Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:13:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708514.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_SRR1708514 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708514.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:13:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708514.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,218,636
Mapped reads	2,231,771 / 69.34%
Unmapped reads	986,865 / 30.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	474 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	114,417 / 3.55%
Duplication rate	3.94%
Clipped reads	431,883 / 13.42%

2.2. ACGT Content

Number/percentage of A's	31,088,211 / 29.02%
Number/percentage of C's	19,769,779 / 18.46%
Number/percentage of T's	34,427,368 / 32.14%
Number/percentage of G's	21,833,884 / 20.38%
Number/percentage of N's	1,419 / 0%
GC Percentage	38.84%

2.3. Coverage

Mean	0.0346

Standard Deviation	0.3617

2.4. Mapping Quality

Mean Mapping Quality	43.06

2.5. Mismatches and indels

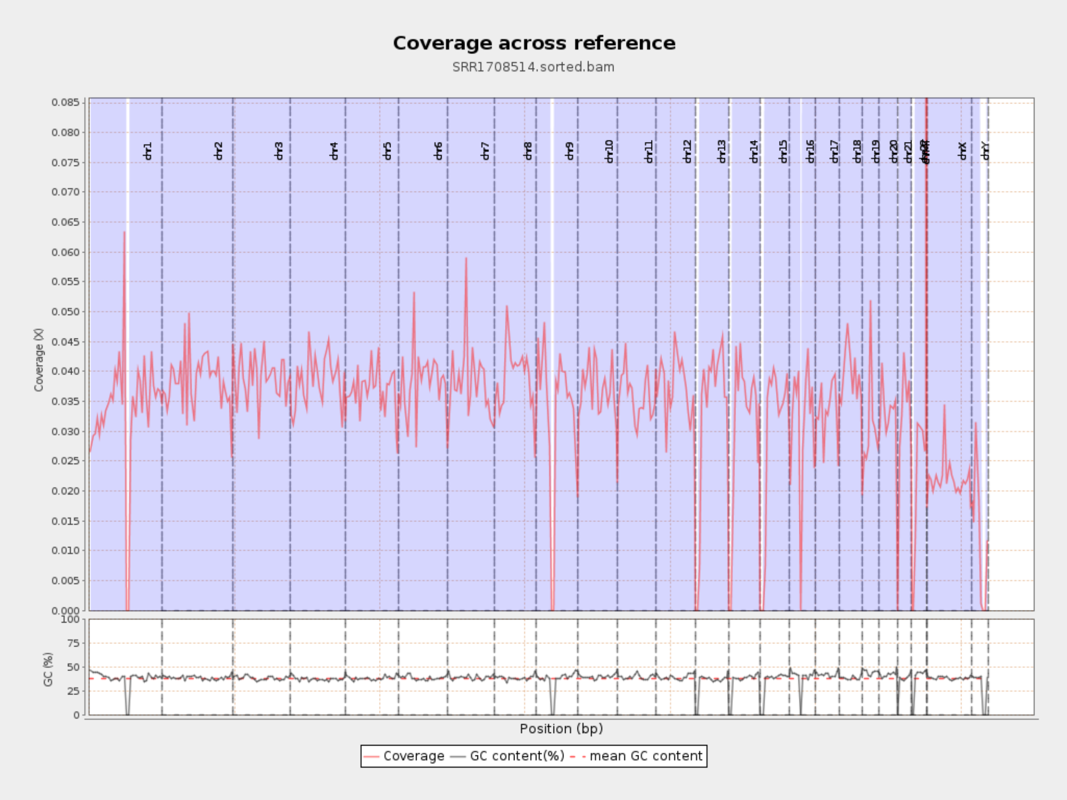
General error rate	0.51%
Mismatches	541,599
Insertions	5,369
Mapped reads with at least one insertion	0.24%
Deletions	13,807
Mapped reads with at least one deletion	0.62%
Homopolymer indels	47.99%

2.6. Chromosome stats

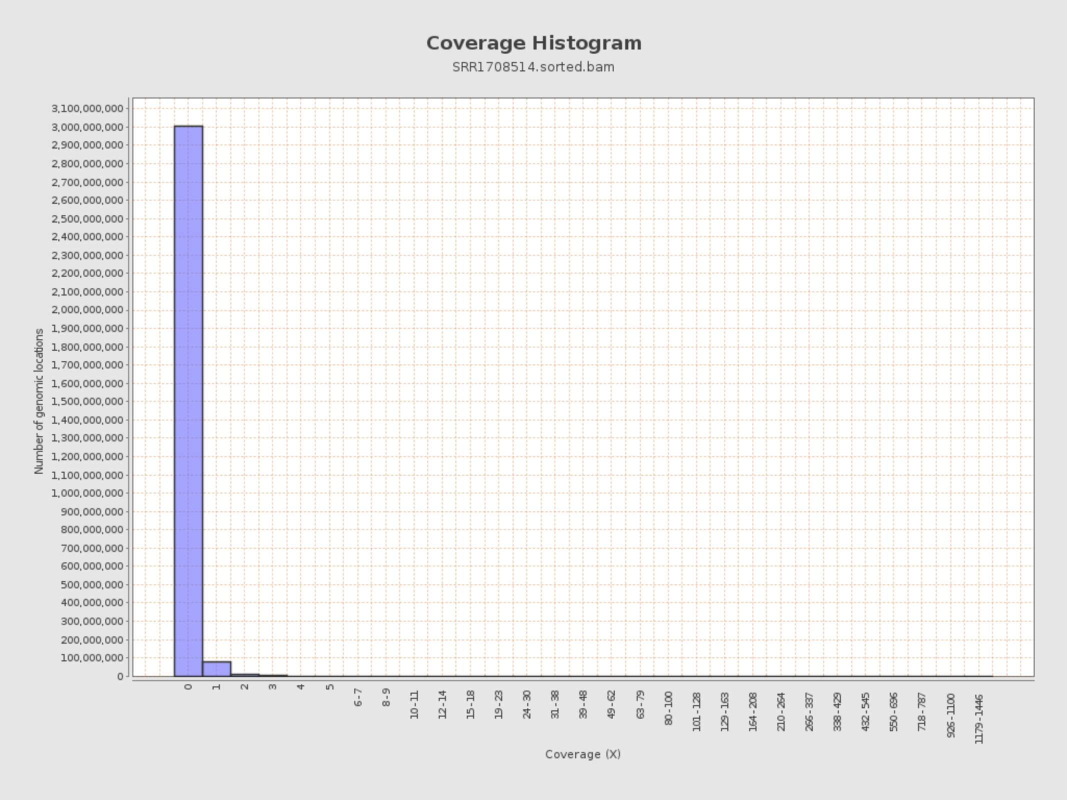
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8408314	0.0337	0.6299
chr2	243199373	9365934	0.0385	0.3812
chr3	198022430	7741615	0.0391	0.2335
chr4	191154276	7403339	0.0387	0.2345
chr5	180915260	6691723	0.037	0.2285
chr6	171115067	6579688	0.0385	0.2776
chr7	159138663	6131159	0.0385	0.3979

chr8	146364022	5708506	0.039	0.7971
chr9	141213431	4733762	0.0335	0.2528
chr10	135534747	5073449	0.0374	0.2815
chr11	135006516	4812918	0.0356	0.3182
chr12	133851895	5000311	0.0374	0.231
chr13	115169878	3778512	0.0328	0.2228
chr14	107349540	3320975	0.0309	0.2135
chr15	102531392	3001433	0.0293	0.2
chr16	90354753	2837622	0.0314	0.2174
chr17	81195210	2694700	0.0332	0.2617
chr18	78077248	3097765	0.0397	0.4178
chr19	59128983	1826116	0.0309	0.4582
chr20	63025520	2096719	0.0333	0.2179
chr21	48129895	1499044	0.0311	0.2518
chr22	51304566	1066697	0.0208	0.1921
chrMT	16571	141997	8.569	5.9865
chrX	155270560	3433749	0.0221	0.2048
chrY	59373566	695424	0.0117	0.1327

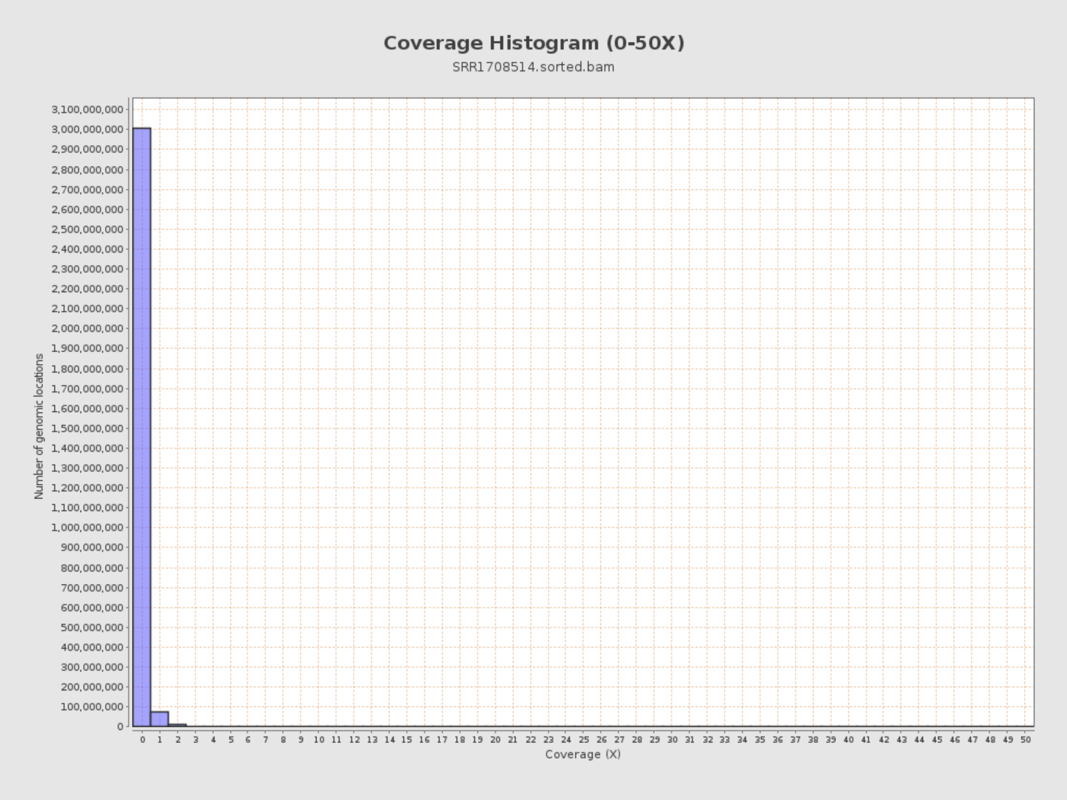
3. Results : Coverage across reference



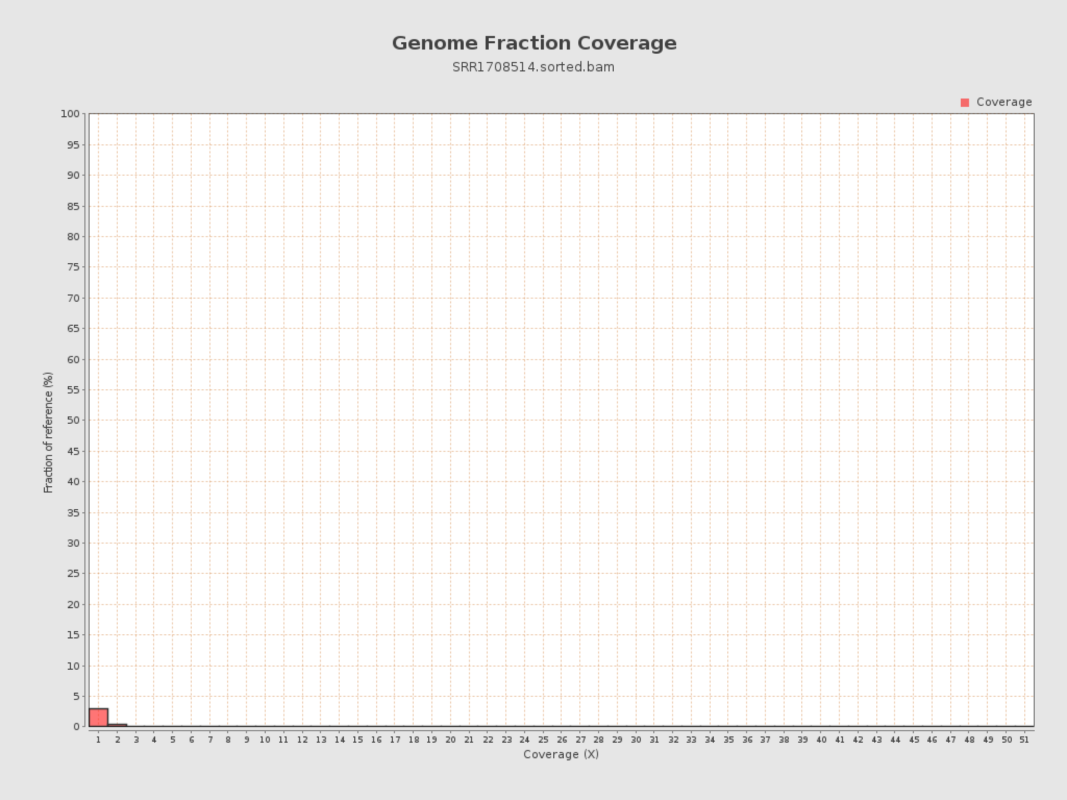
4. Results : Coverage Histogram



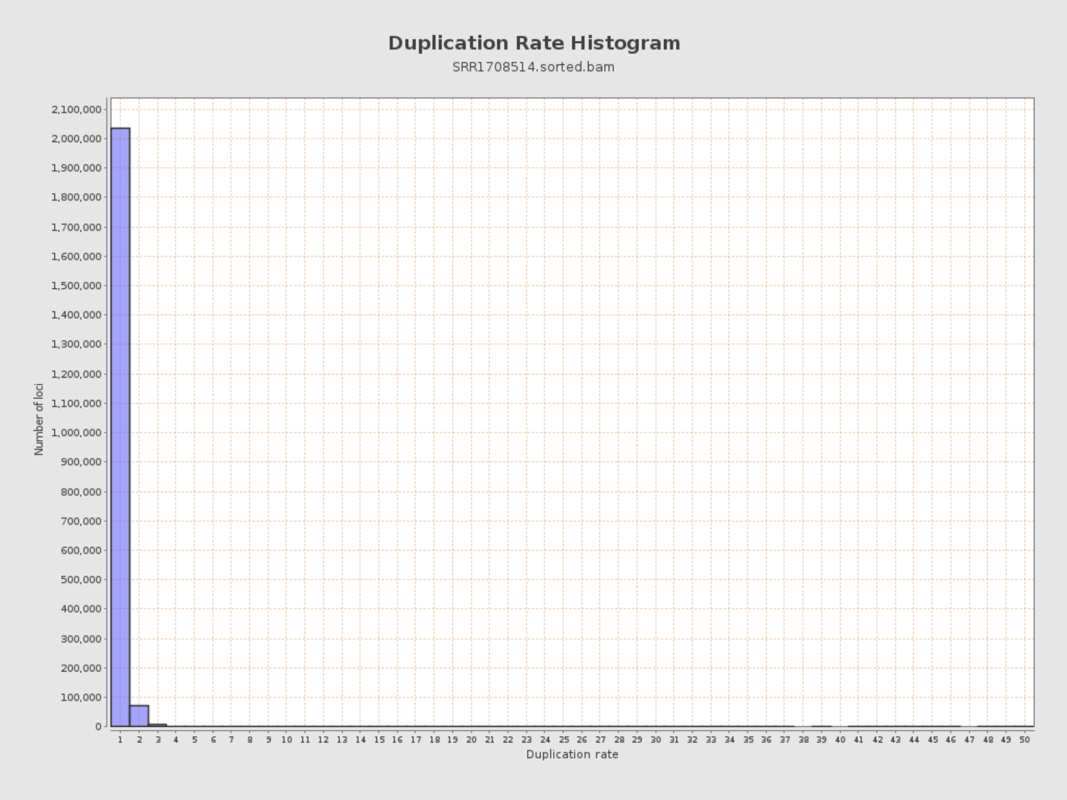
5. Results : Coverage Histogram (0-50X)



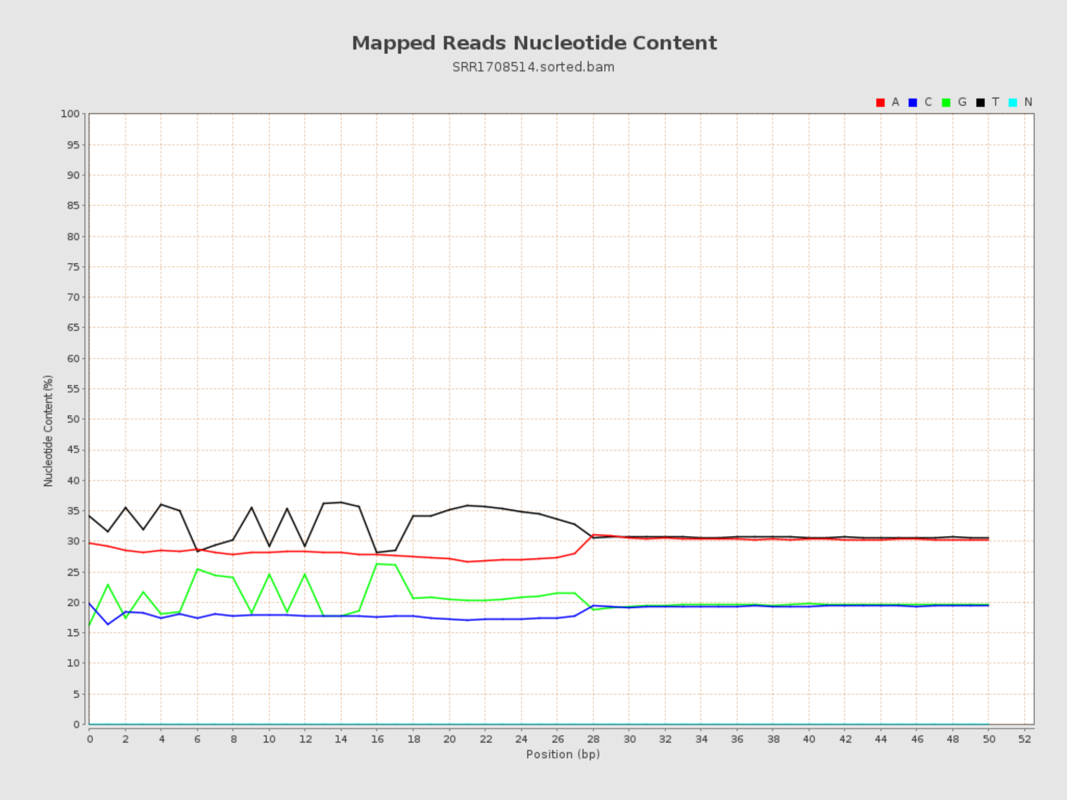
6. Results : Genome Fraction Coverage



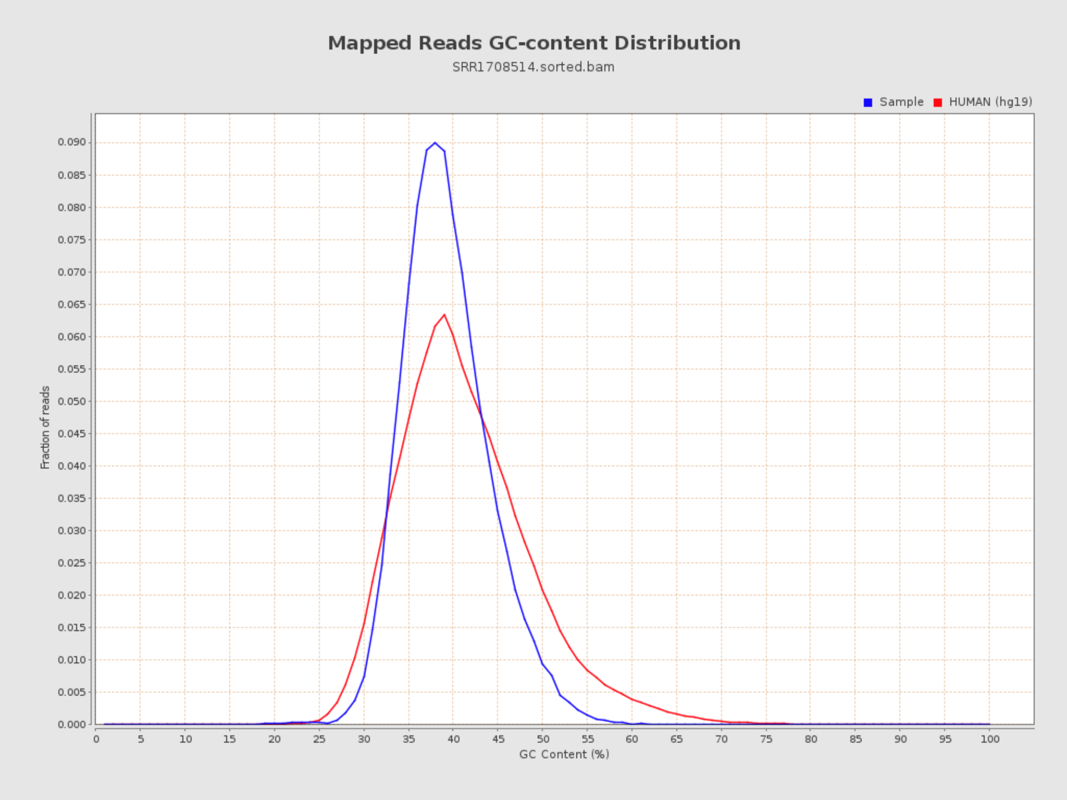
7. Results : Duplication Rate Histogram



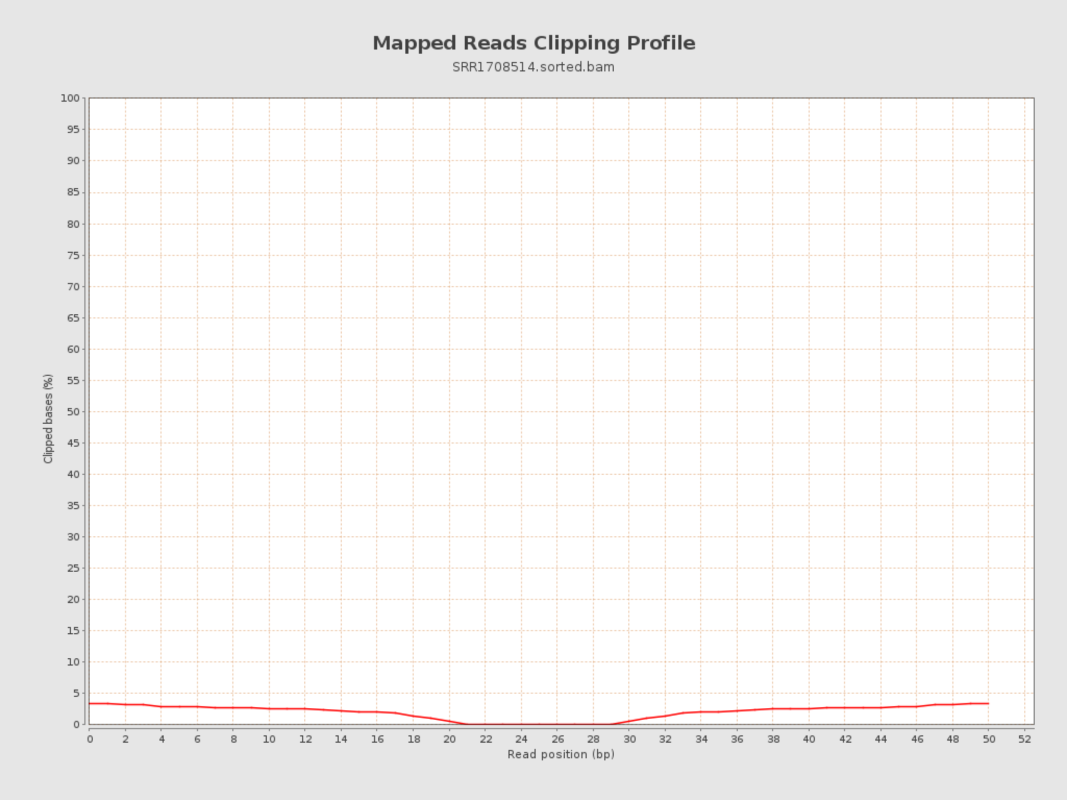
8. Results : Mapped Reads Nucleotide Content



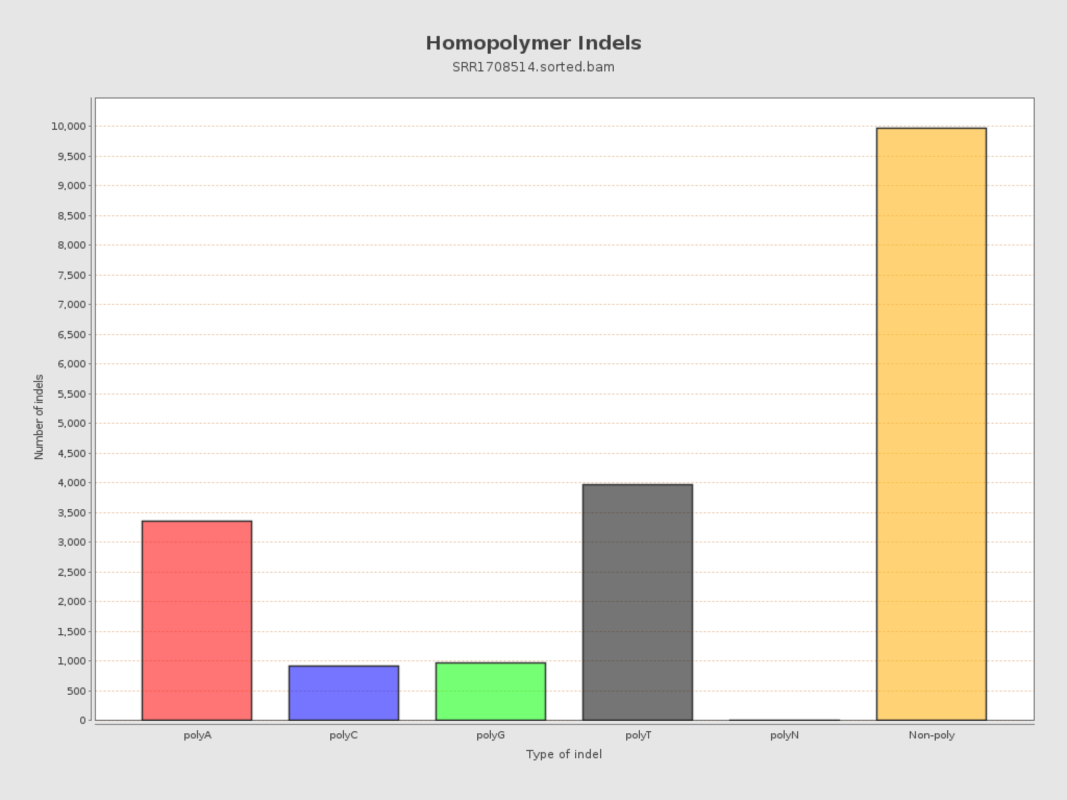
9. Results : Mapped Reads GC-content Distribution



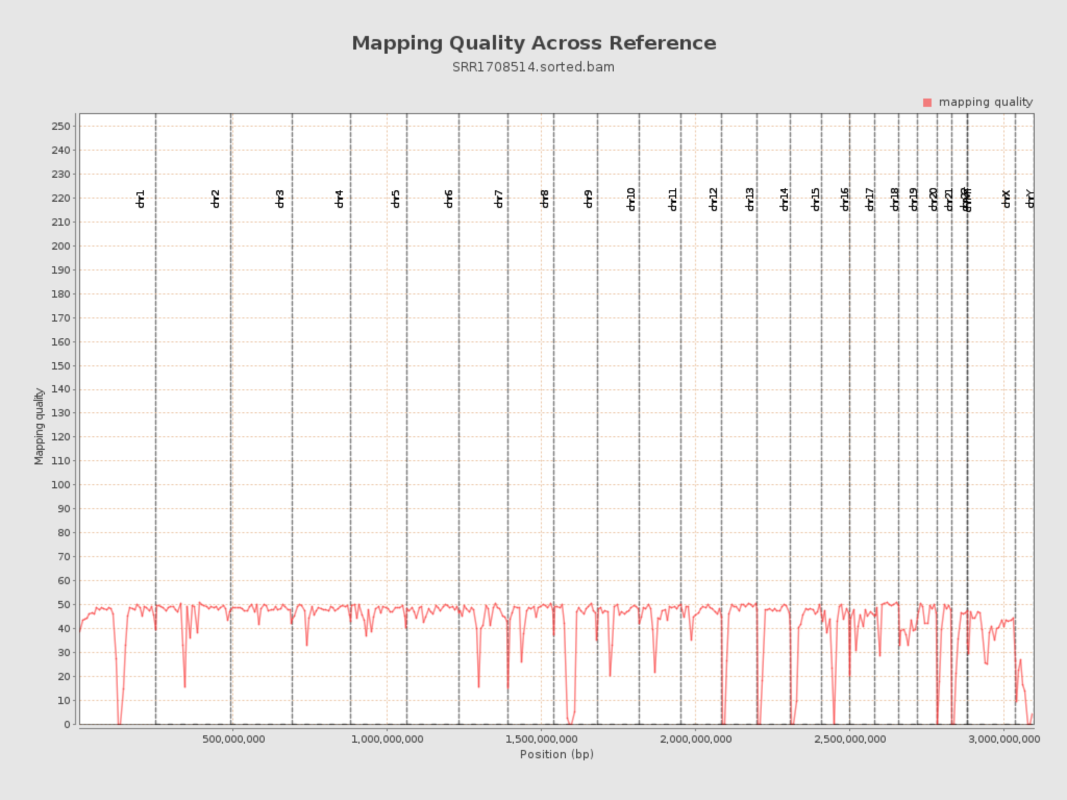
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram