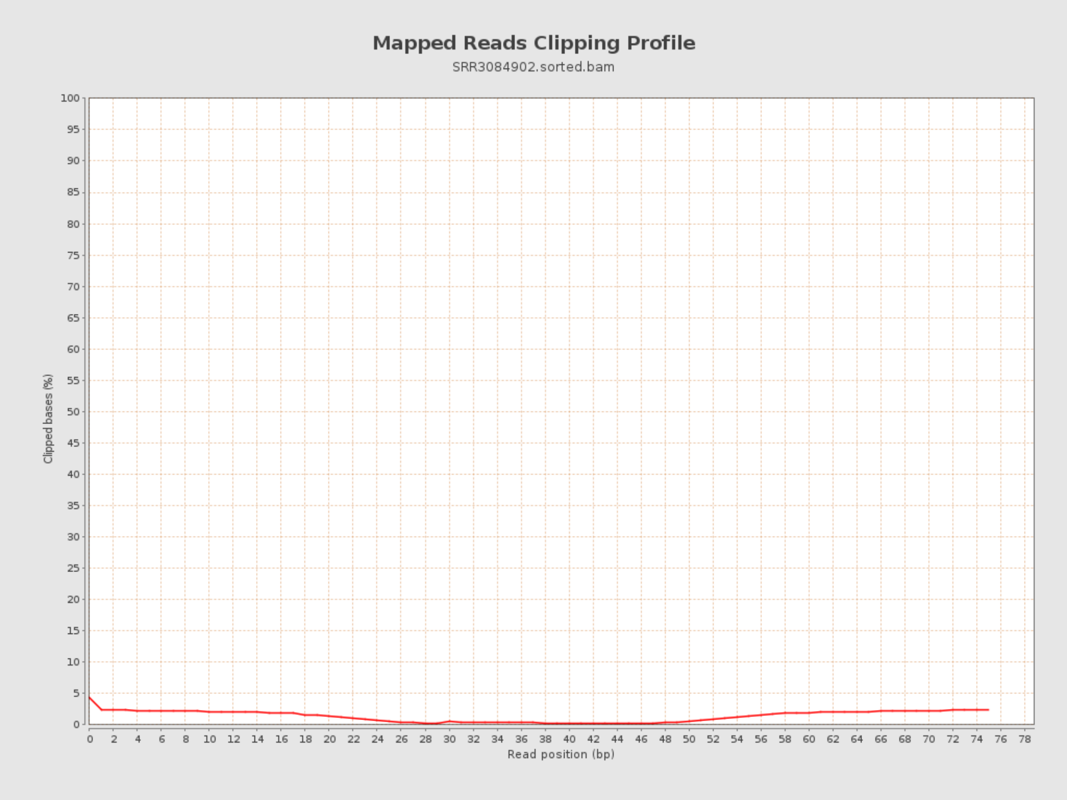
8. Results : Mapped Reads Nucleotide Content



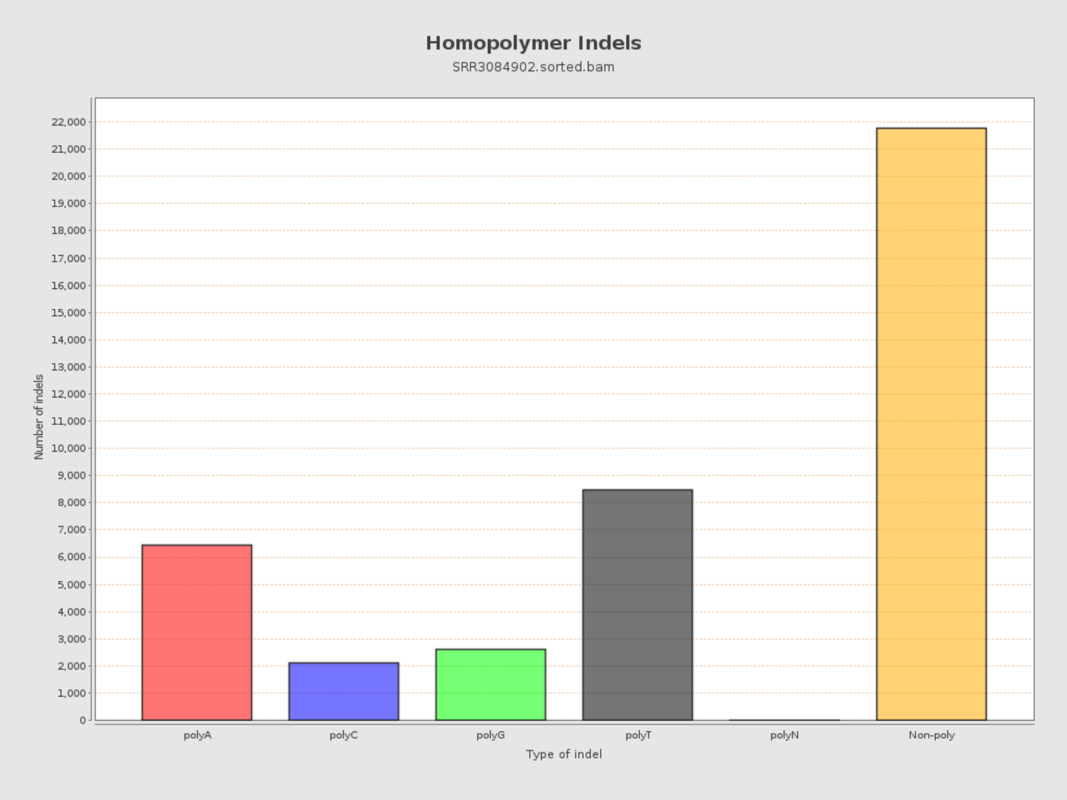
9. Results : Mapped Reads GC-content Distribution



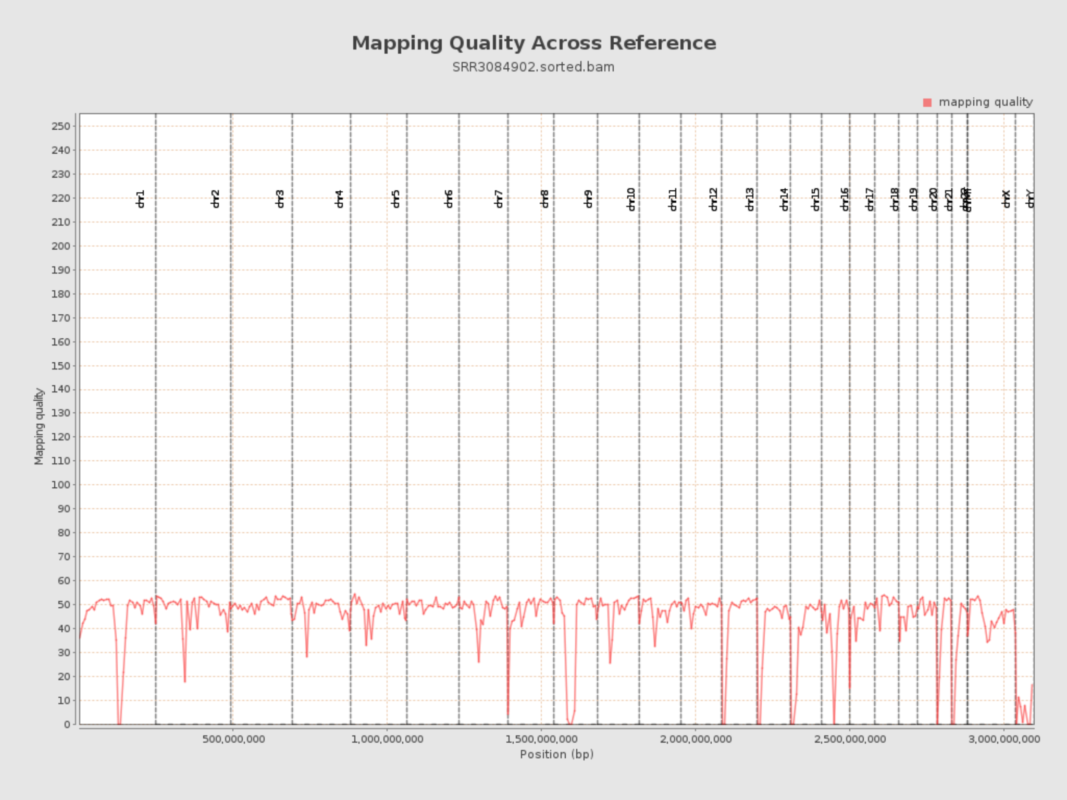
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram