Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:15:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084908.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_SRR3084908 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084908.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:15:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084908.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,404,961
Mapped reads	2,131,943 / 88.65%
Unmapped reads	273,018 / 11.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,665 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	103,503 / 4.3%
Duplication rate	3.17%
Clipped reads	1,028,796 / 42.78%

2.2. ACGT Content

Number/percentage of A's	39,210,061 / 27.79%
Number/percentage of C's	26,803,534 / 19%
Number/percentage of T's	42,479,309 / 30.1%
Number/percentage of G's	32,593,961 / 23.1%
Number/percentage of N's	21,077 / 0.01%
GC Percentage	42.09%

2.3. Coverage

Mean	0.0456

Standard Deviation	0.6065

2.4. Mapping Quality

Mean Mapping Quality	43.02

2.5. Mismatches and indels

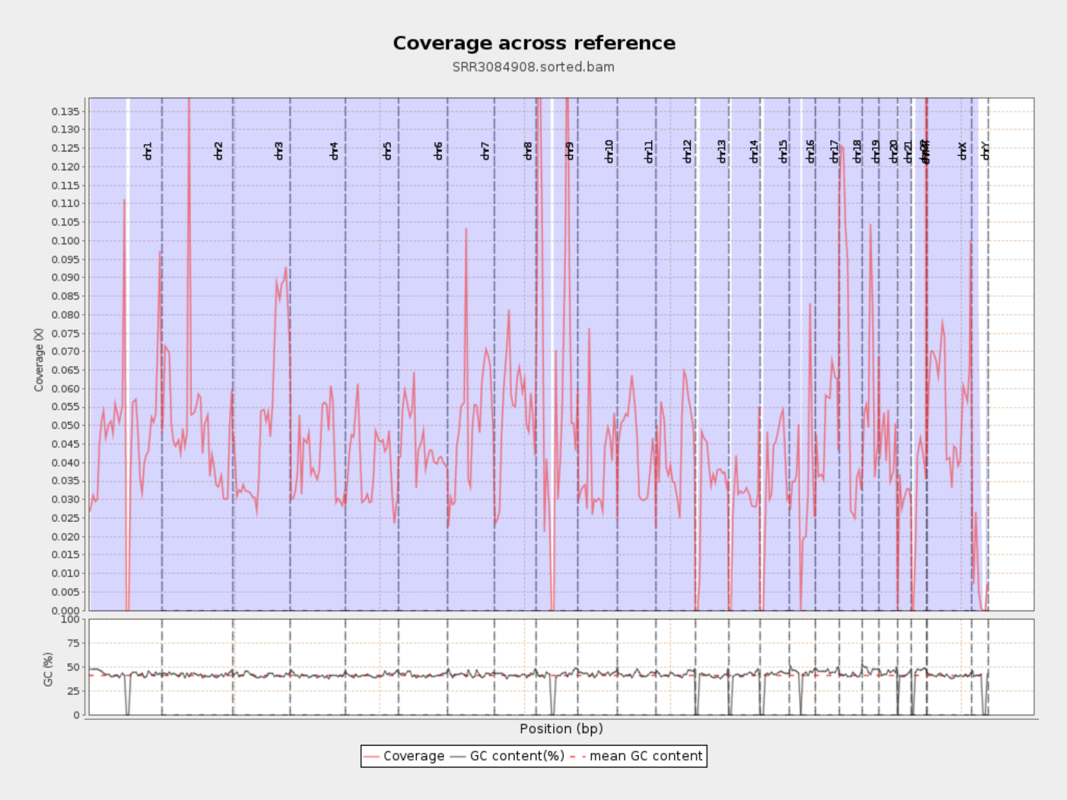
General error rate	0.91%
Mismatches	1,267,255
Insertions	12,293
Mapped reads with at least one insertion	0.57%
Deletions	27,976
Mapped reads with at least one deletion	1.3%
Homopolymer indels	43.77%

2.6. Chromosome stats

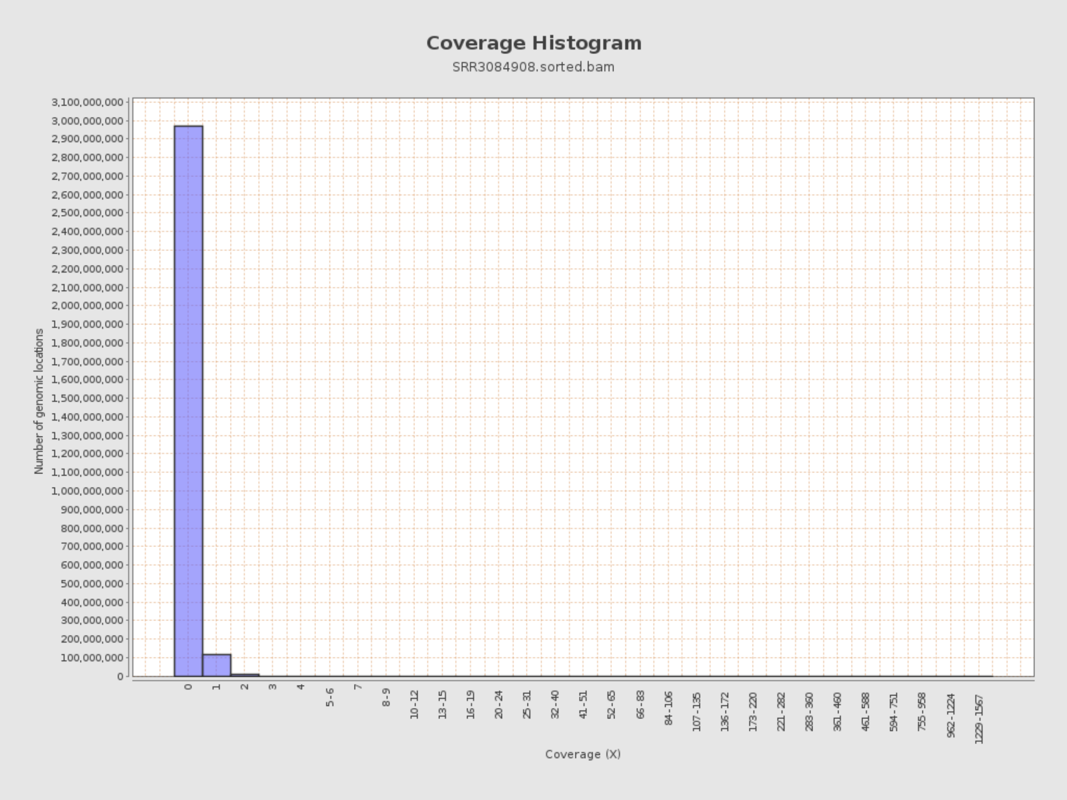
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11772136	0.0472	1.3617
chr2	243199373	12314280	0.0506	0.7782
chr3	198022430	10369866	0.0524	0.2506
chr4	191154276	7844054	0.041	0.235
chr5	180915260	7212779	0.0399	0.2425
chr6	171115067	7778034	0.0455	0.2626
chr7	159138663	8261973	0.0519	0.6936

chr8	146364022	7765972	0.0531	0.6421
chr9	141213431	9233360	0.0654	0.6404
chr10	135534747	5153854	0.038	0.4244
chr11	135006516	5918860	0.0438	0.5155
chr12	133851895	6071610	0.0454	0.2521
chr13	115169878	3758542	0.0326	0.1922
chr14	107349540	2968236	0.0277	0.254
chr15	102531392	3593448	0.035	0.2124
chr16	90354753	3079157	0.0341	0.2783
chr17	81195210	4209617	0.0518	0.3062
chr18	78077248	5210090	0.0667	1.2281
chr19	59128983	3558353	0.0602	0.8104
chr20	63025520	2821607	0.0448	0.258
chr21	48129895	1382703	0.0287	0.2336
chr22	51304566	1508000	0.0294	0.1818
chrMT	16571	82204	4.9607	3.5128
chrX	155270560	8838796	0.0569	0.3557
chrY	59373566	448528	0.0076	0.2592

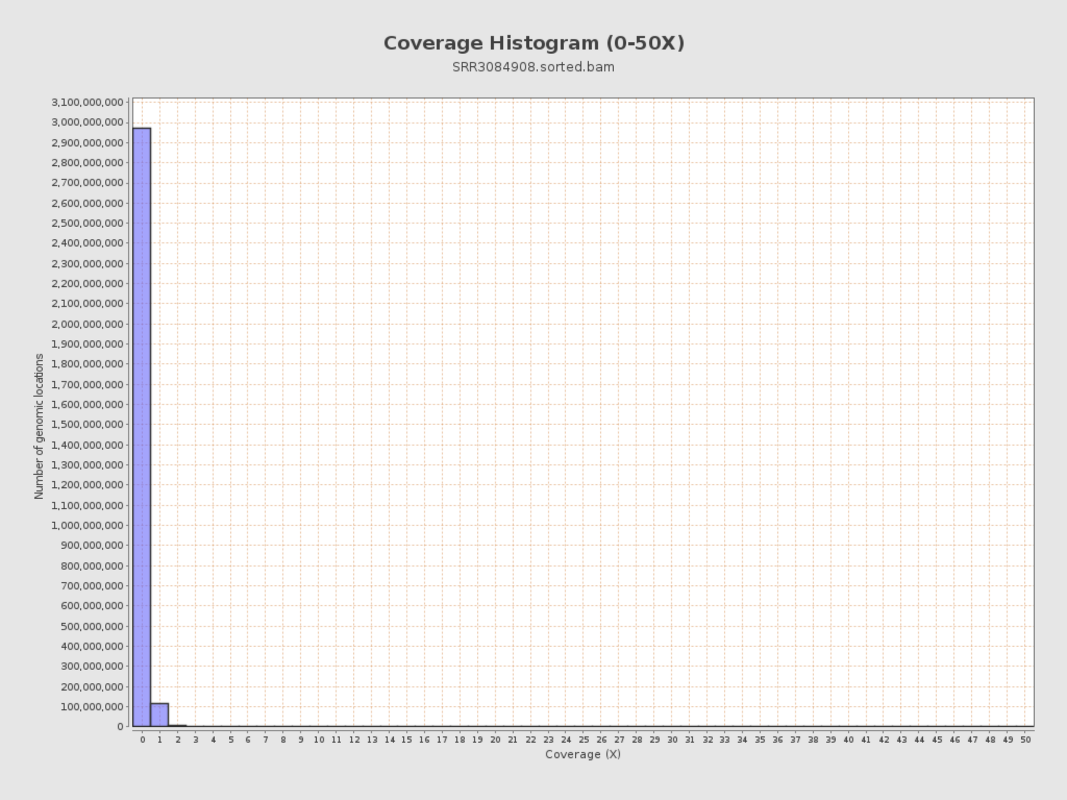
3. Results : Coverage across reference



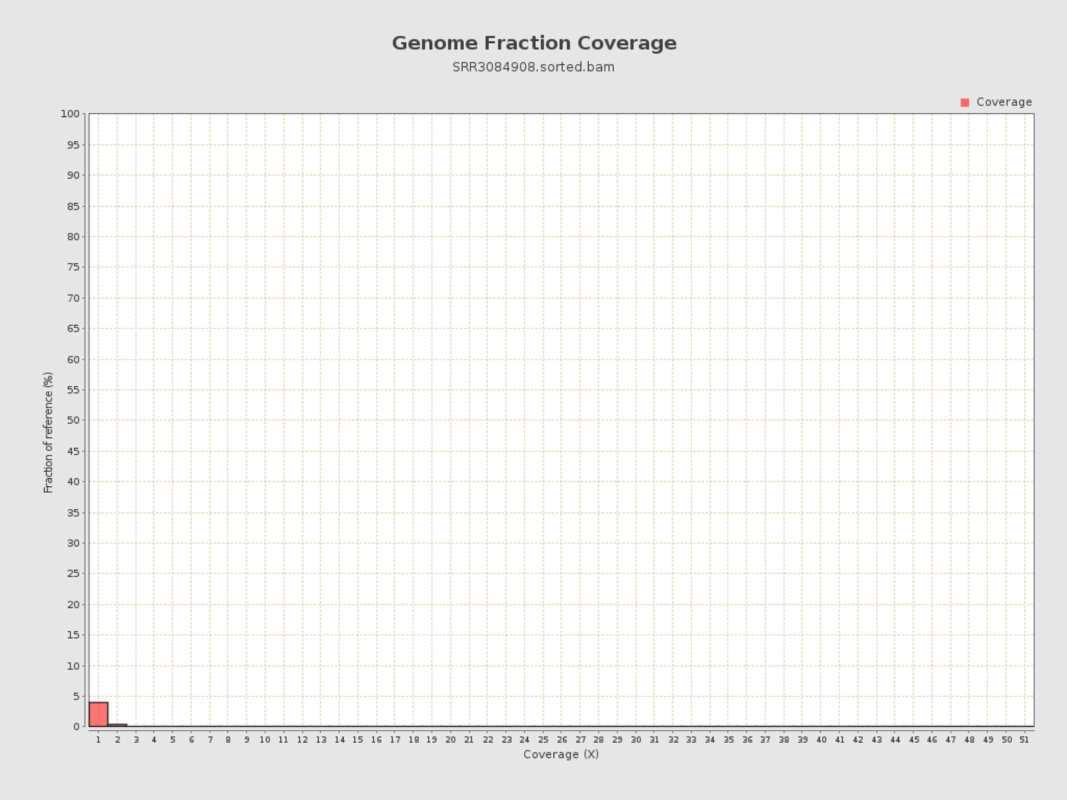
4. Results : Coverage Histogram



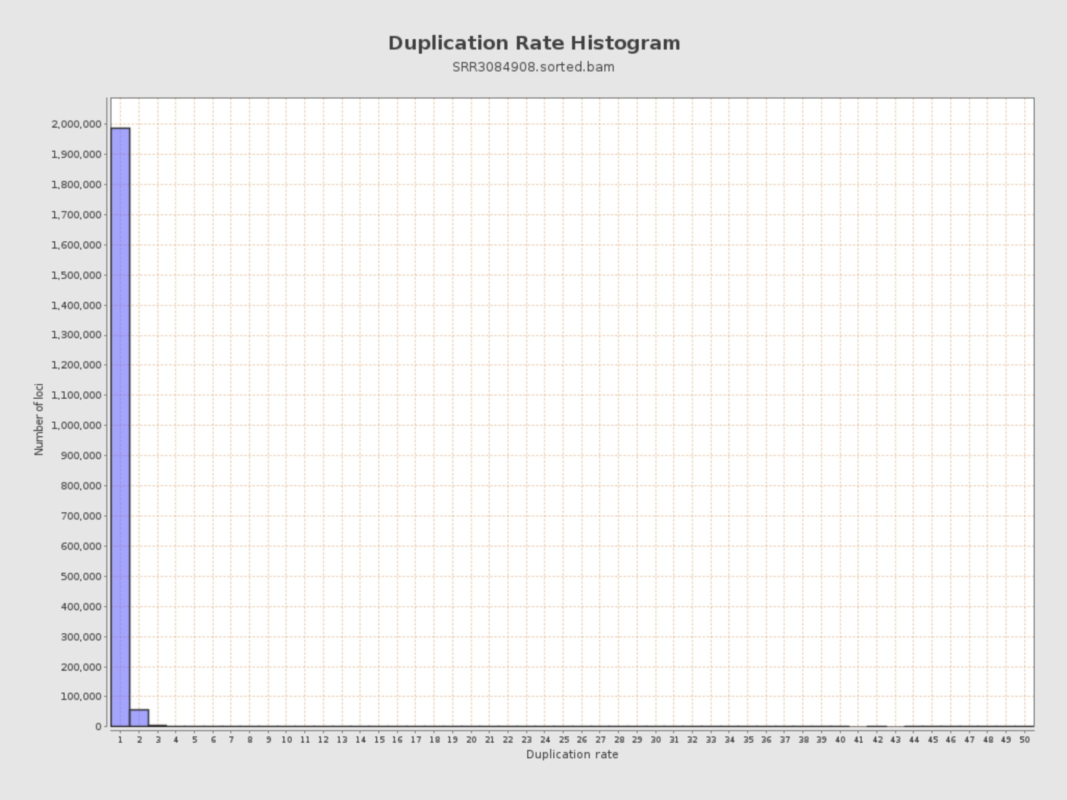
5. Results : Coverage Histogram (0-50X)



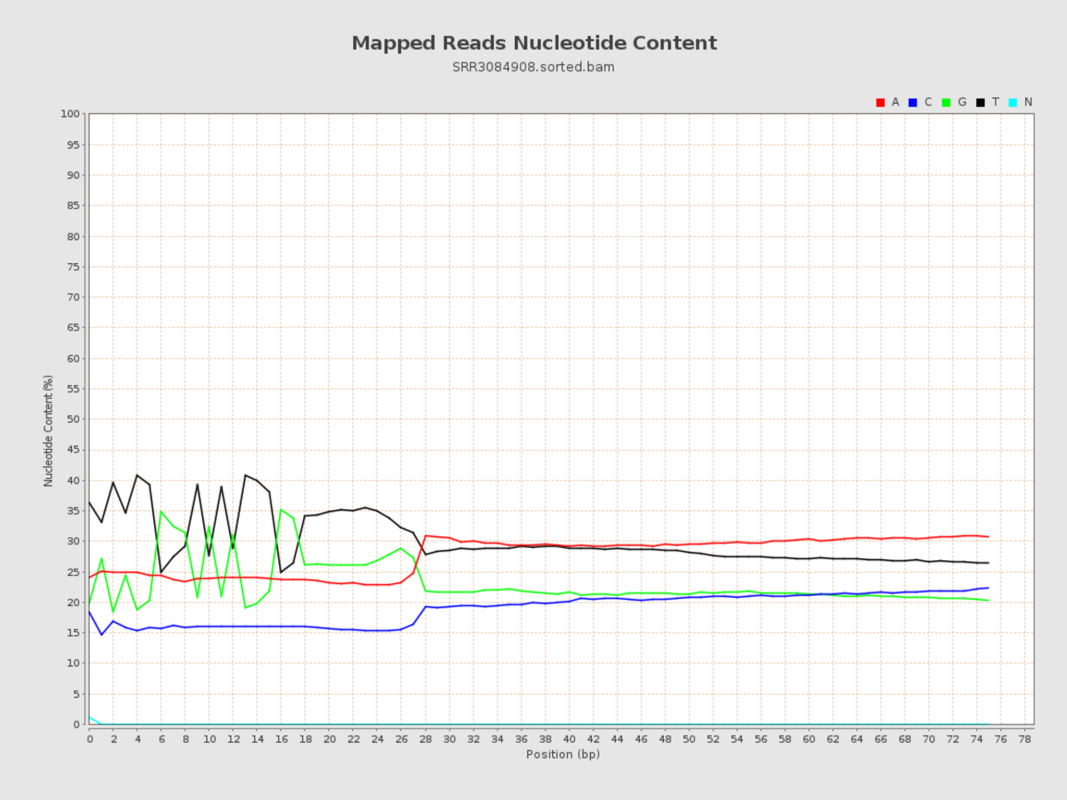
6. Results : Genome Fraction Coverage



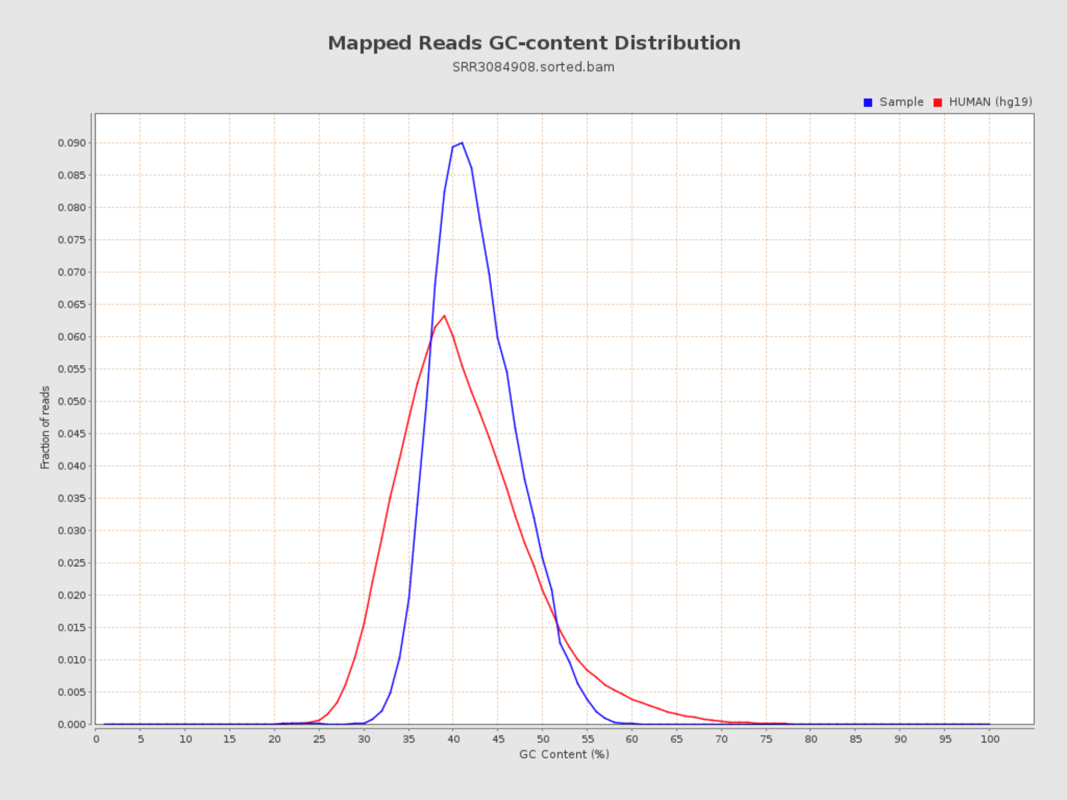
7. Results : Duplication Rate Histogram



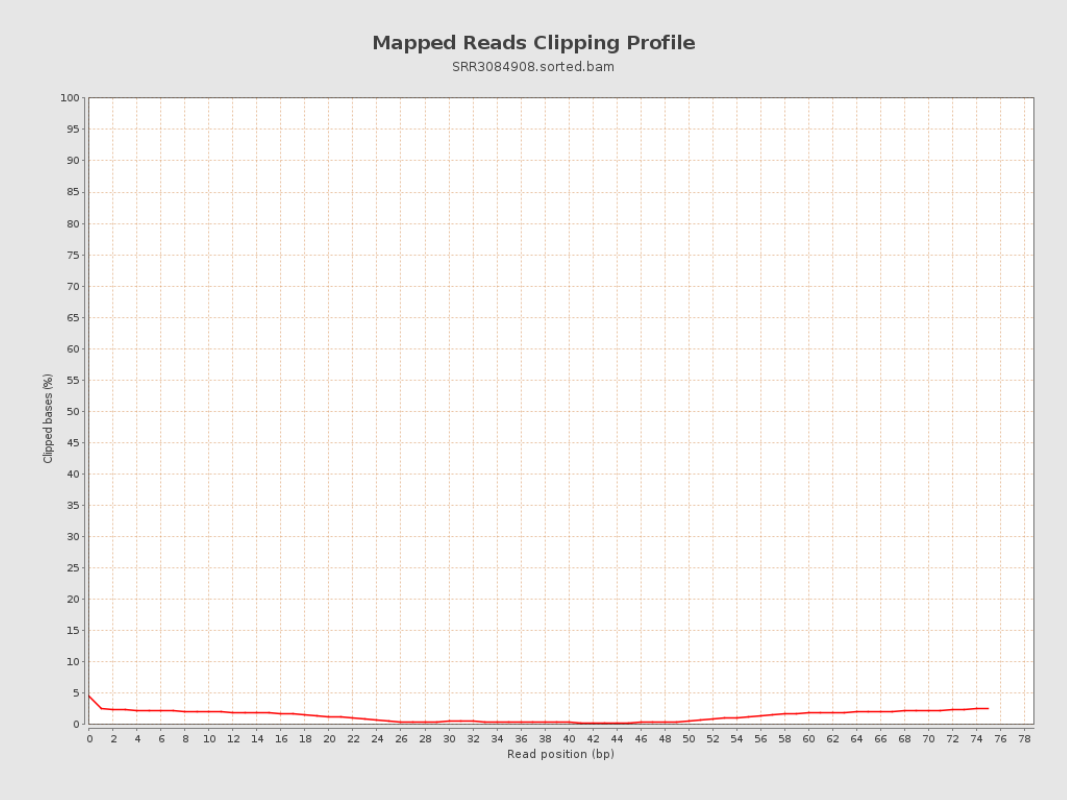
8. Results : Mapped Reads Nucleotide Content



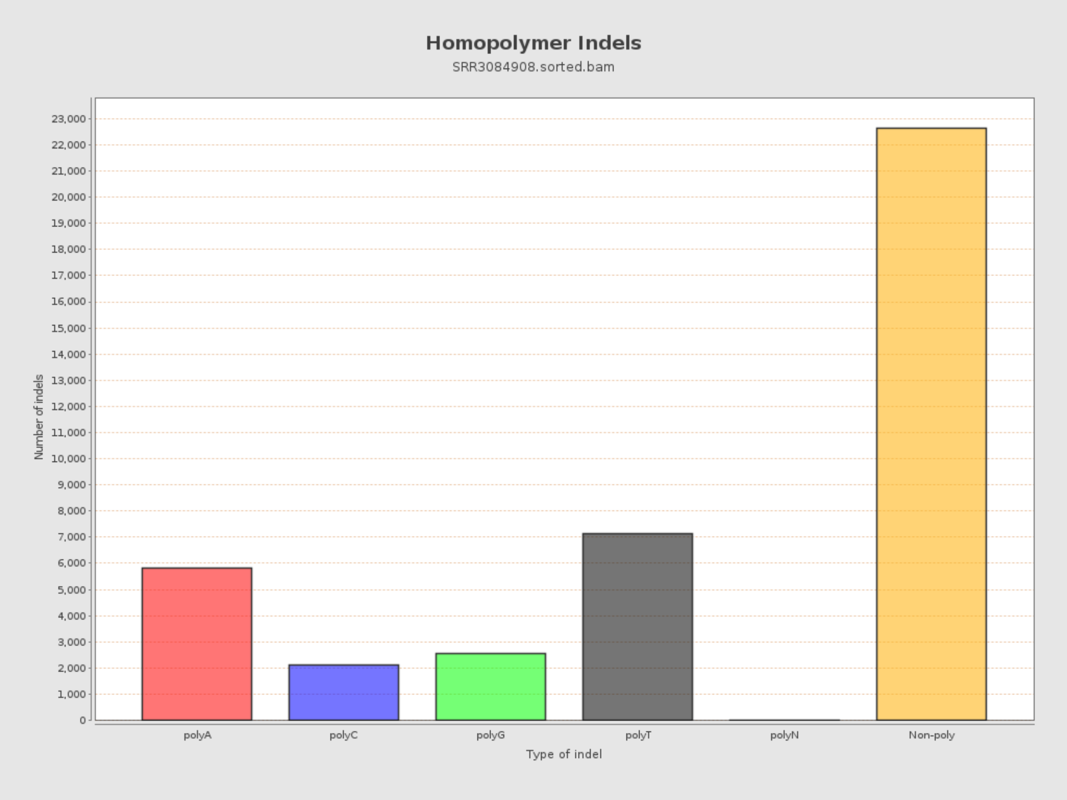
9. Results : Mapped Reads GC-content Distribution



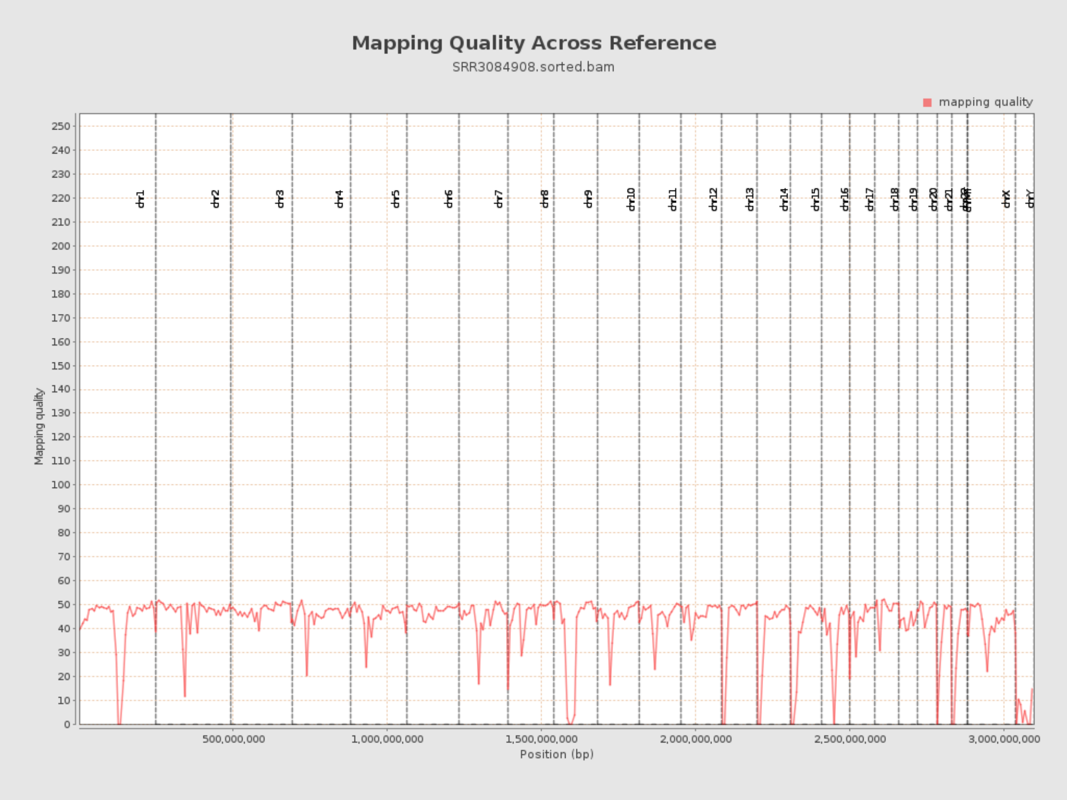
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram