Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 01:58:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708509.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_SRR1708509 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708509.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 01:58:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708509.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,084,965
Mapped reads	2,078,990 / 67.39%
Unmapped reads	1,005,975 / 32.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	370 / 0.01%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	114,555 / 3.71%
Duplication rate	4.2%
Clipped reads	460,410 / 14.92%

2.2. ACGT Content

Number/percentage of A's	28,007,413 / 28.38%
Number/percentage of C's	18,188,844 / 18.43%
Number/percentage of T's	31,745,036 / 32.16%
Number/percentage of G's	20,751,848 / 21.03%
Number/percentage of N's	1,349 / 0%
GC Percentage	39.46%

2.3. Coverage

Mean	0.0319

Standard Deviation	0.3262

2.4. Mapping Quality

Mean Mapping Quality	40.57

2.5. Mismatches and indels

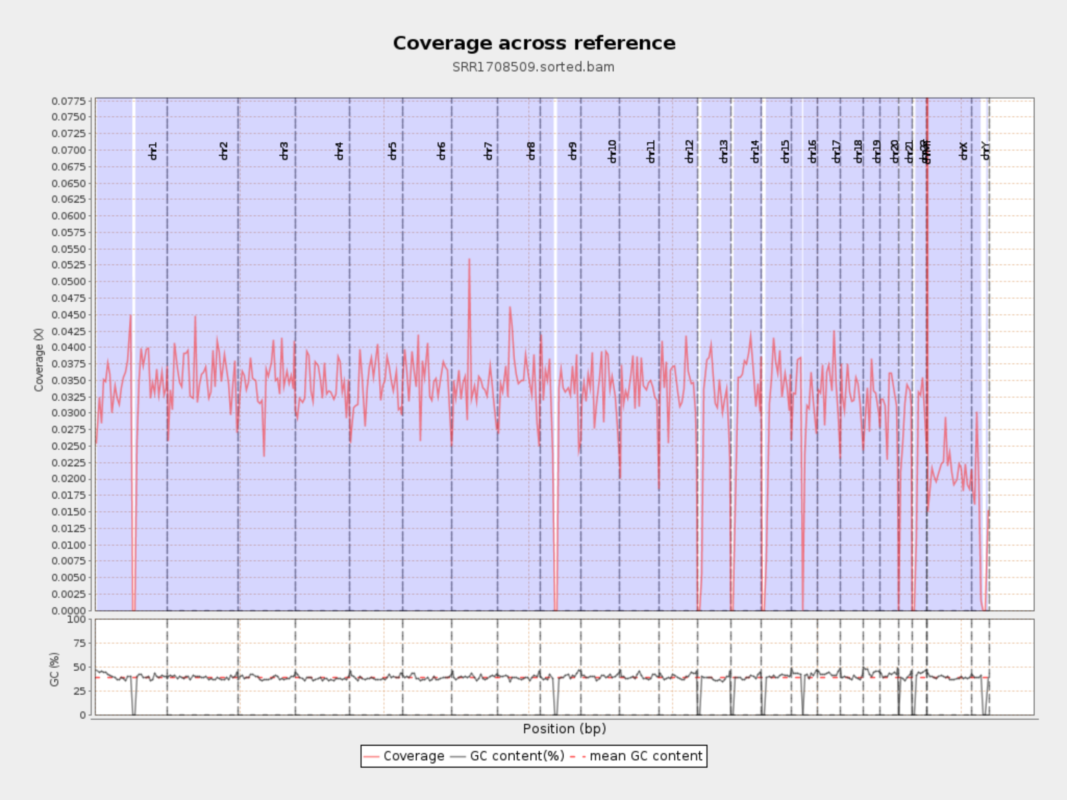
General error rate	0.51%
Mismatches	498,893
Insertions	5,199
Mapped reads with at least one insertion	0.25%
Deletions	15,172
Mapped reads with at least one deletion	0.73%
Homopolymer indels	48.42%

2.6. Chromosome stats

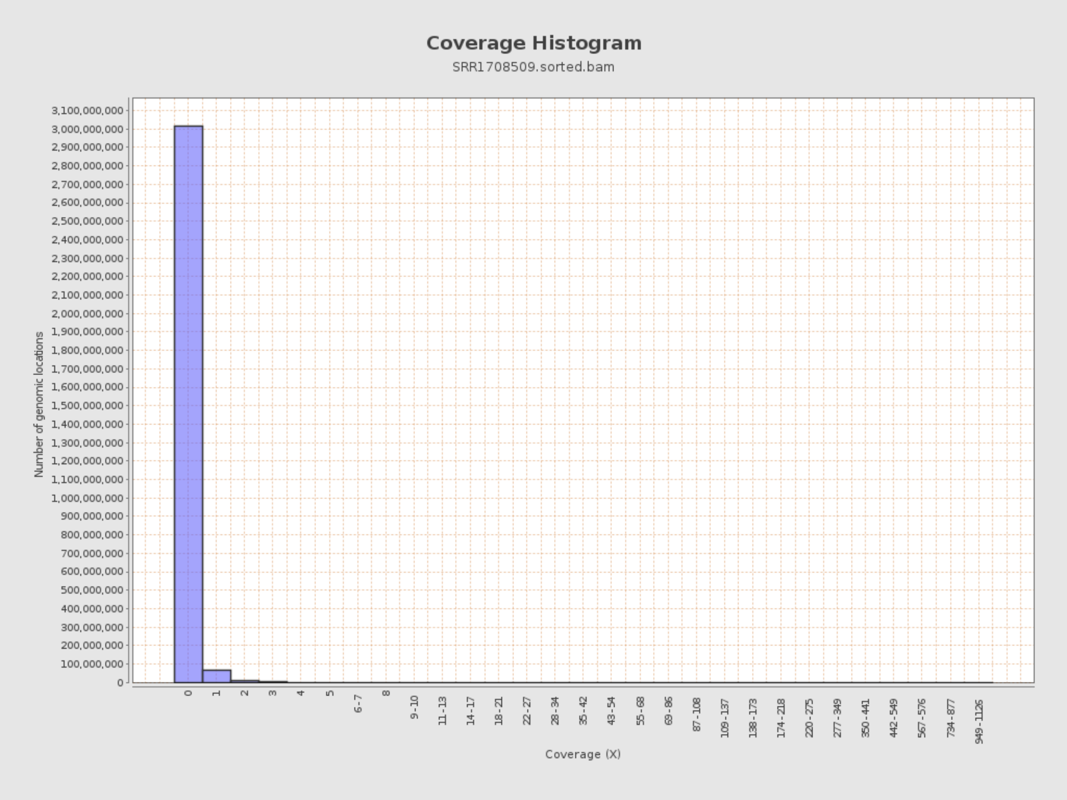
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8076332	0.0324	0.4349
chr2	243199373	8643466	0.0355	0.5029
chr3	198022430	6897320	0.0348	0.2316
chr4	191154276	6525975	0.0341	0.2371
chr5	180915260	6205356	0.0343	0.2241
chr6	171115067	6026941	0.0352	0.2939
chr7	159138663	5445436	0.0342	0.3707

chr8	146364022	5149882	0.0352	0.6433
chr9	141213431	4281899	0.0303	0.2491
chr10	135534747	4557994	0.0336	0.2496
chr11	135006516	4586086	0.034	0.2885
chr12	133851895	4607431	0.0344	0.2264
chr13	115169878	3238071	0.0281	0.2313
chr14	107349540	3201794	0.0298	0.2154
chr15	102531392	2908837	0.0284	0.2069
chr16	90354753	2640848	0.0292	0.2097
chr17	81195210	2757201	0.034	0.2636
chr18	78077248	2577430	0.033	0.3578
chr19	59128983	1870808	0.0316	0.3387
chr20	63025520	1977305	0.0314	0.2155
chr21	48129895	1283503	0.0267	0.2066
chr22	51304566	1127127	0.022	0.1792
chrMT	16571	135142	8.1553	5.8078
chrX	155270560	3261298	0.021	0.1984
chrY	59373566	733819	0.0124	0.151

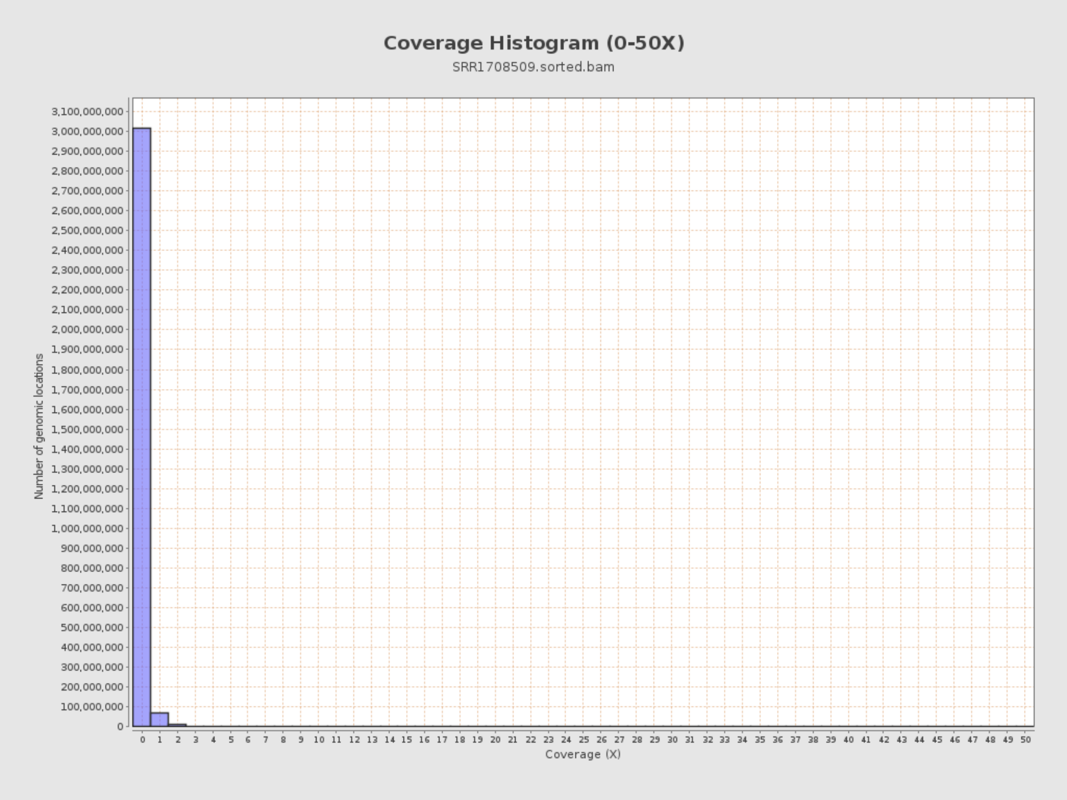
3. Results : Coverage across reference



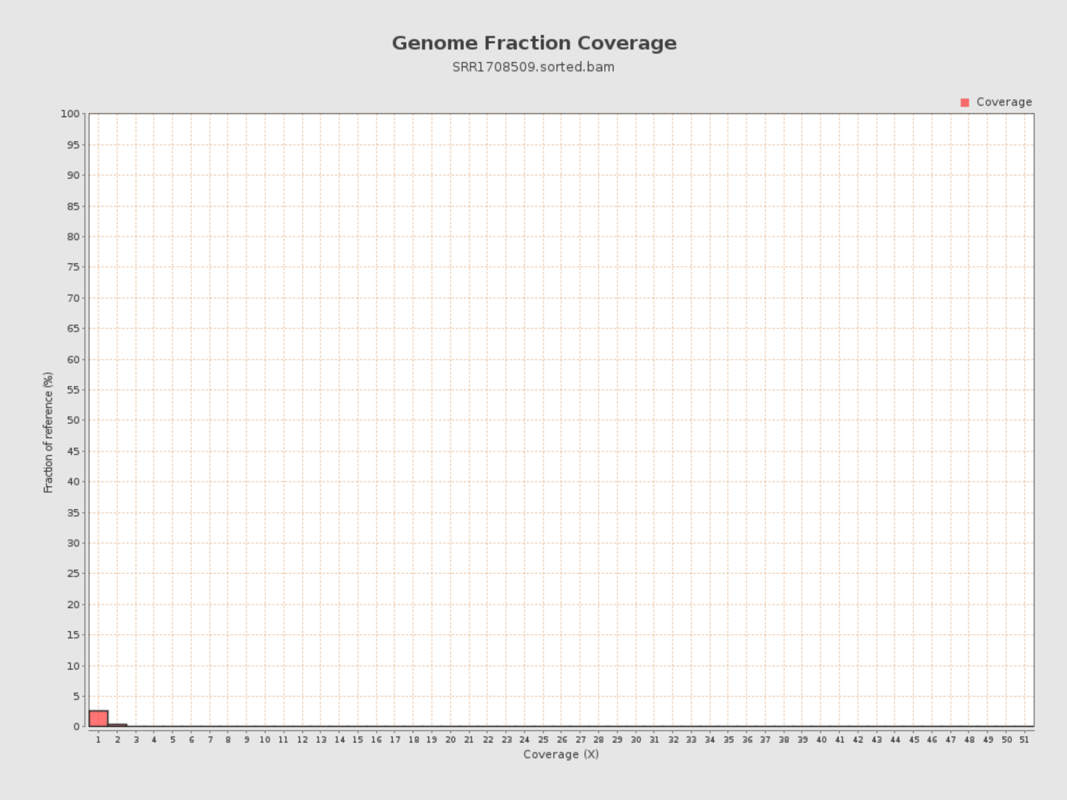
4. Results : Coverage Histogram



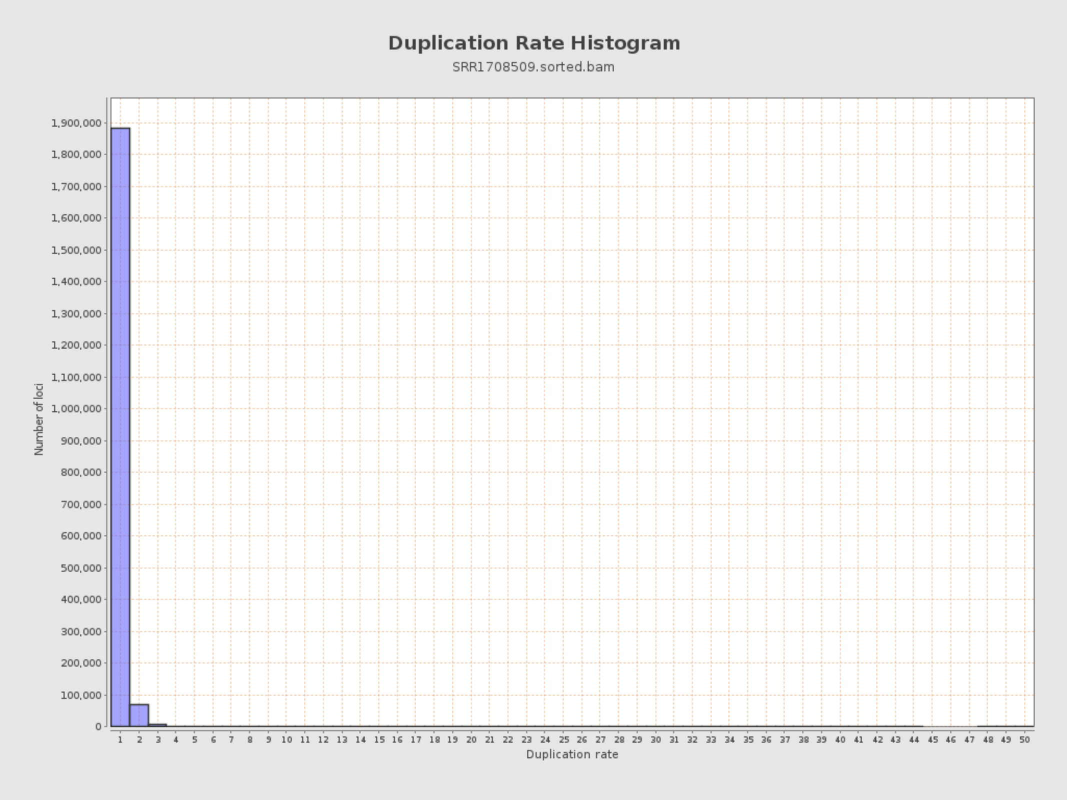
5. Results : Coverage Histogram (0-50X)



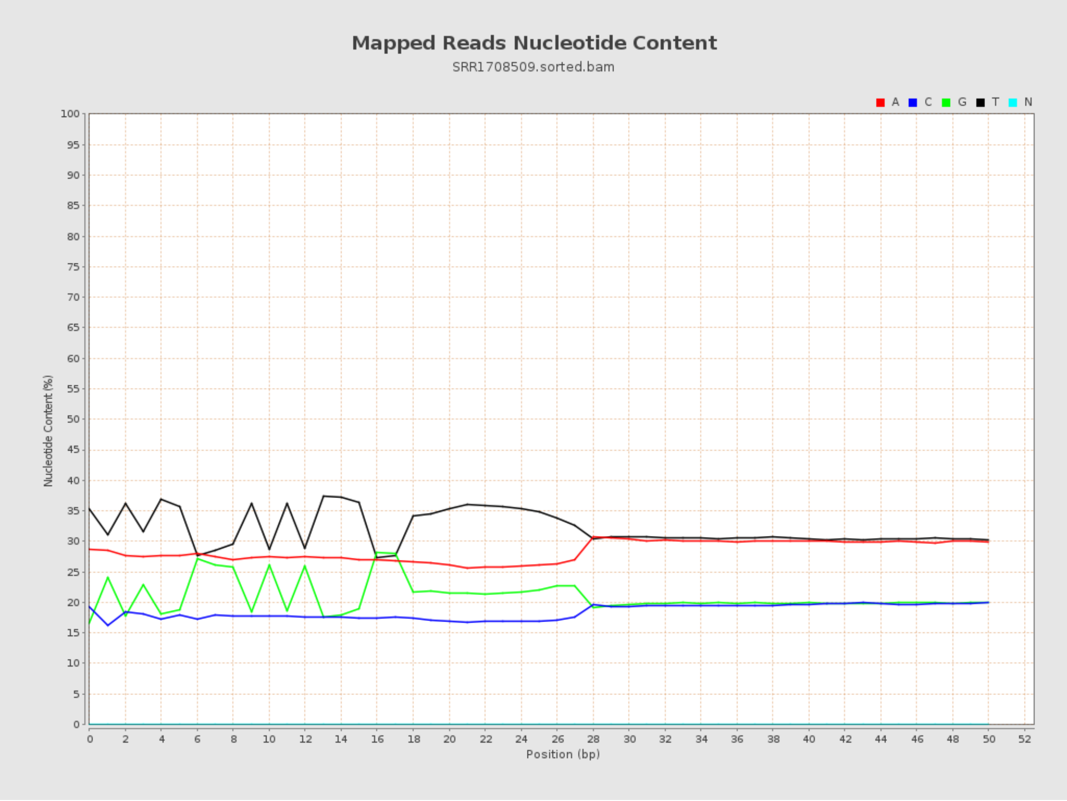
6. Results : Genome Fraction Coverage



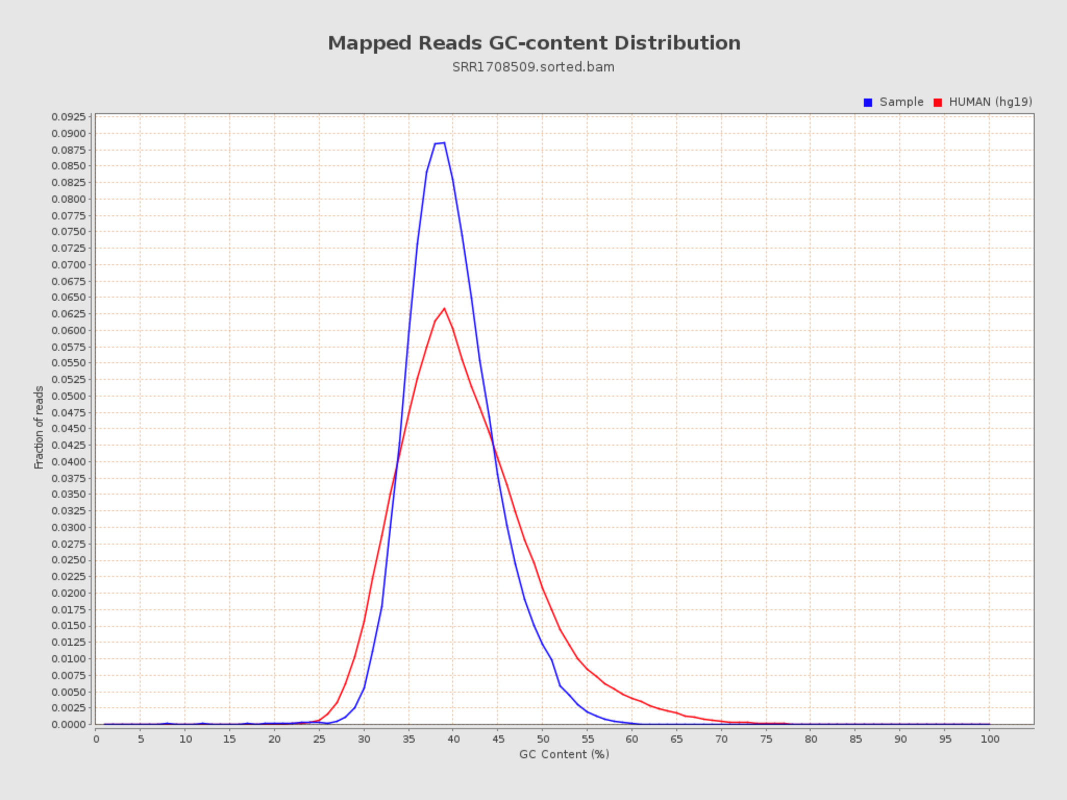
7. Results : Duplication Rate Histogram



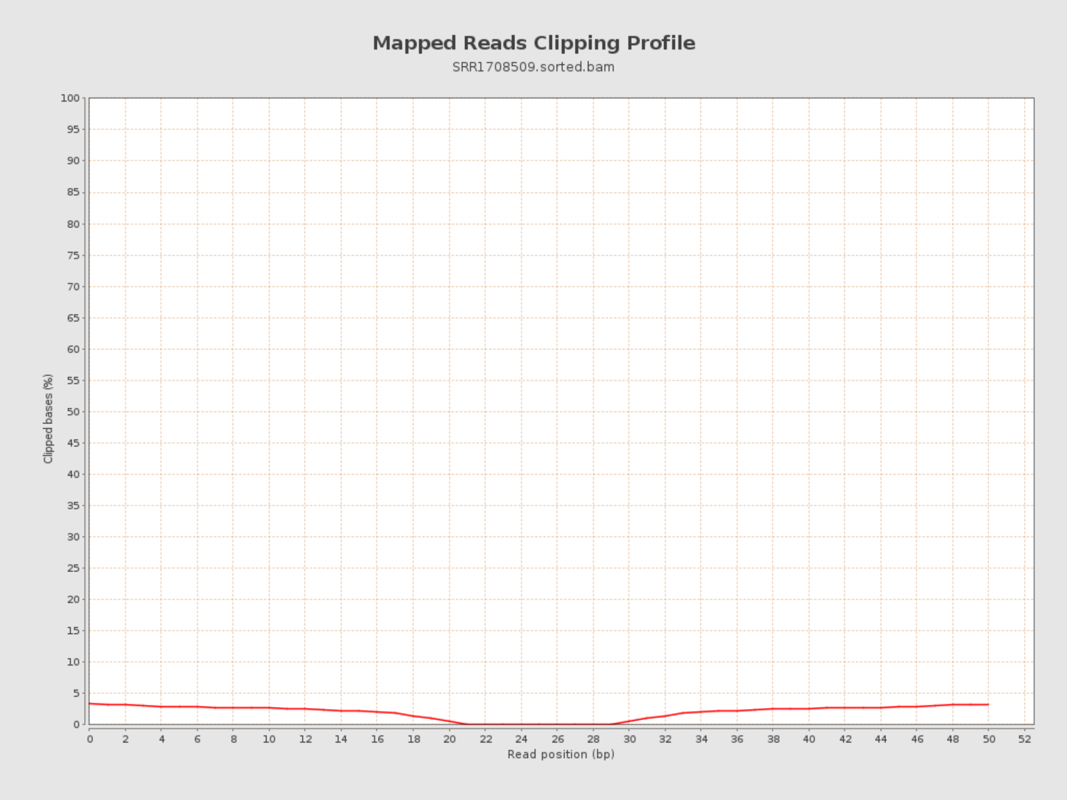
8. Results : Mapped Reads Nucleotide Content



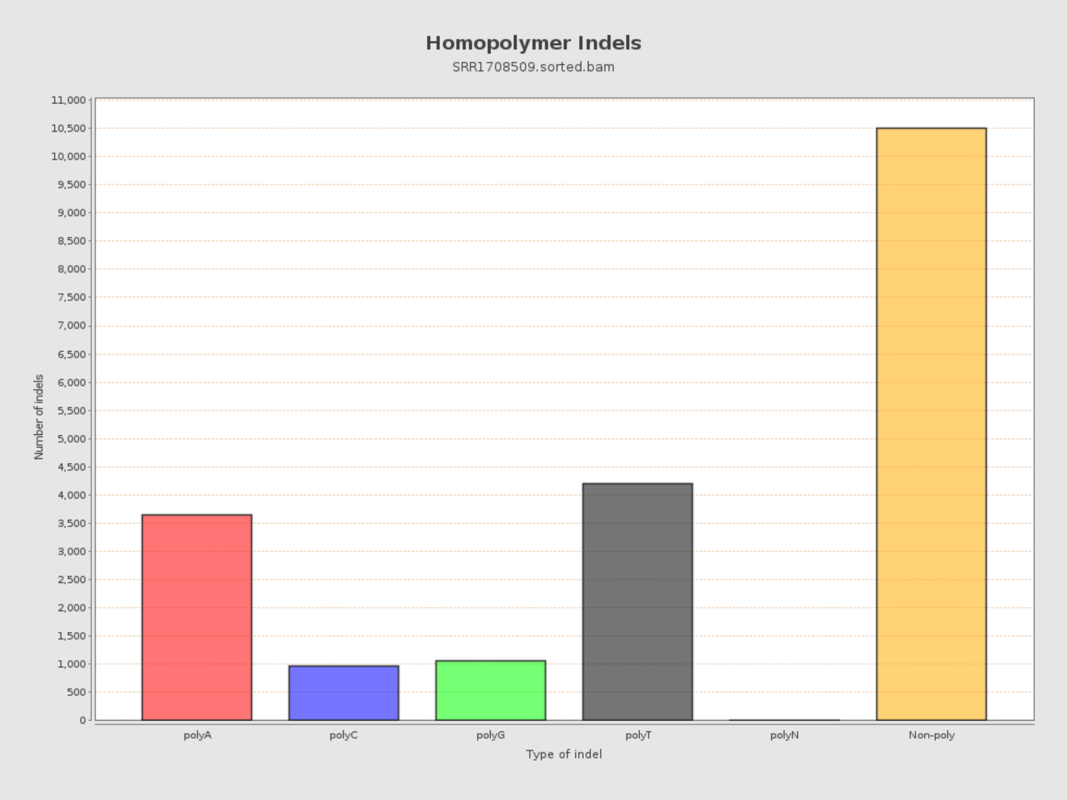
9. Results : Mapped Reads GC-content Distribution



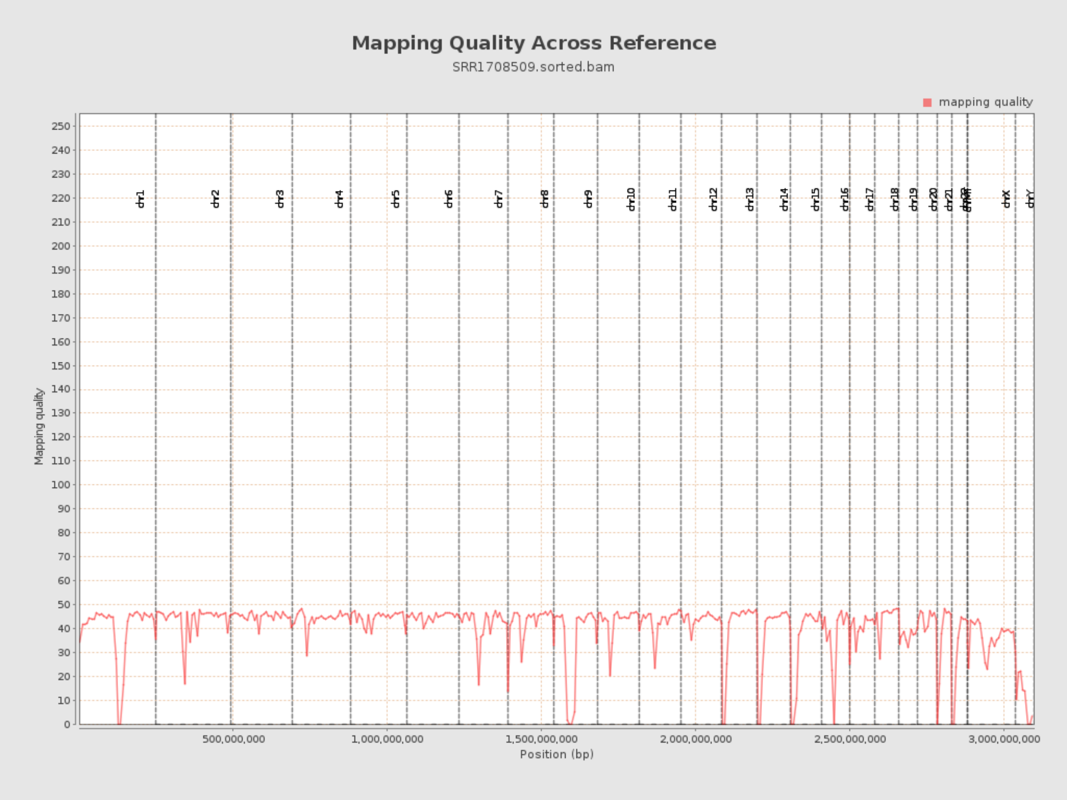
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram