Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:15:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081908.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_SRR3081908 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081908.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:15:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081908.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,539,821
Mapped reads	2,337,853 / 92.05%
Unmapped reads	201,968 / 7.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,536 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	83,175 / 3.27%
Duplication rate	2.48%
Clipped reads	908,659 / 35.78%

2.2. ACGT Content

Number/percentage of A's	46,038,303 / 28.84%
Number/percentage of C's	30,212,615 / 18.92%
Number/percentage of T's	49,290,165 / 30.87%
Number/percentage of G's	34,116,726 / 21.37%
Number/percentage of N's	1,820 / 0%
GC Percentage	40.29%

2.3. Coverage

Mean	0.0516

Standard Deviation	0.4655

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

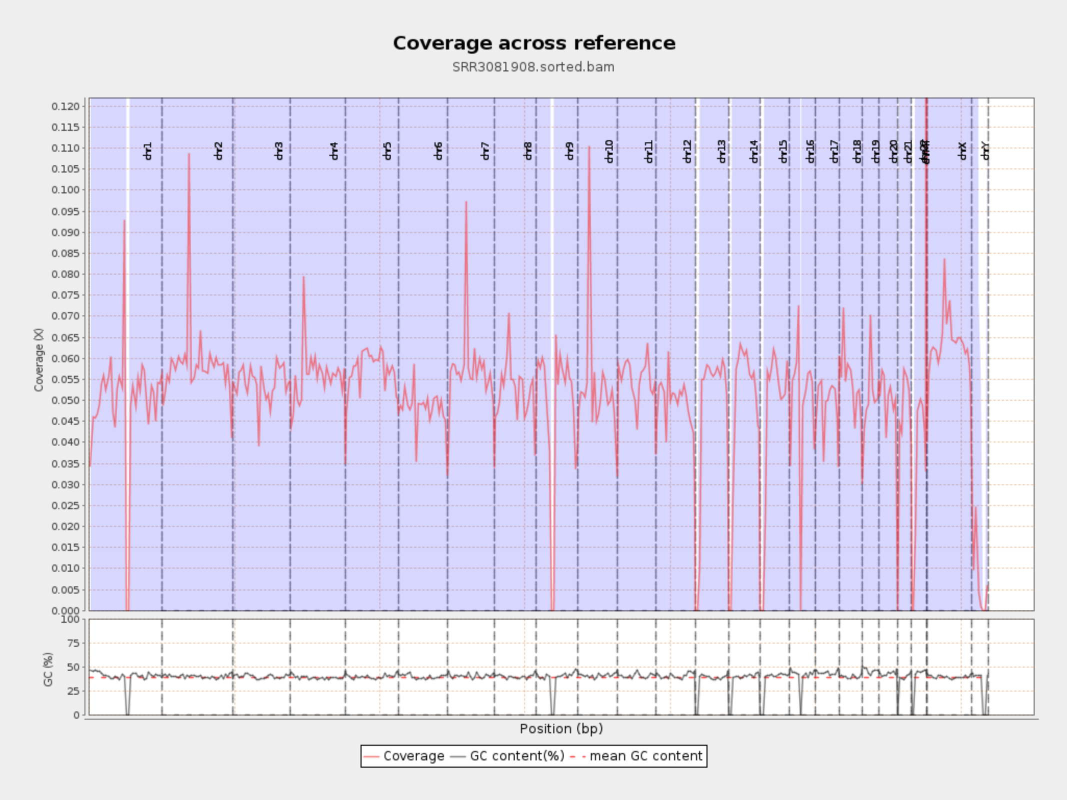
General error rate	0.86%
Mismatches	1,349,538
Insertions	12,347
Mapped reads with at least one insertion	0.52%
Deletions	35,654
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46.44%

2.6. Chromosome stats

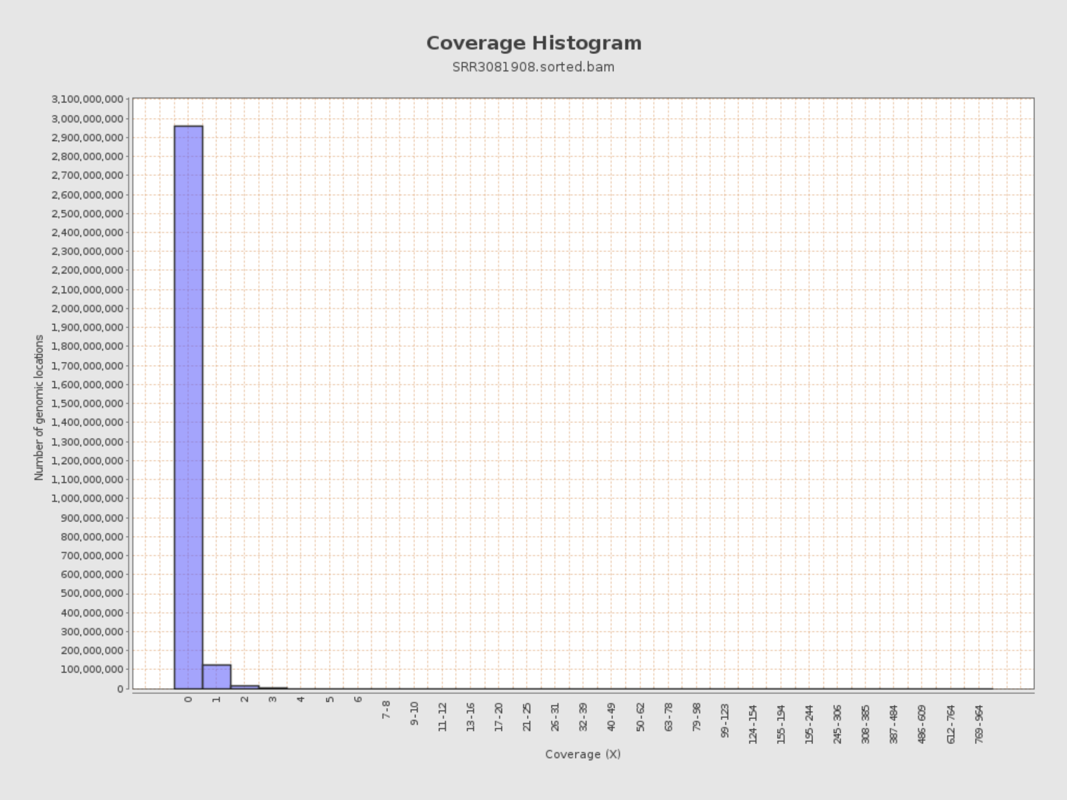
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12265643	0.0492	0.8474
chr2	243199373	14342317	0.059	0.5377
chr3	198022430	10709420	0.0541	0.2627
chr4	191154276	10670612	0.0558	0.3027
chr5	180915260	10414456	0.0576	0.269
chr6	171115067	8244615	0.0482	0.271
chr7	159138663	9237959	0.058	0.6562

chr8	146364022	7642874	0.0522	0.6287
chr9	141213431	6805396	0.0482	0.4353
chr10	135534747	7260647	0.0536	0.5391
chr11	135006516	7400178	0.0548	0.3671
chr12	133851895	6656199	0.0497	0.2517
chr13	115169878	5388294	0.0468	0.2392
chr14	107349540	5121096	0.0477	0.2674
chr15	102531392	4627876	0.0451	0.2397
chr16	90354753	4442466	0.0492	0.3119
chr17	81195210	3952426	0.0487	0.2683
chr18	78077248	4291503	0.055	0.8612
chr19	59128983	3013191	0.051	0.6478
chr20	63025520	3141980	0.0499	0.2636
chr21	48129895	2147910	0.0446	0.2729
chr22	51304566	1664238	0.0324	0.1978
chrMT	16571	16632	1.0037	1.2431
chrX	155270560	9813403	0.0632	0.3138
chrY	59373566	451153	0.0076	0.2033

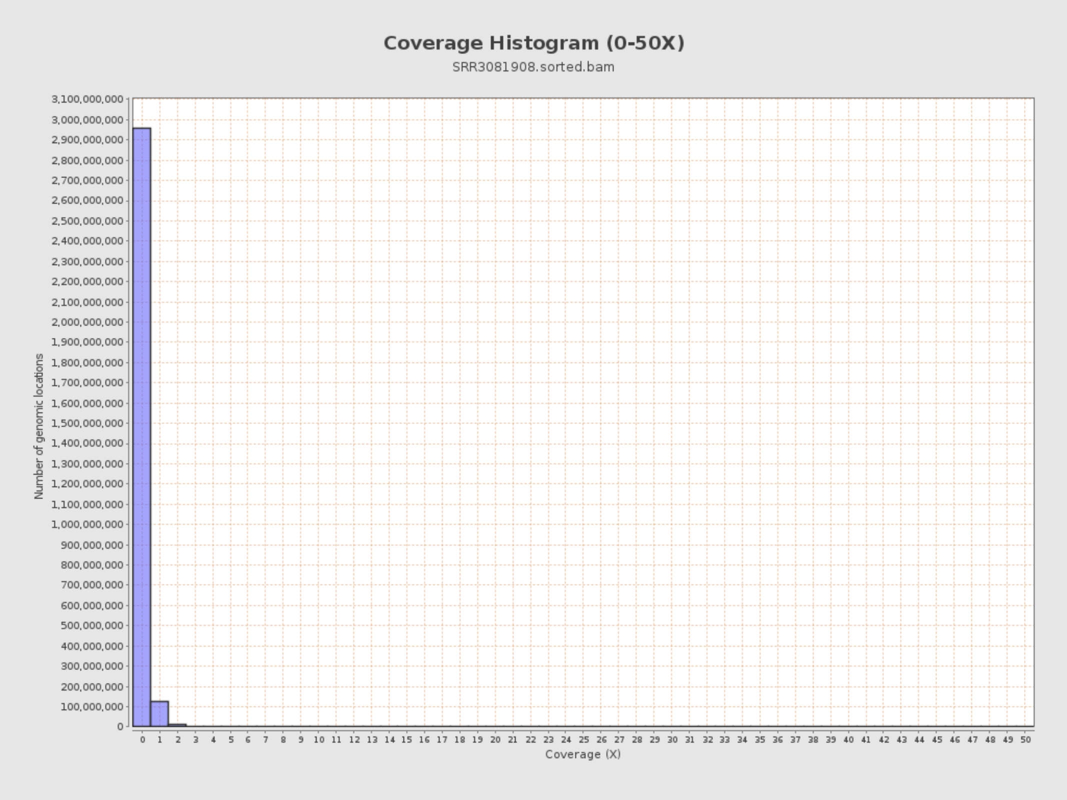
3. Results : Coverage across reference



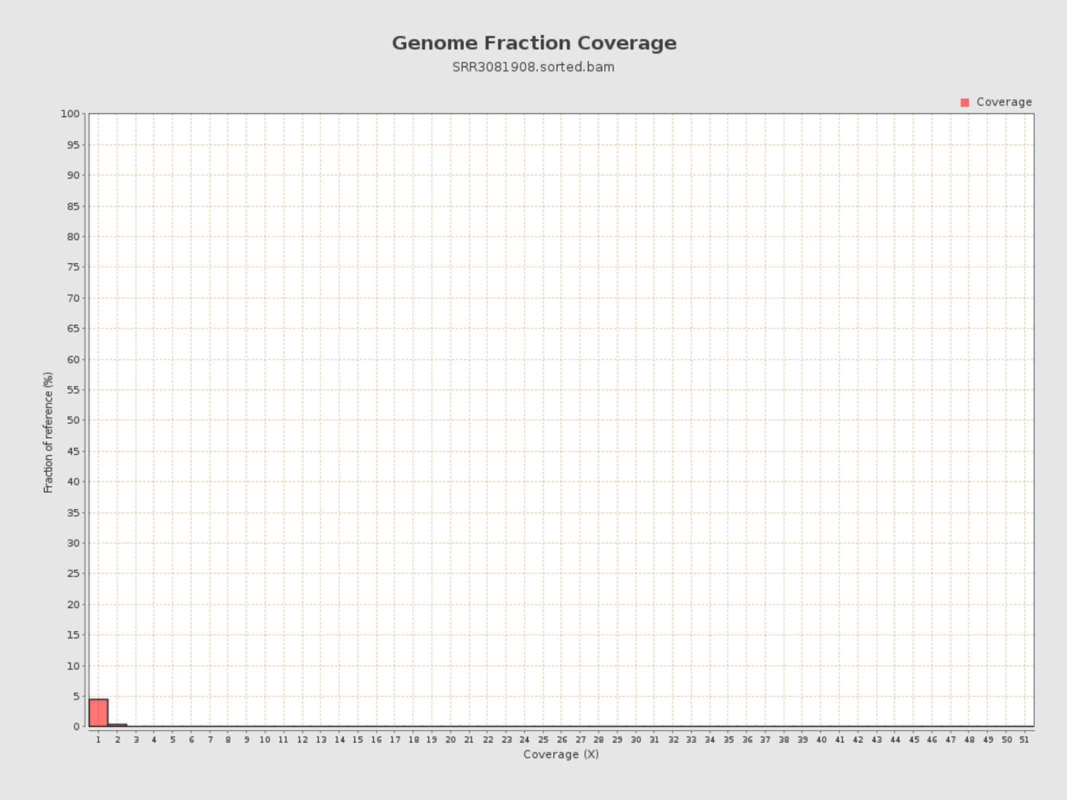
4. Results : Coverage Histogram



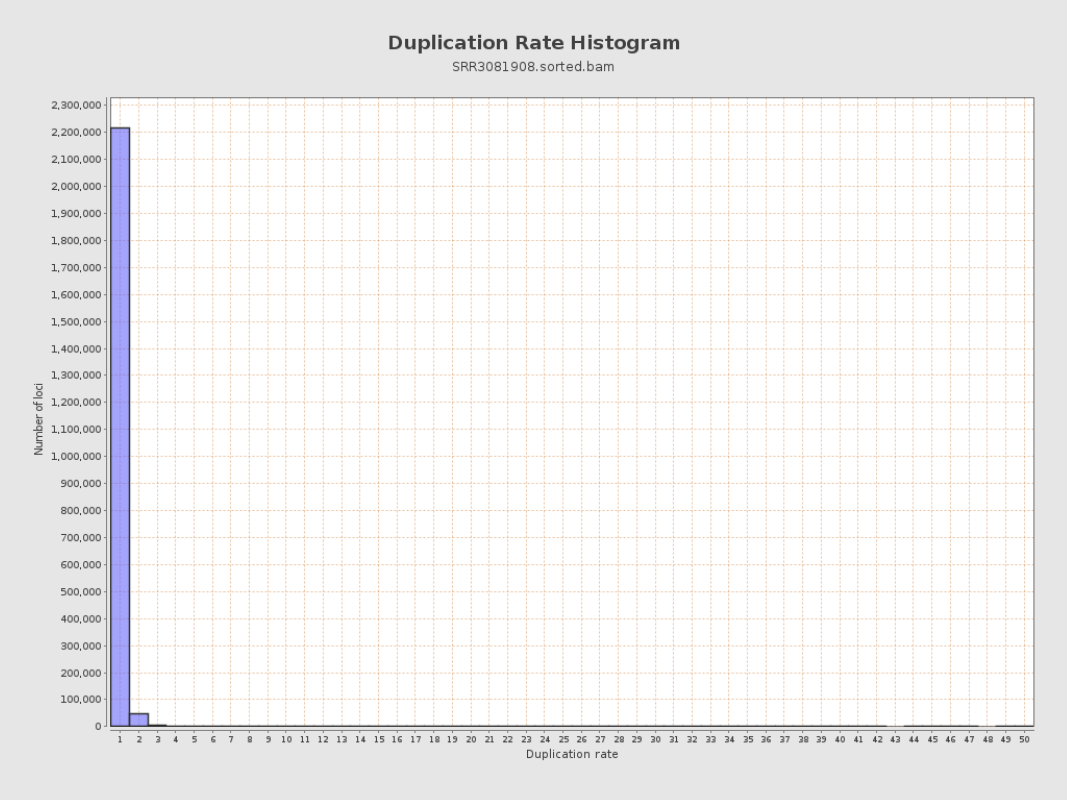
5. Results : Coverage Histogram (0-50X)



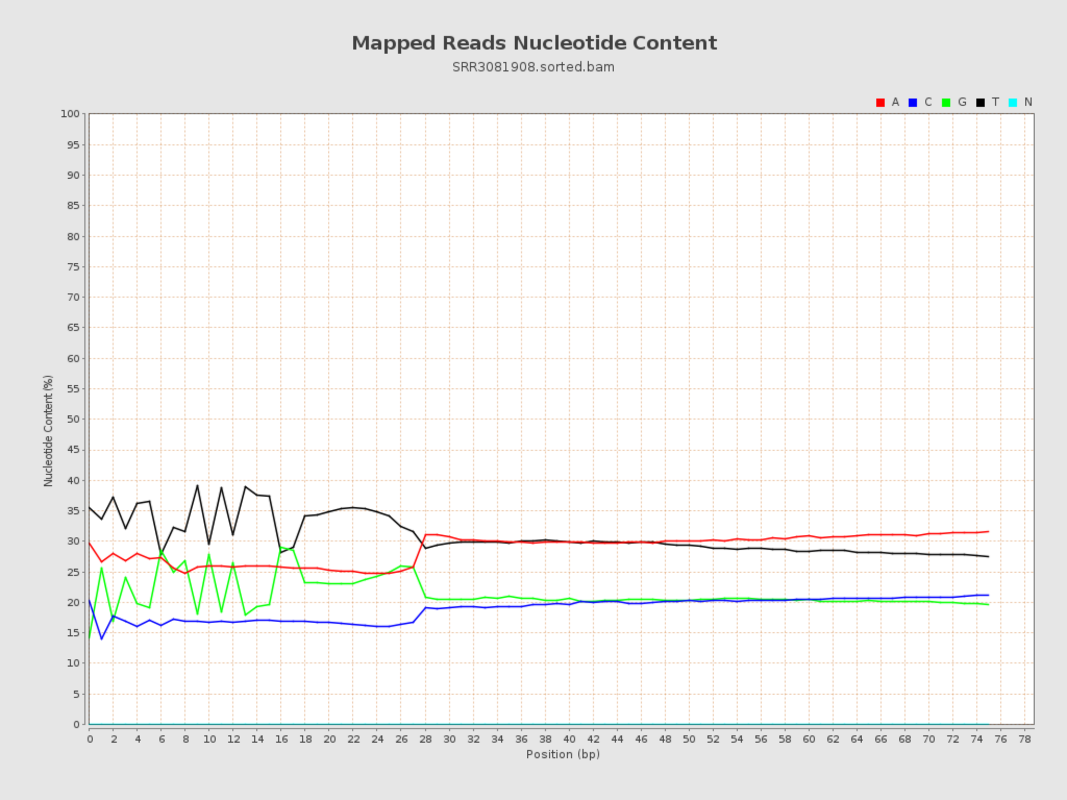
6. Results : Genome Fraction Coverage



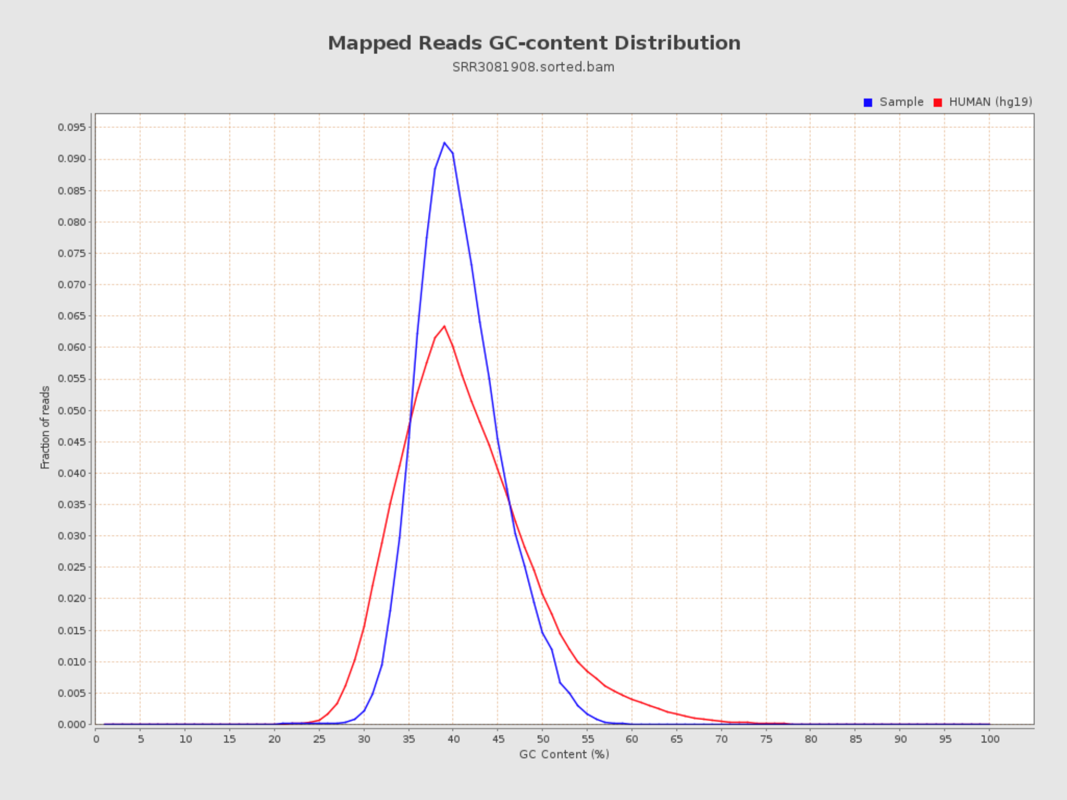
7. Results : Duplication Rate Histogram



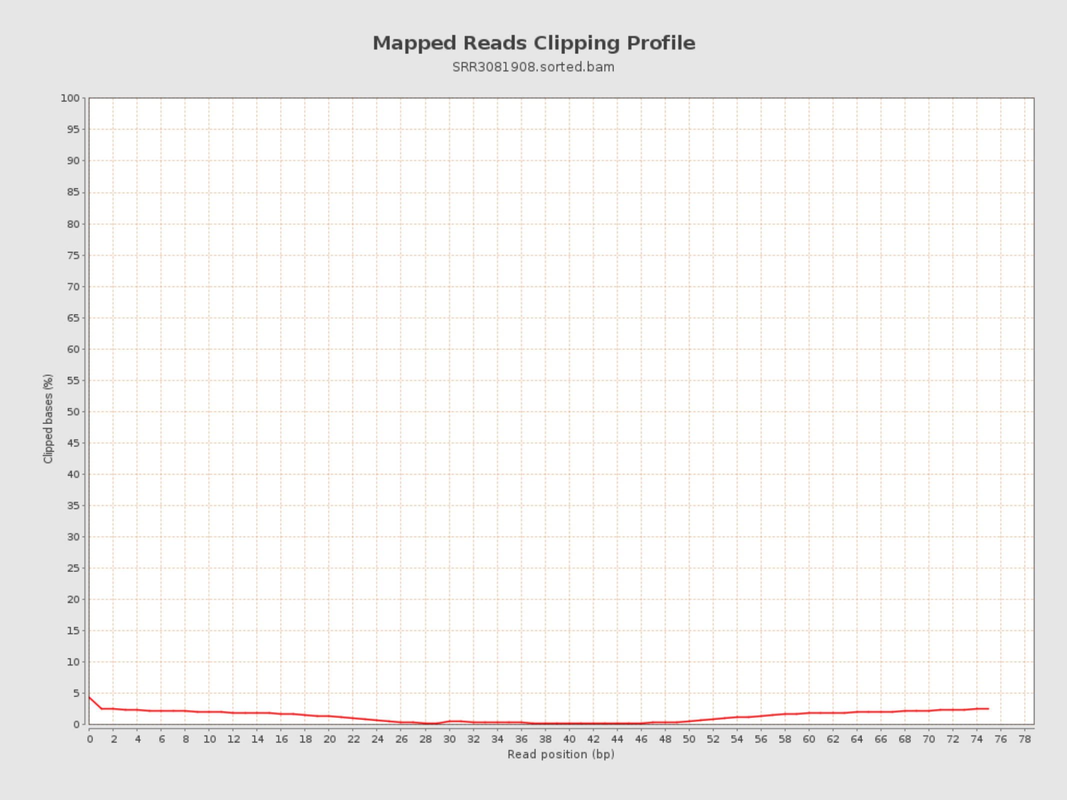
8. Results : Mapped Reads Nucleotide Content



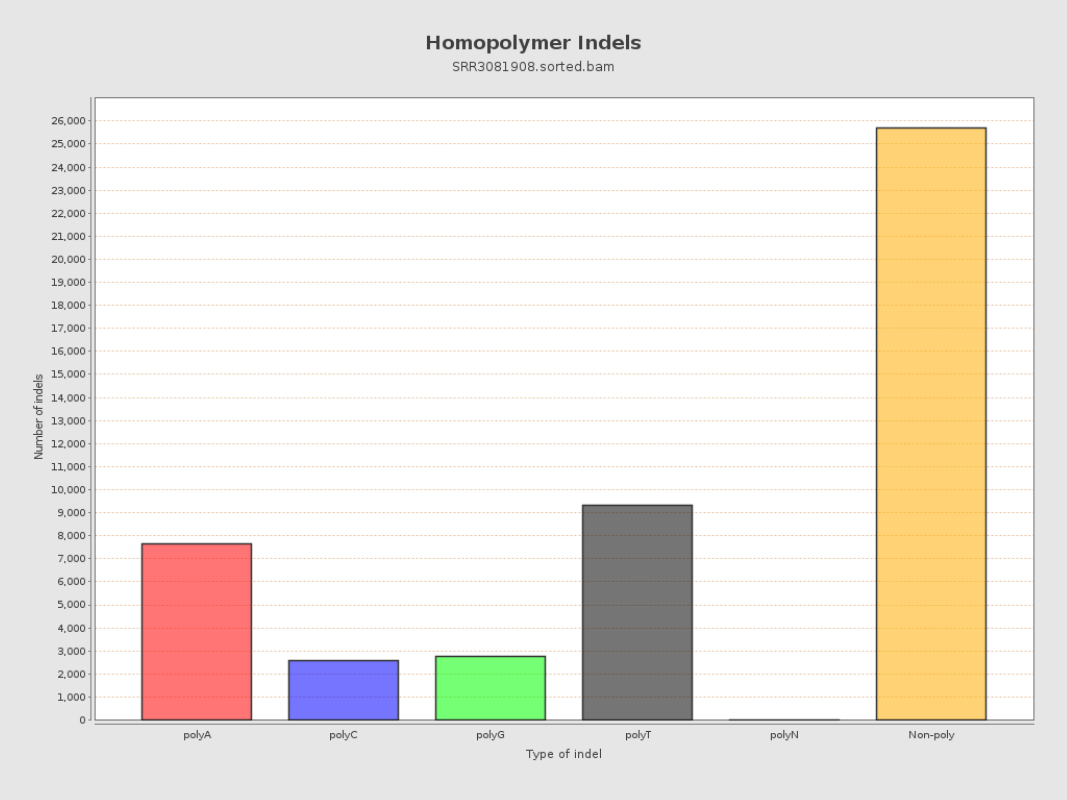
9. Results : Mapped Reads GC-content Distribution



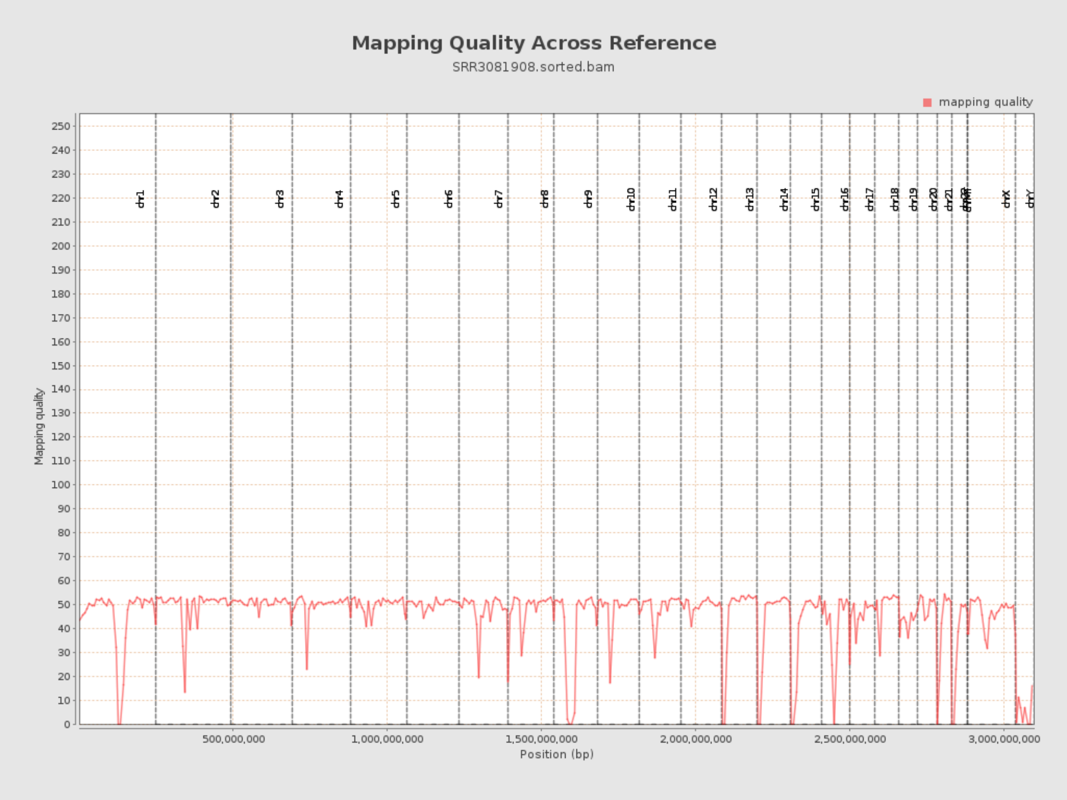
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram