Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 01:12:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708506.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_SRR1708506 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708506.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 01:12:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708506.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,867,942
Mapped reads	1,932,191 / 67.37%
Unmapped reads	935,751 / 32.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	371 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	102,019 / 3.56%
Duplication rate	3.98%
Clipped reads	406,359 / 14.17%

2.2. ACGT Content

Number/percentage of A's	26,443,345 / 28.7%
Number/percentage of C's	16,918,422 / 18.36%
Number/percentage of T's	29,679,263 / 32.21%
Number/percentage of G's	19,107,347 / 20.74%
Number/percentage of N's	1,395 / 0%
GC Percentage	39.09%

2.3. Coverage

Mean	0.0298

Standard Deviation	0.3242

2.4. Mapping Quality

Mean Mapping Quality	40.81

2.5. Mismatches and indels

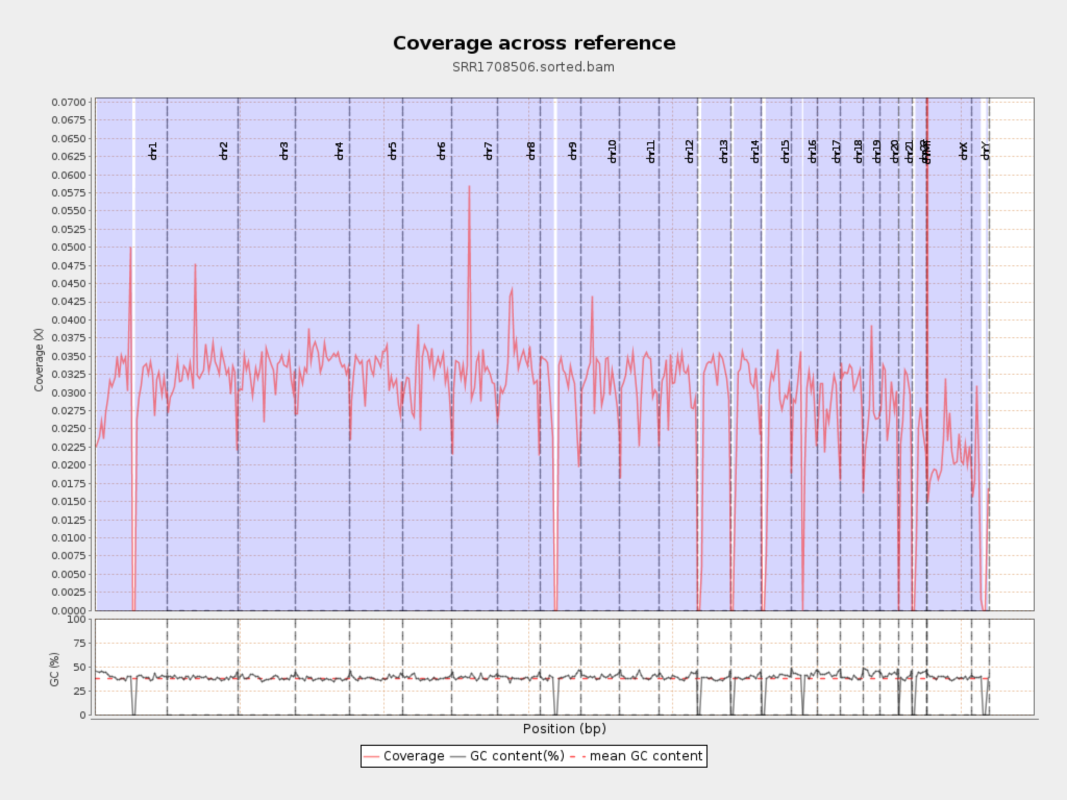
General error rate	0.53%
Mismatches	476,648
Insertions	4,776
Mapped reads with at least one insertion	0.25%
Deletions	13,952
Mapped reads with at least one deletion	0.72%
Homopolymer indels	47.59%

2.6. Chromosome stats

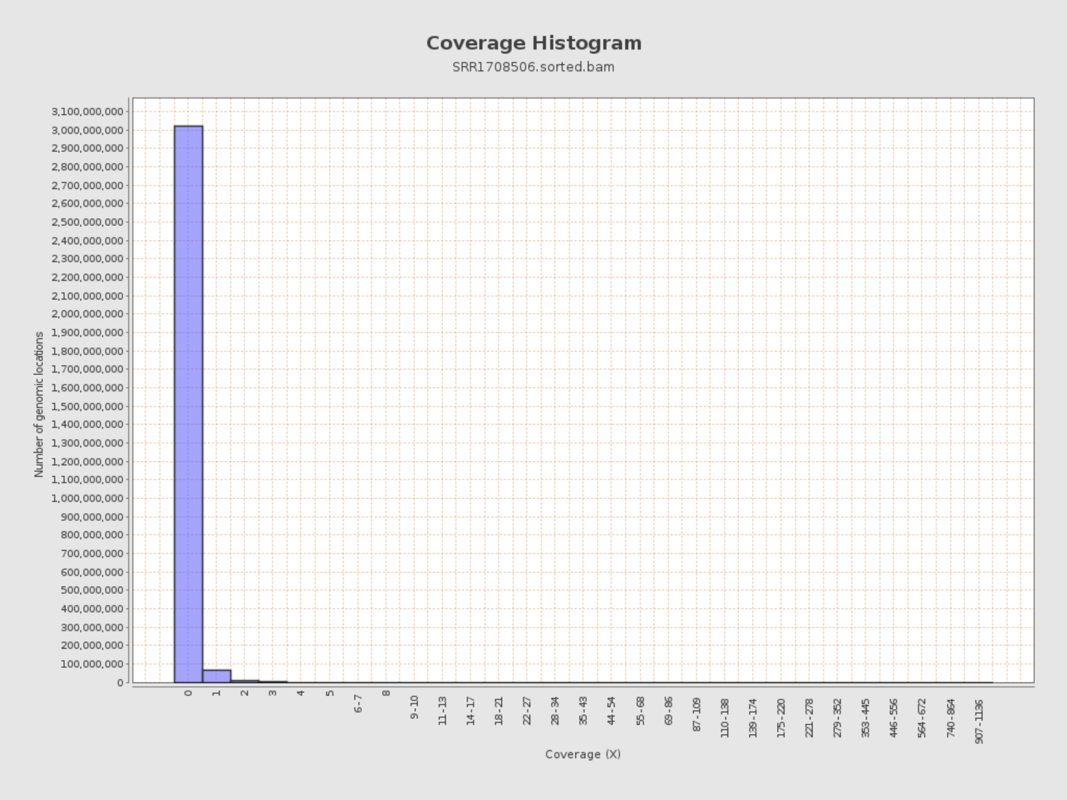
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7280908	0.0292	0.4945
chr2	243199373	8030725	0.033	0.4442
chr3	198022430	6491476	0.0328	0.2208
chr4	191154276	6491721	0.034	0.2354
chr5	180915260	5915069	0.0327	0.2179
chr6	171115067	5555552	0.0325	0.2659
chr7	159138663	5285544	0.0332	0.3985

chr8	146364022	4931047	0.0337	0.6472
chr9	141213431	3929248	0.0278	0.2401
chr10	135534747	4332565	0.032	0.251
chr11	135006516	4256509	0.0315	0.286
chr12	133851895	4195306	0.0313	0.2153
chr13	115169878	3172649	0.0275	0.2236
chr14	107349540	2875549	0.0268	0.1995
chr15	102531392	2554597	0.0249	0.1889
chr16	90354753	2365907	0.0262	0.1985
chr17	81195210	2245093	0.0277	0.2377
chr18	78077248	2508728	0.0321	0.3564
chr19	59128983	1603828	0.0271	0.3505
chr20	63025520	1800391	0.0286	0.207
chr21	48129895	1226671	0.0255	0.2115
chr22	51304566	881874	0.0172	0.164
chrMT	16571	157583	9.5096	6.4901
chrX	155270560	3323506	0.0214	0.1966
chrY	59373566	758816	0.0128	0.1559

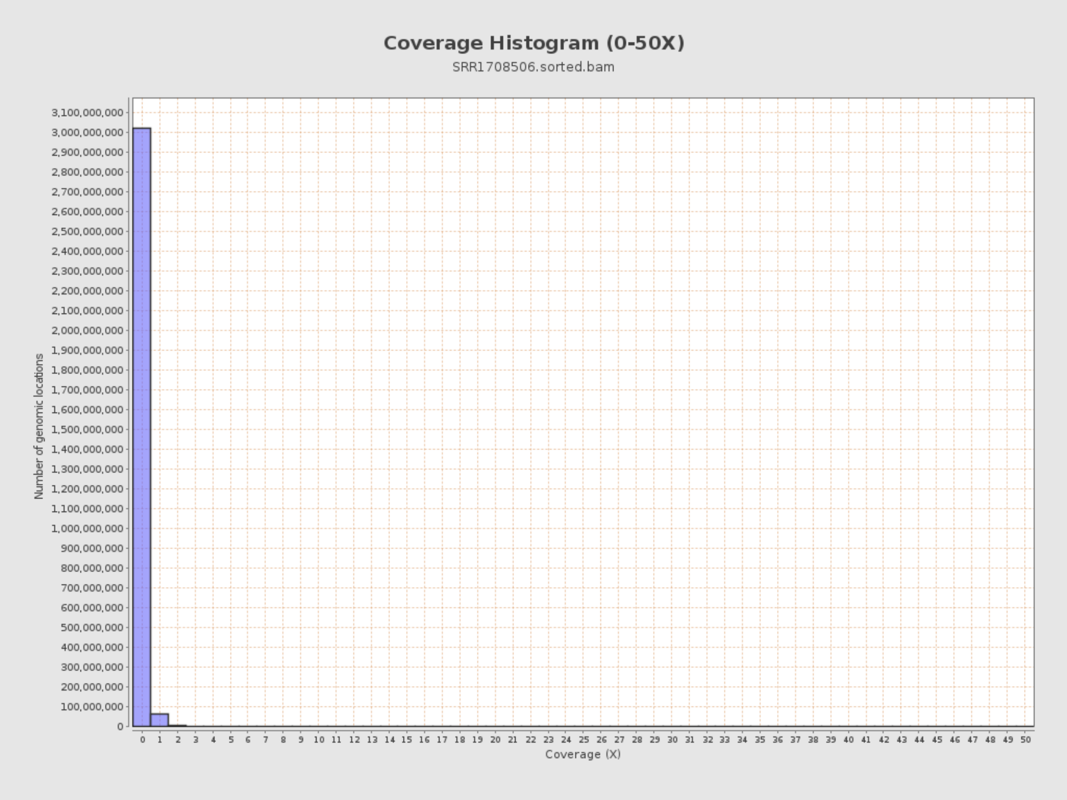
3. Results : Coverage across reference



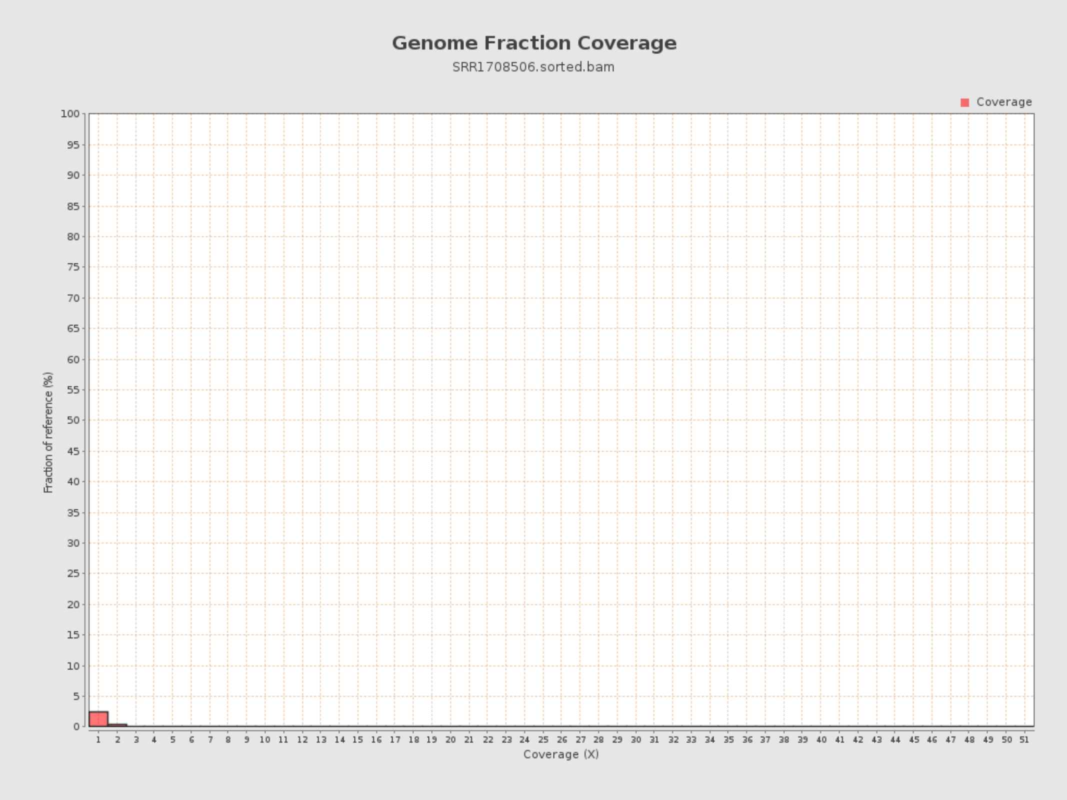
4. Results : Coverage Histogram



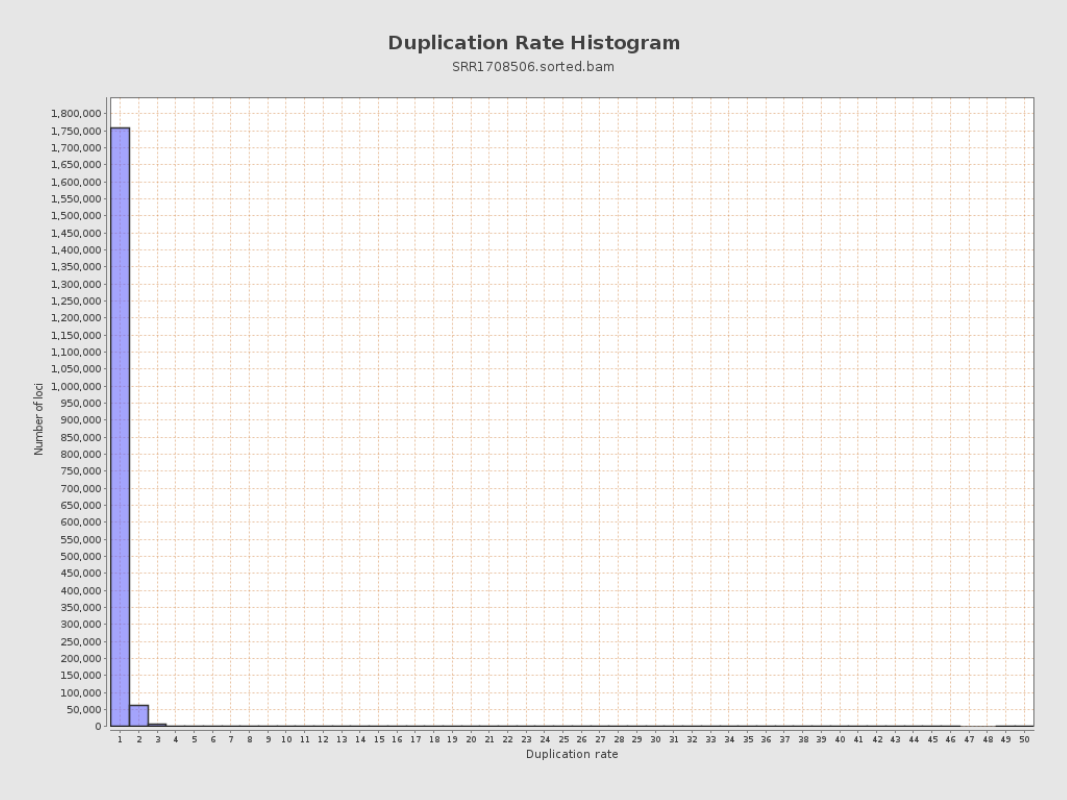
5. Results : Coverage Histogram (0-50X)



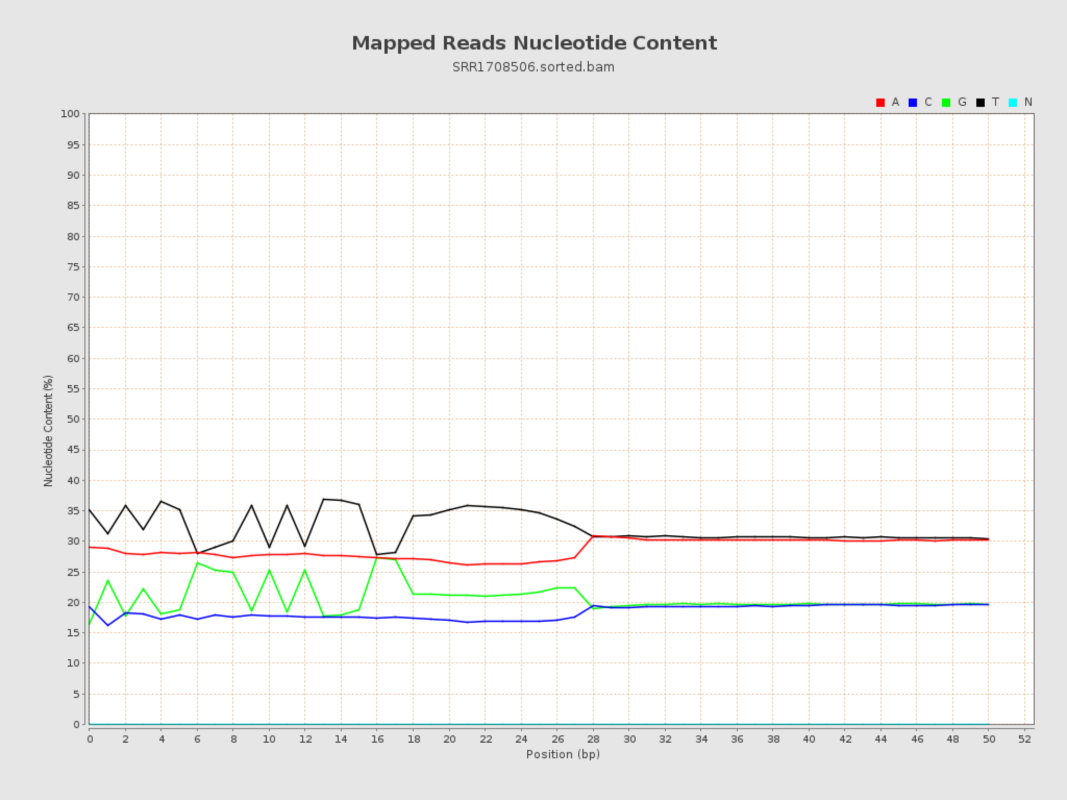
6. Results : Genome Fraction Coverage



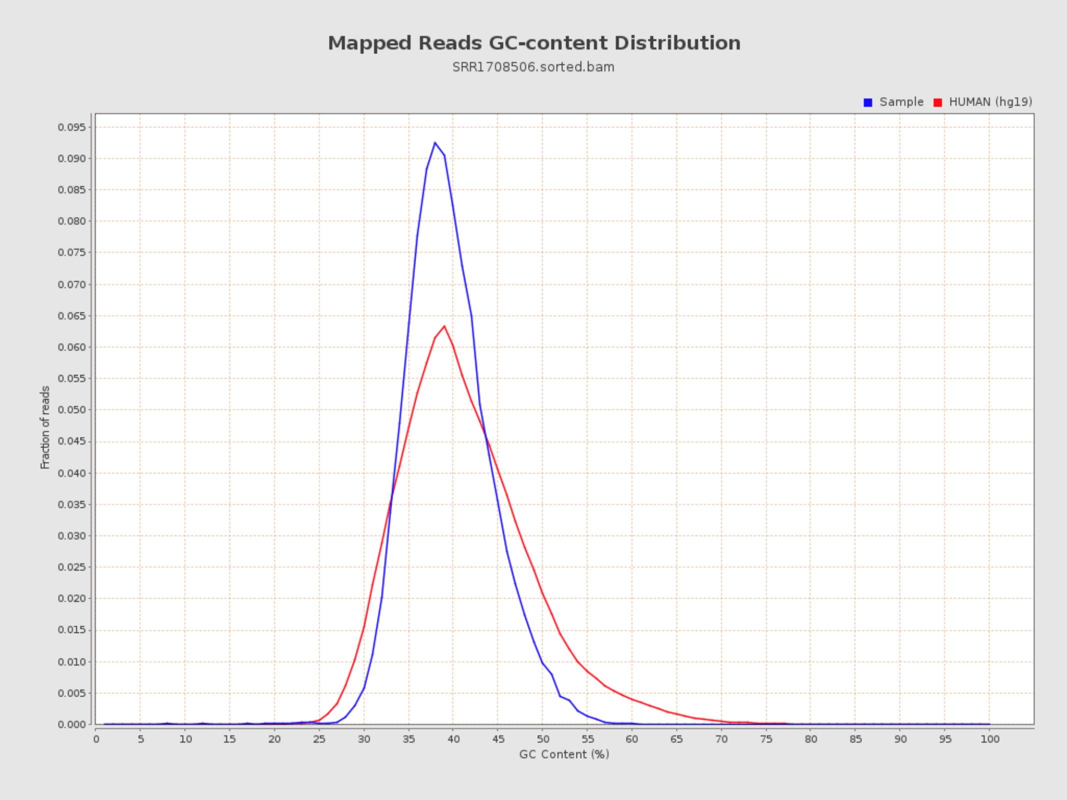
7. Results : Duplication Rate Histogram



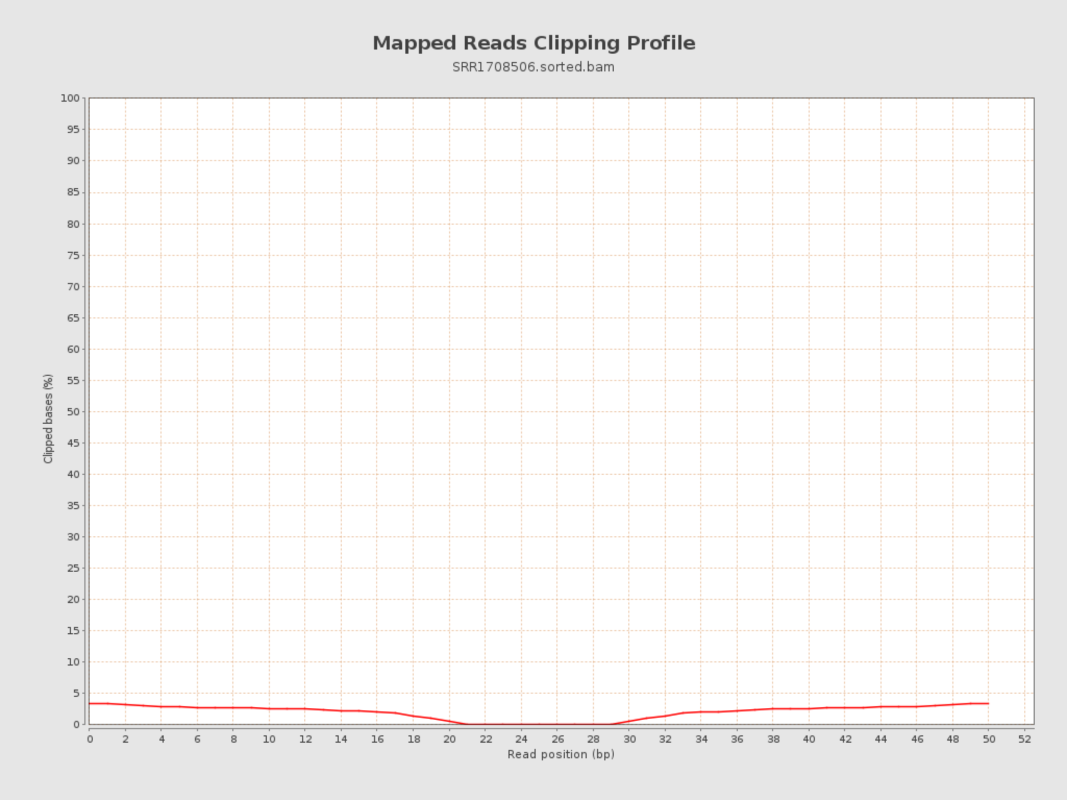
8. Results : Mapped Reads Nucleotide Content



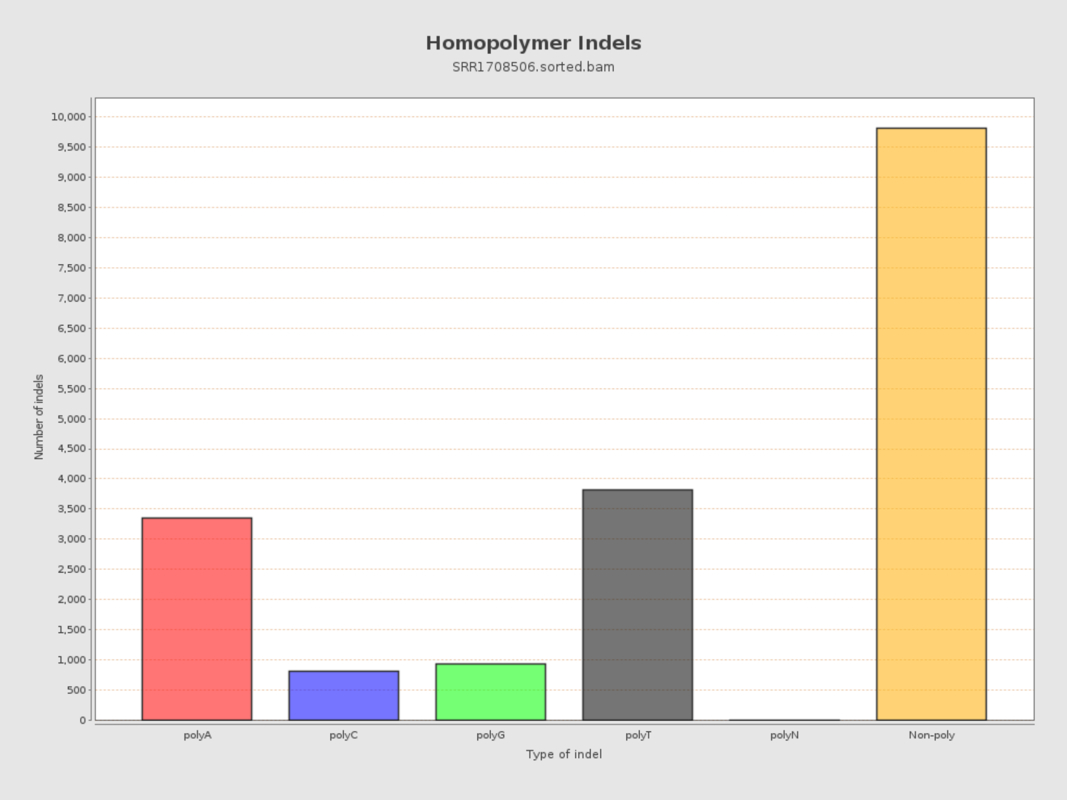
9. Results : Mapped Reads GC-content Distribution



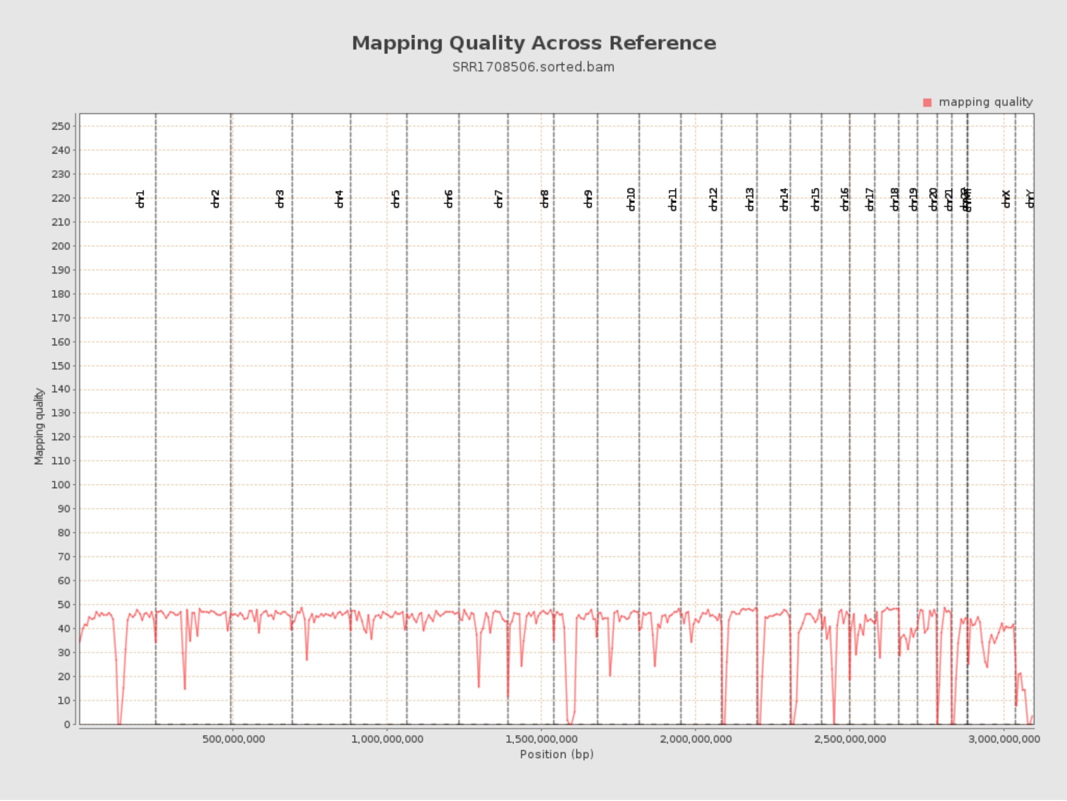
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram