Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:13:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082708.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_SRR3082708 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082708.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:13:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082708.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,763,601
Mapped reads	2,536,688 / 91.79%
Unmapped reads	226,913 / 8.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,736 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	102,928 / 3.72%
Duplication rate	2.79%
Clipped reads	1,249,414 / 45.21%

2.2. ACGT Content

Number/percentage of A's	45,472,901 / 27.23%
Number/percentage of C's	28,821,363 / 17.26%
Number/percentage of T's	55,495,509 / 33.23%
Number/percentage of G's	37,174,474 / 22.26%
Number/percentage of N's	42,896 / 0.03%
GC Percentage	39.52%

2.3. Coverage

Mean	0.054

Standard Deviation	0.494

2.4. Mapping Quality

Mean Mapping Quality	46.59

2.5. Mismatches and indels

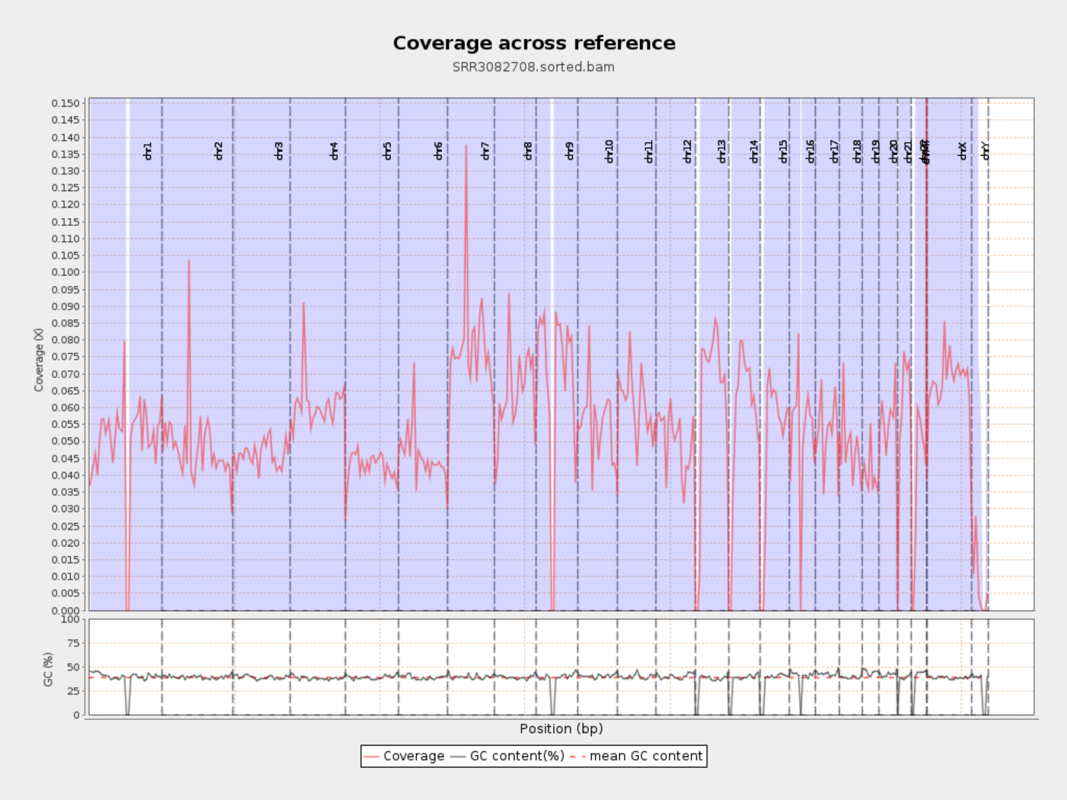
General error rate	0.94%
Mismatches	1,543,530
Insertions	16,626
Mapped reads with at least one insertion	0.65%
Deletions	41,281
Mapped reads with at least one deletion	1.61%
Homopolymer indels	48.26%

2.6. Chromosome stats

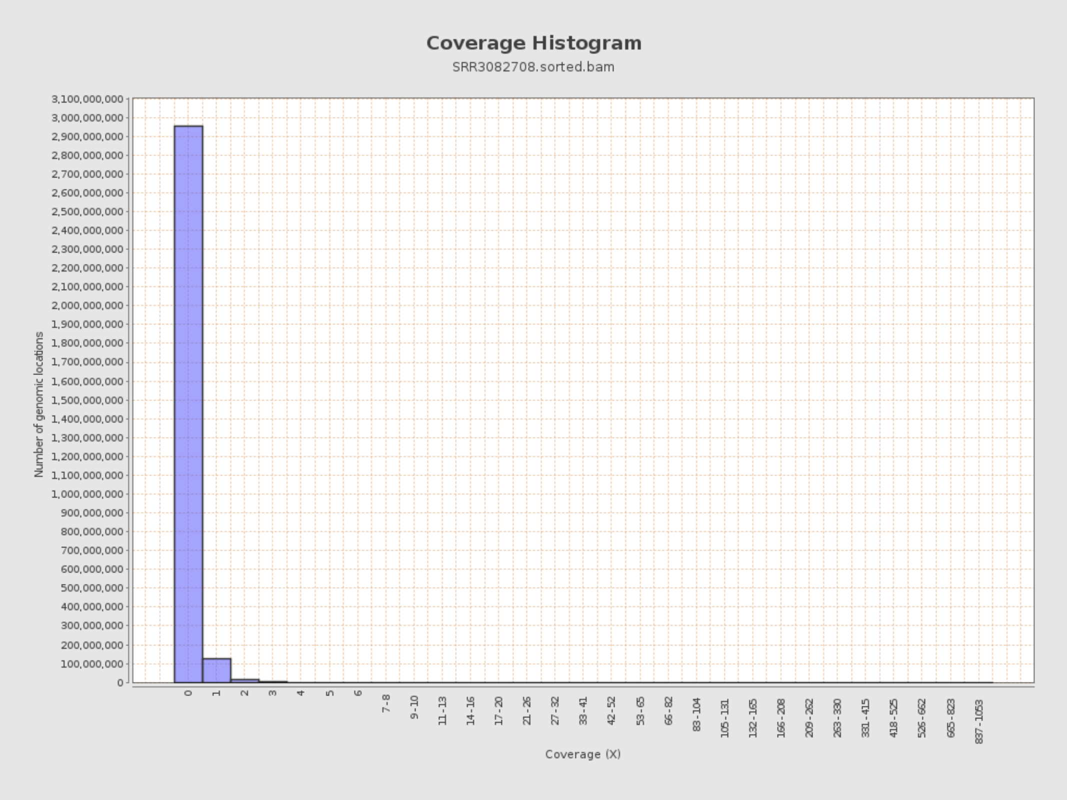
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12371608	0.0496	0.6208
chr2	243199373	11816645	0.0486	0.5721
chr3	198022430	9158301	0.0462	0.2435
chr4	191154276	11673573	0.0611	0.3208
chr5	180915260	7748724	0.0428	0.237
chr6	171115067	7866578	0.046	0.3572
chr7	159138663	12501188	0.0786	1.0668

chr8	146364022	9402228	0.0642	0.5014
chr9	141213431	9533389	0.0675	0.6321
chr10	135534747	7480613	0.0552	0.3923
chr11	135006516	8209211	0.0608	0.4538
chr12	133851895	6706326	0.0501	0.2697
chr13	115169878	7022817	0.061	0.2791
chr14	107349540	6047944	0.0563	0.3361
chr15	102531392	5076392	0.0495	0.251
chr16	90354753	4779488	0.0529	0.3452
chr17	81195210	4282326	0.0527	0.3344
chr18	78077248	3781934	0.0484	1.0485
chr19	59128983	2388547	0.0404	0.4855
chr20	63025520	3576606	0.0567	0.2965
chr21	48129895	2807310	0.0583	0.327
chr22	51304566	1893093	0.0369	0.2151
chrMT	16571	4016	0.2424	0.493
chrX	155270560	10472362	0.0674	0.3545
chrY	59373566	472655	0.008	0.2419

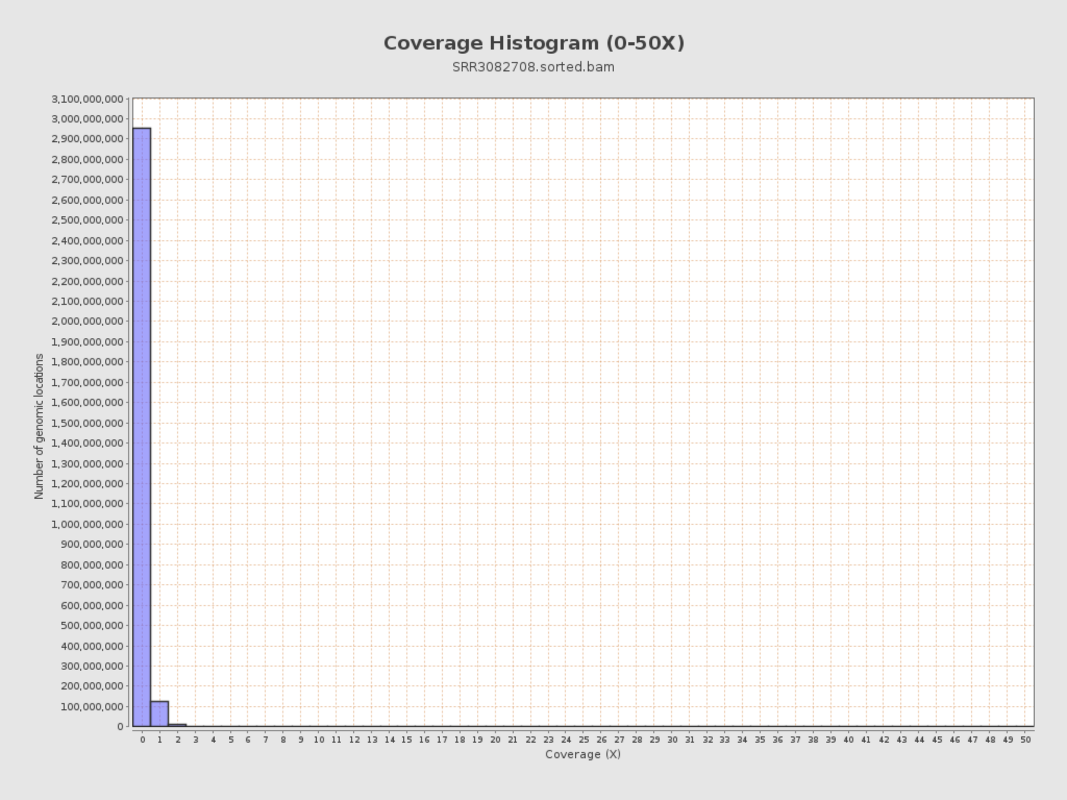
3. Results : Coverage across reference



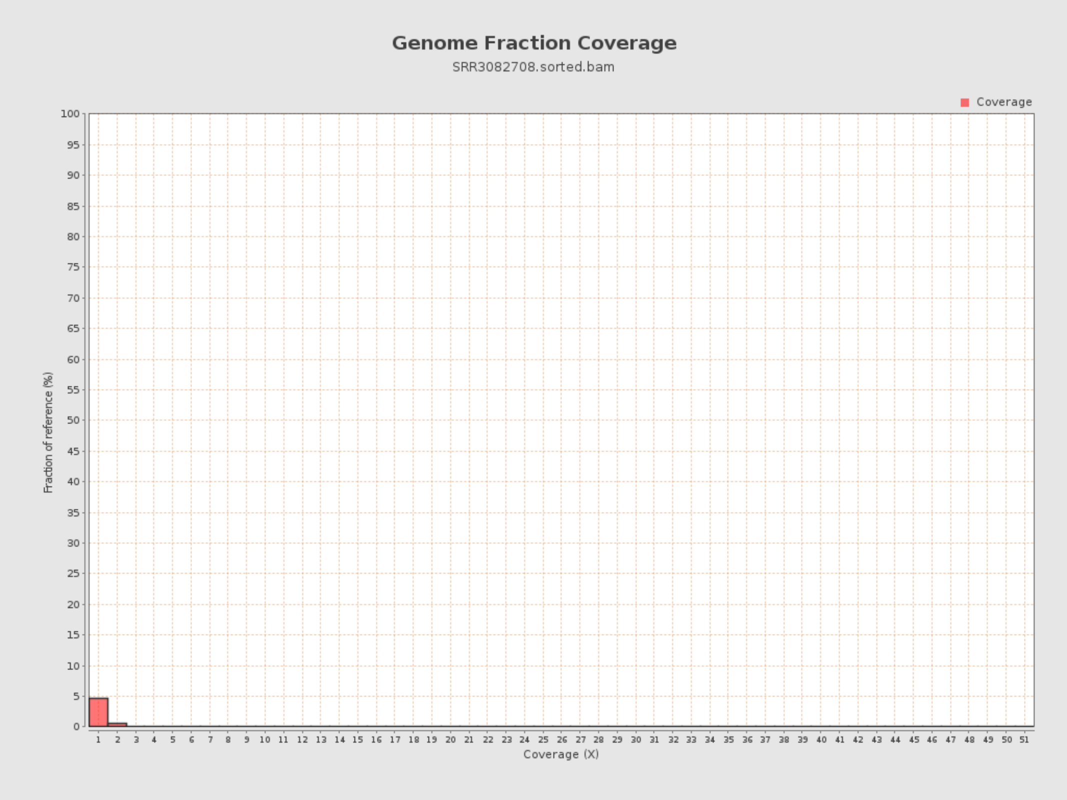
4. Results : Coverage Histogram



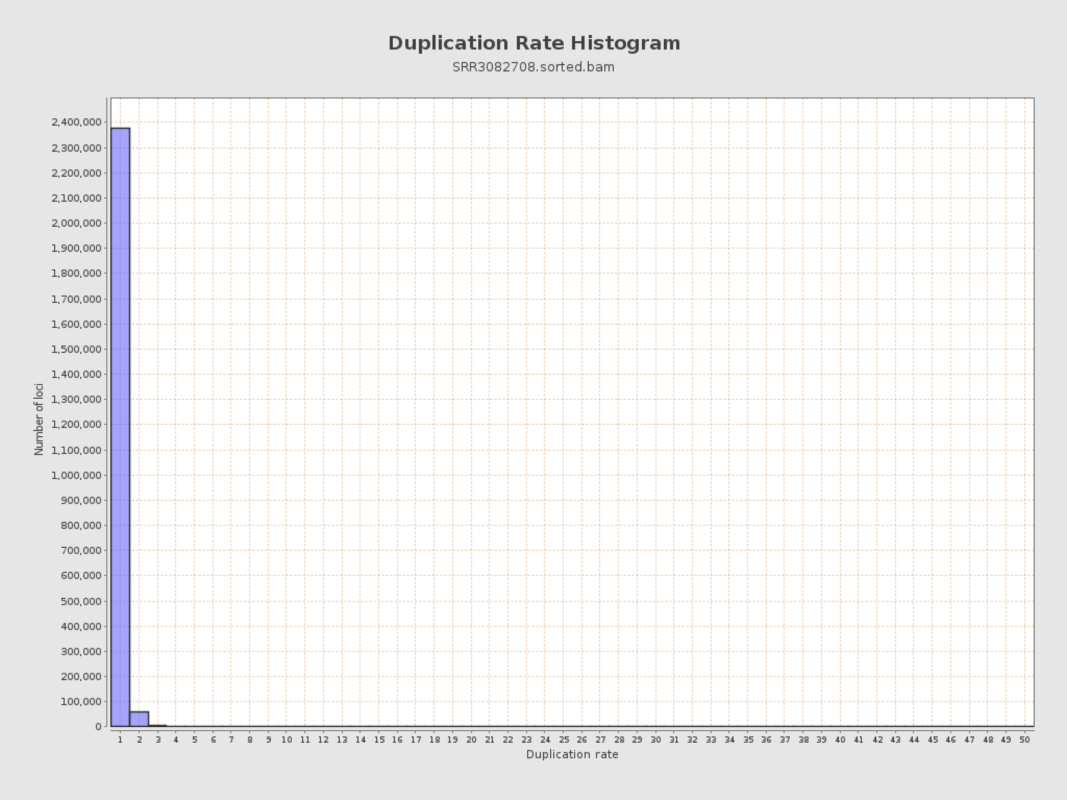
5. Results : Coverage Histogram (0-50X)



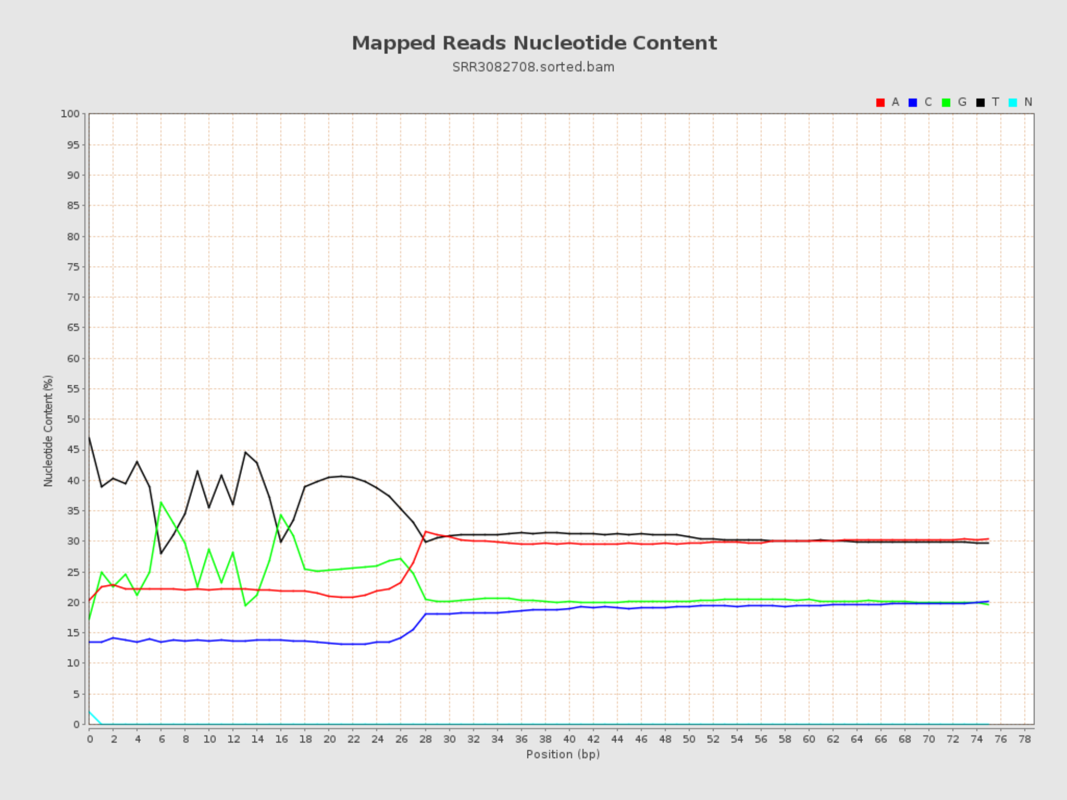
6. Results : Genome Fraction Coverage



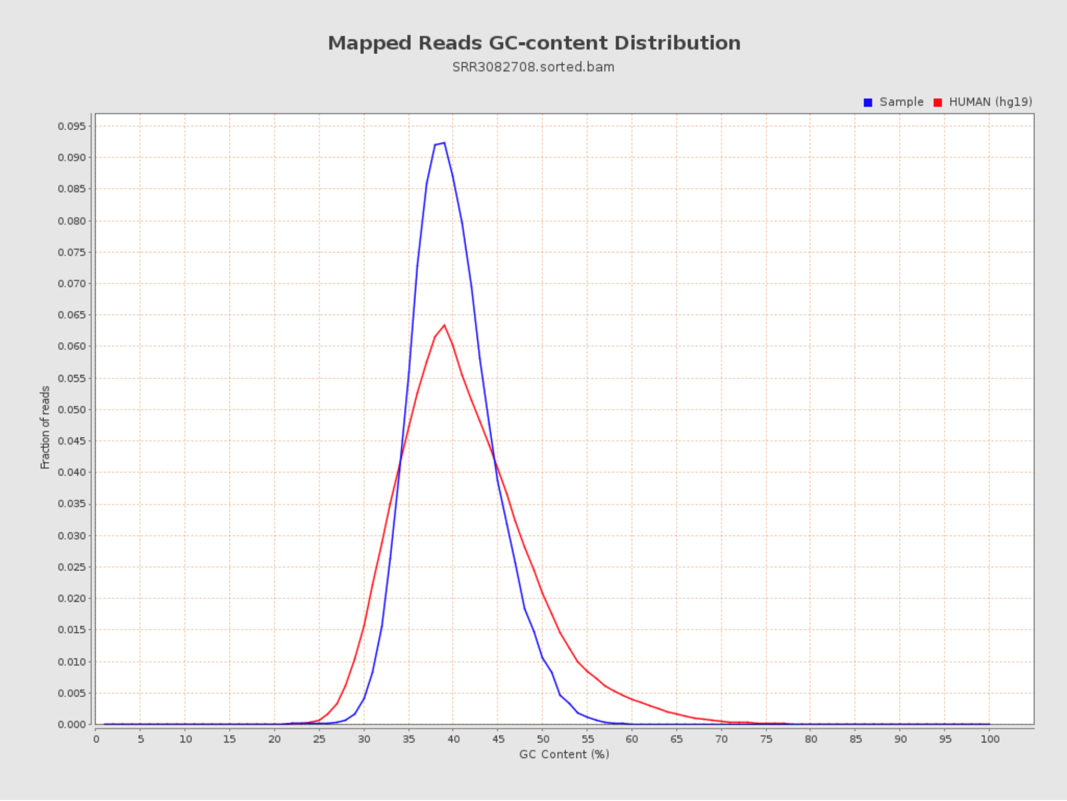
7. Results : Duplication Rate Histogram



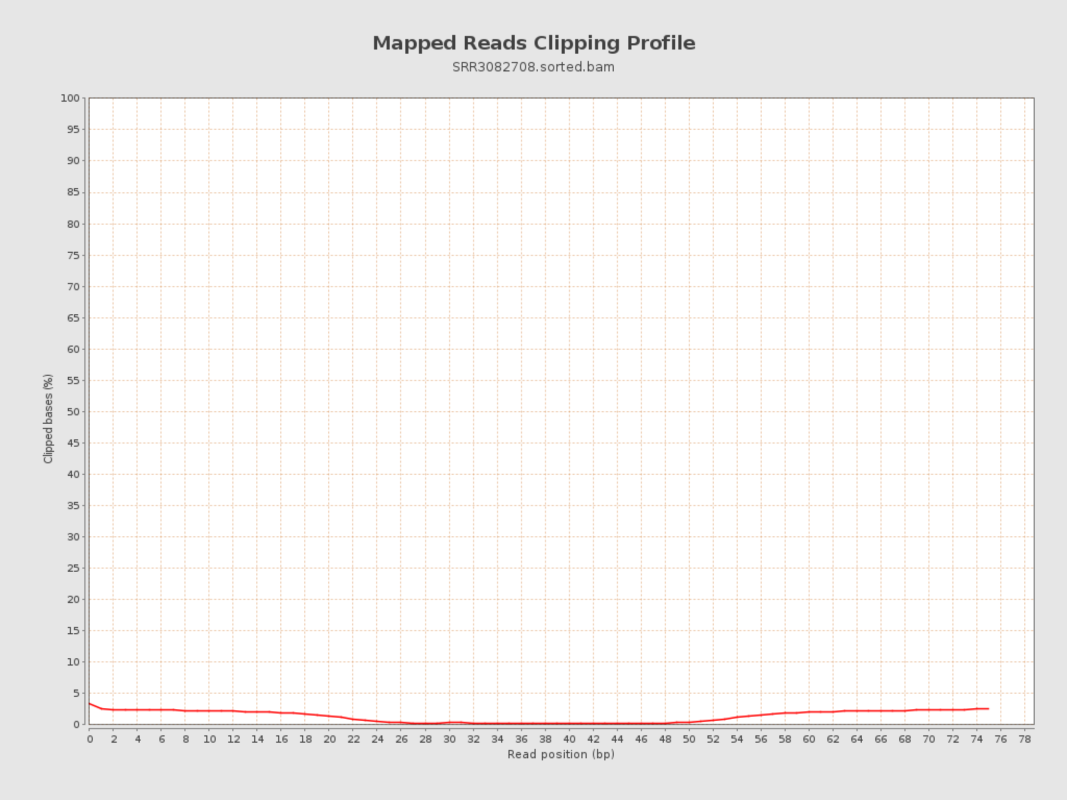
8. Results : Mapped Reads Nucleotide Content



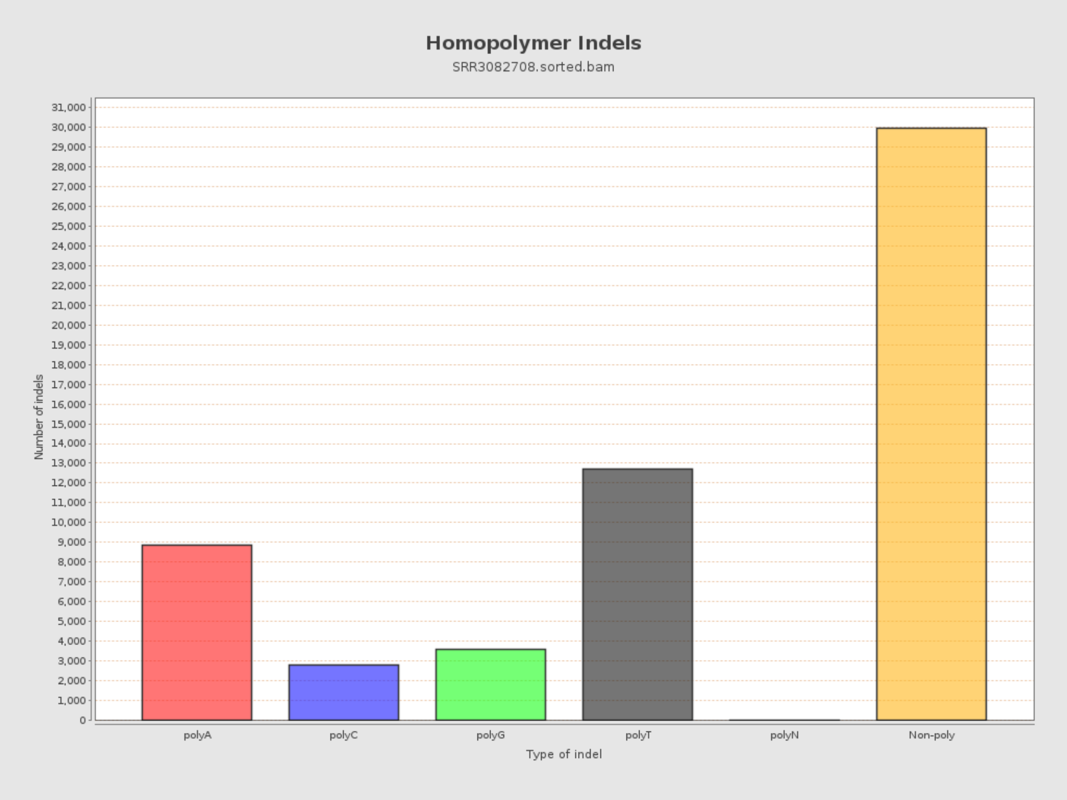
9. Results : Mapped Reads GC-content Distribution



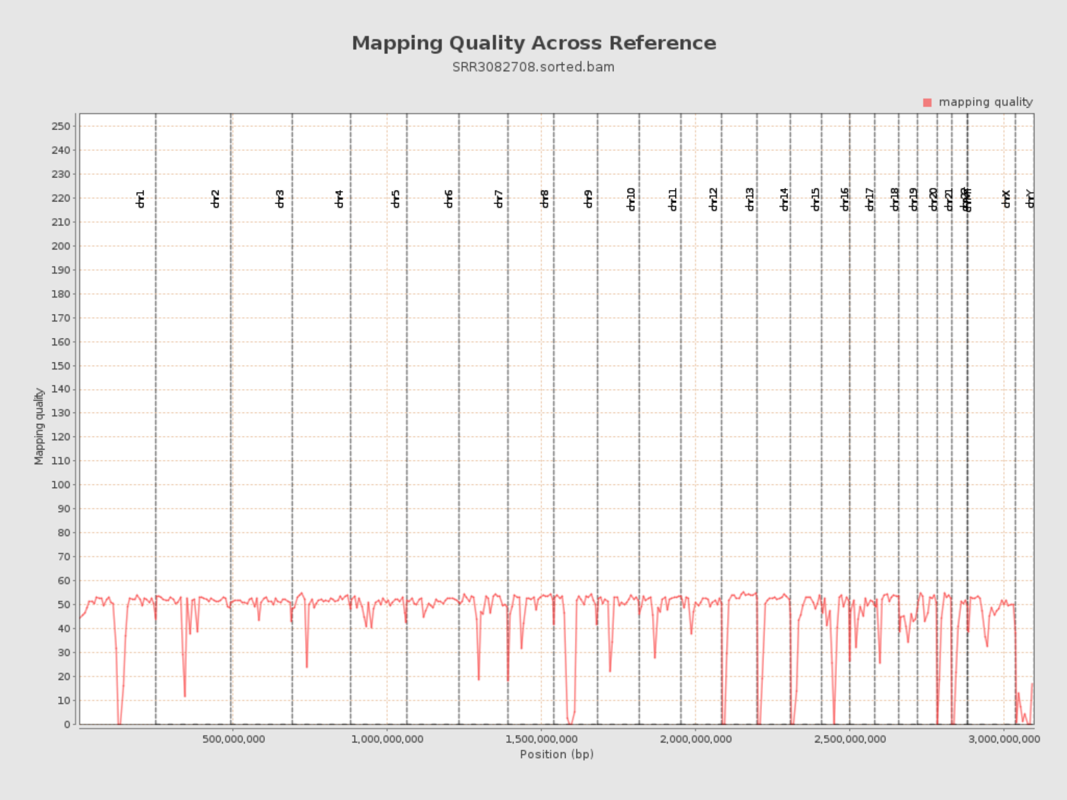
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram