Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 00:49:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708504.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_SRR1708504 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708504.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 00:49:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708504.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,300,309
Mapped reads	2,156,623 / 65.35%
Unmapped reads	1,143,686 / 34.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,082 / 0.03%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	90,115 / 2.73%
Duplication rate	2.97%
Clipped reads	525,338 / 15.92%

2.2. ACGT Content

Number/percentage of A's	28,583,376 / 28.03%
Number/percentage of C's	19,241,351 / 18.87%
Number/percentage of T's	32,259,416 / 31.64%
Number/percentage of G's	21,882,979 / 21.46%
Number/percentage of N's	1,369 / 0%
GC Percentage	40.33%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.3109

2.4. Mapping Quality

Mean Mapping Quality	38.92

2.5. Mismatches and indels

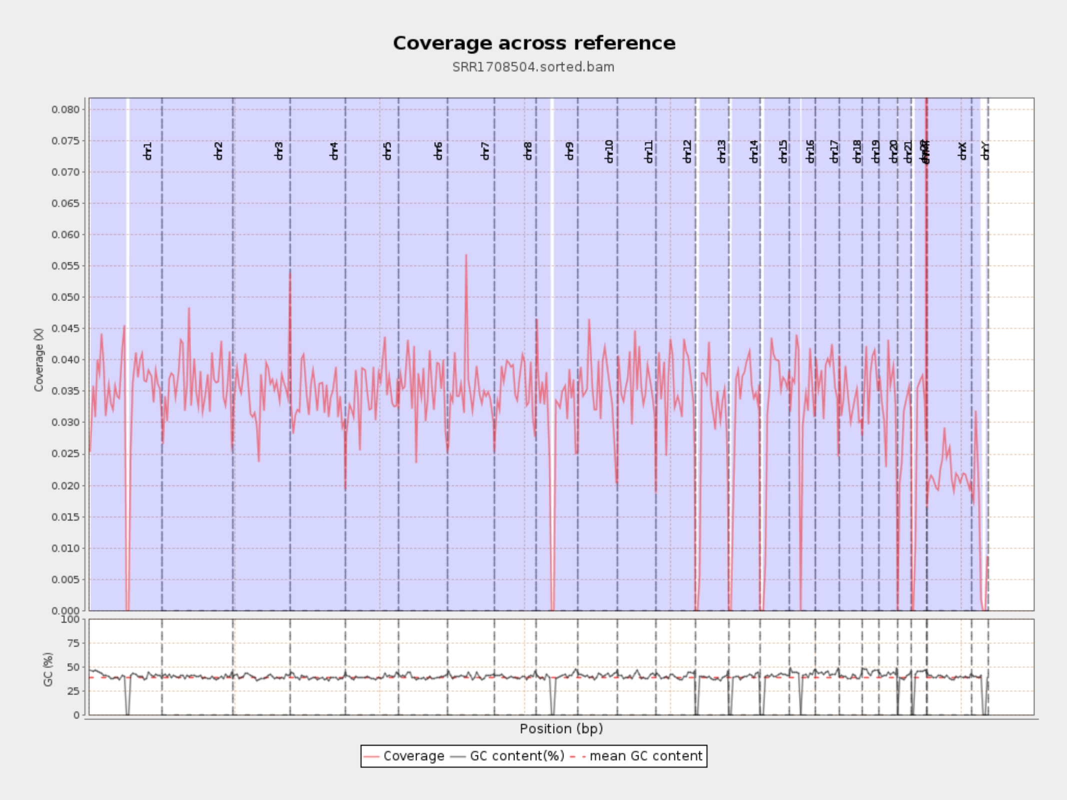
General error rate	0.54%
Mismatches	538,741
Insertions	5,968
Mapped reads with at least one insertion	0.28%
Deletions	16,572
Mapped reads with at least one deletion	0.77%
Homopolymer indels	46.65%

2.6. Chromosome stats

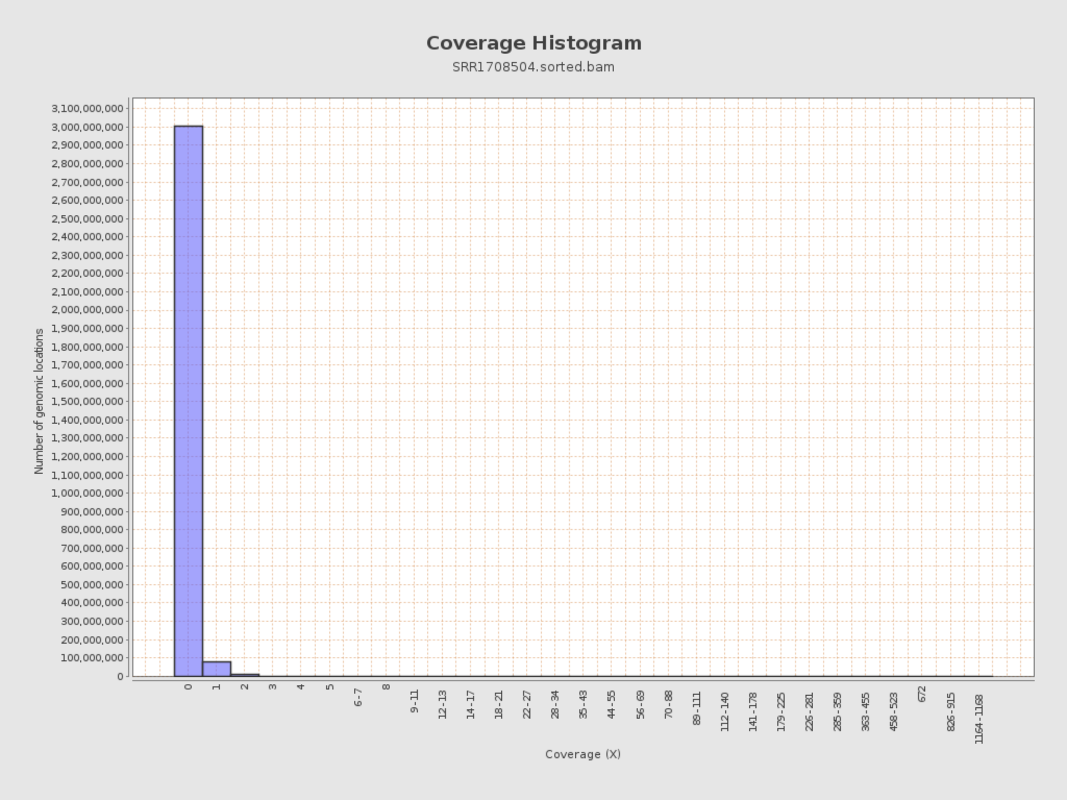
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8501301	0.0341	0.4202
chr2	243199373	8830709	0.0363	0.539
chr3	198022430	6952743	0.0351	0.222
chr4	191154276	6493268	0.034	0.2222
chr5	180915260	6269916	0.0347	0.2161
chr6	171115067	6103643	0.0357	0.3456
chr7	159138663	5650799	0.0355	0.3774

chr8	146364022	5224917	0.0357	0.3694
chr9	141213431	4233663	0.03	0.2645
chr10	135534747	4803074	0.0354	0.2633
chr11	135006516	4854279	0.036	0.2705
chr12	133851895	4864185	0.0363	0.2228
chr13	115169878	3267537	0.0284	0.2618
chr14	107349540	3272788	0.0305	0.2096
chr15	102531392	3080576	0.03	0.2093
chr16	90354753	2988703	0.0331	0.2245
chr17	81195210	2990946	0.0368	0.2411
chr18	78077248	2618401	0.0335	0.3464
chr19	59128983	2189432	0.037	0.3391
chr20	63025520	2113275	0.0335	0.2196
chr21	48129895	1281105	0.0266	0.197
chr22	51304566	1240521	0.0242	0.1819
chrMT	16571	97815	5.9028	4.1896
chrX	155270560	3367002	0.0217	0.2097
chrY	59373566	703334	0.0118	0.1421

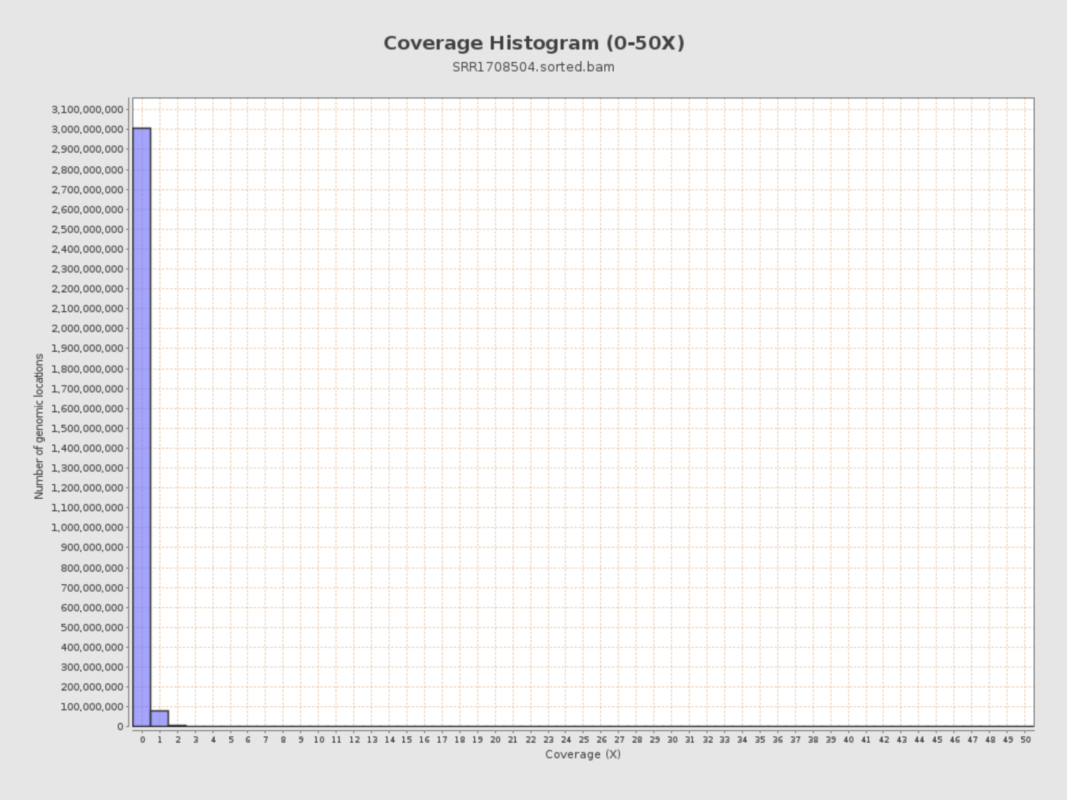
3. Results : Coverage across reference



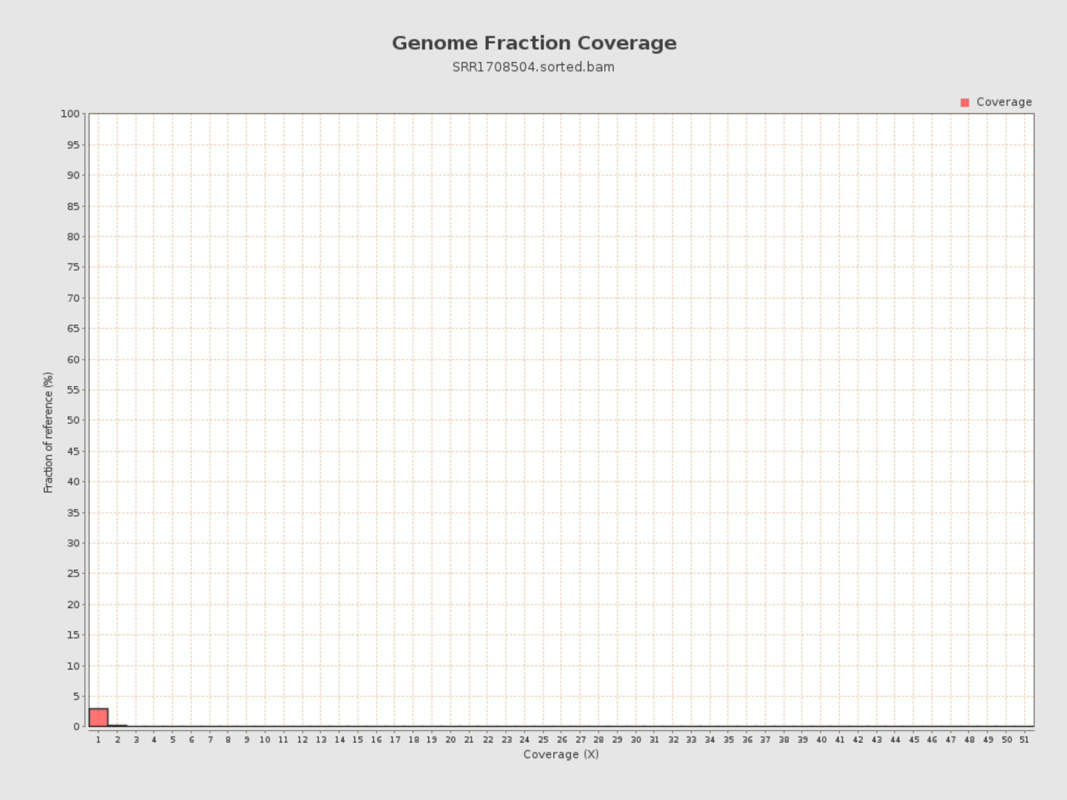
4. Results : Coverage Histogram



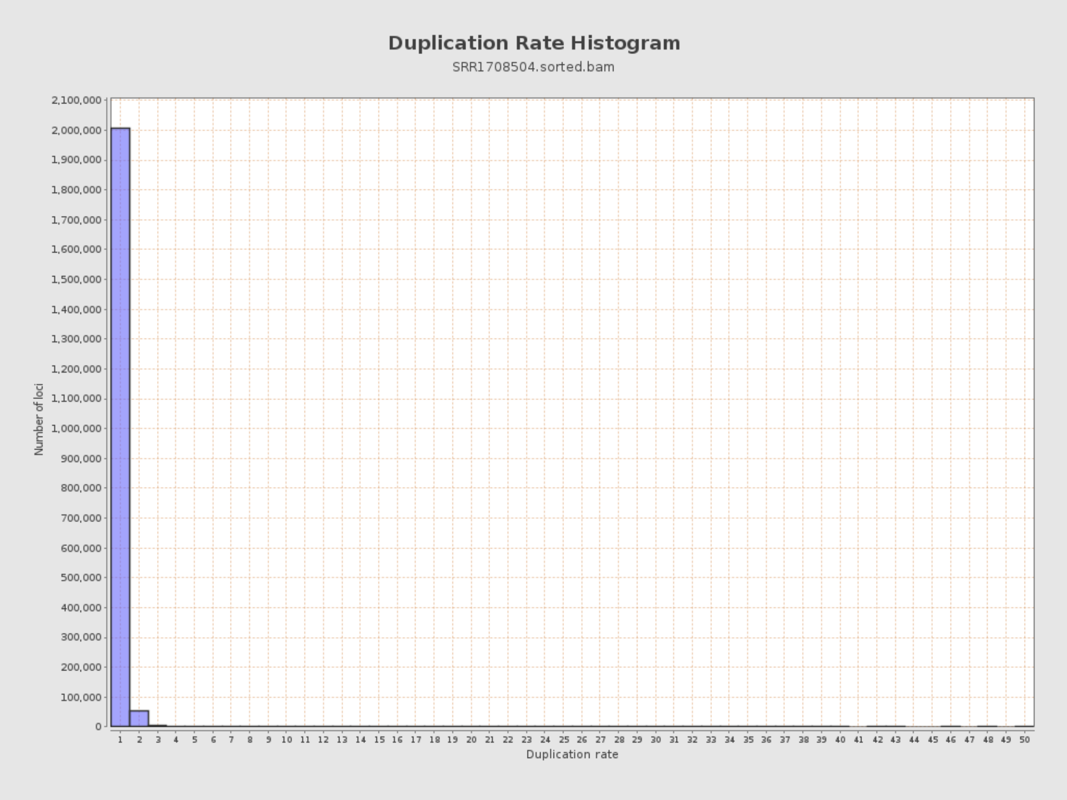
5. Results : Coverage Histogram (0-50X)



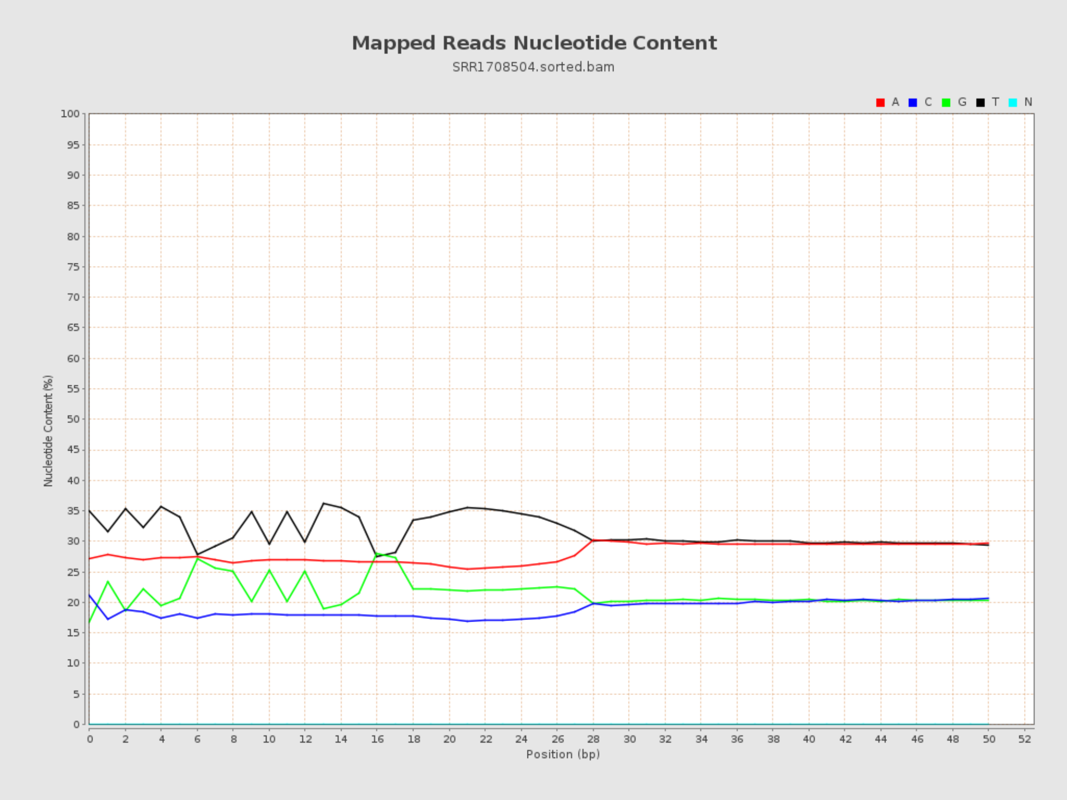
6. Results : Genome Fraction Coverage



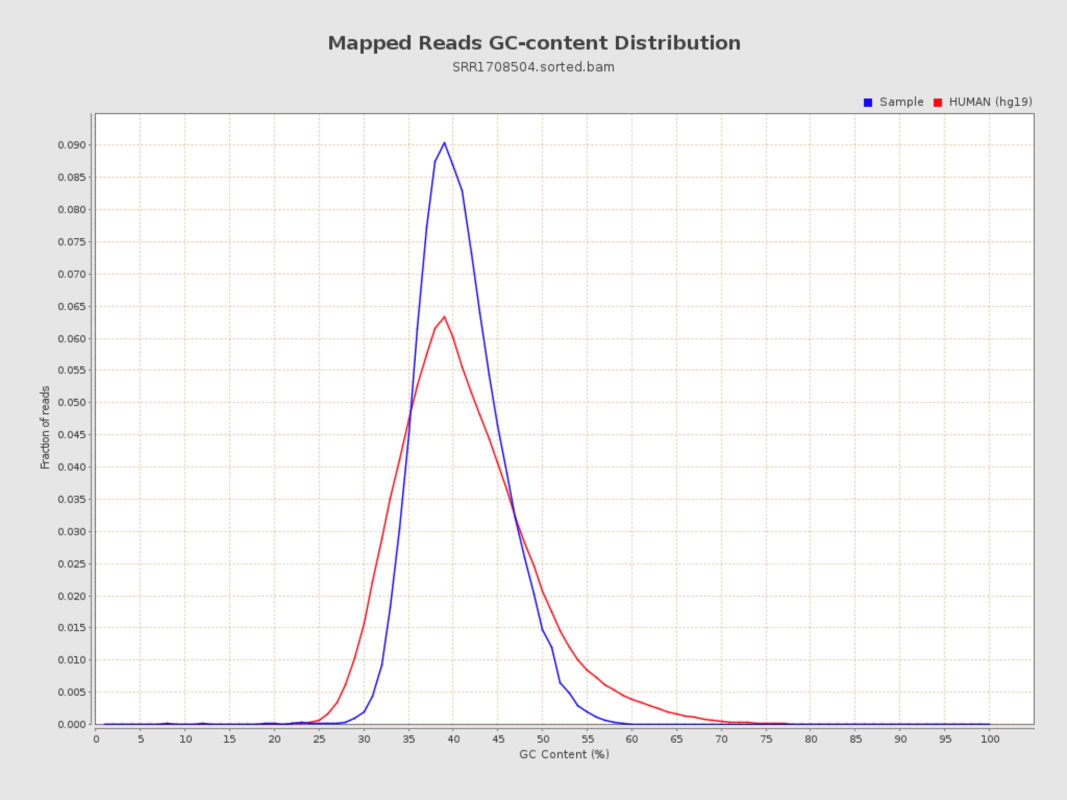
7. Results : Duplication Rate Histogram



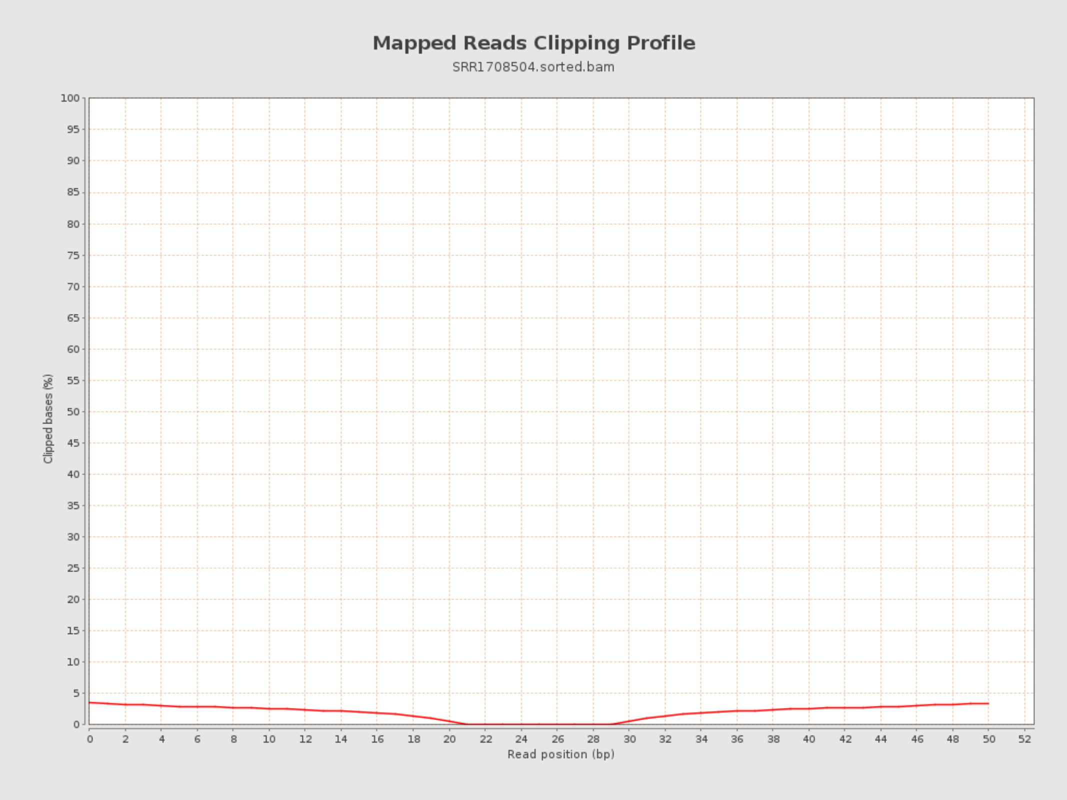
8. Results : Mapped Reads Nucleotide Content



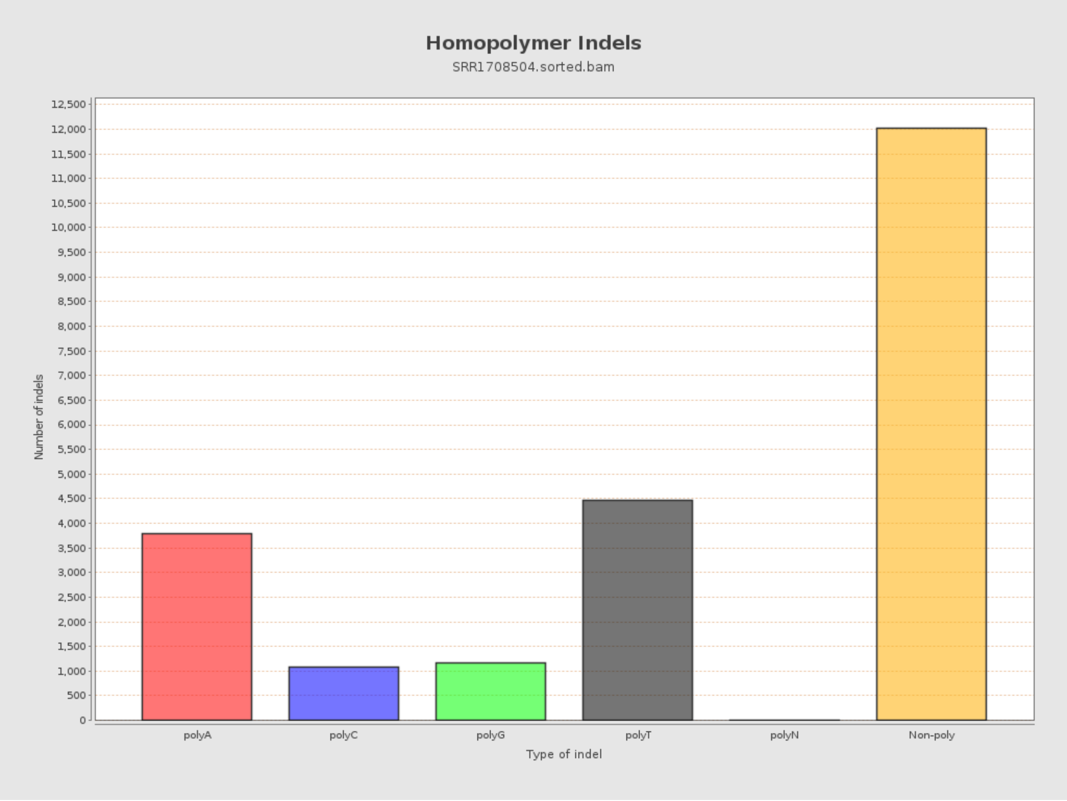
9. Results : Mapped Reads GC-content Distribution



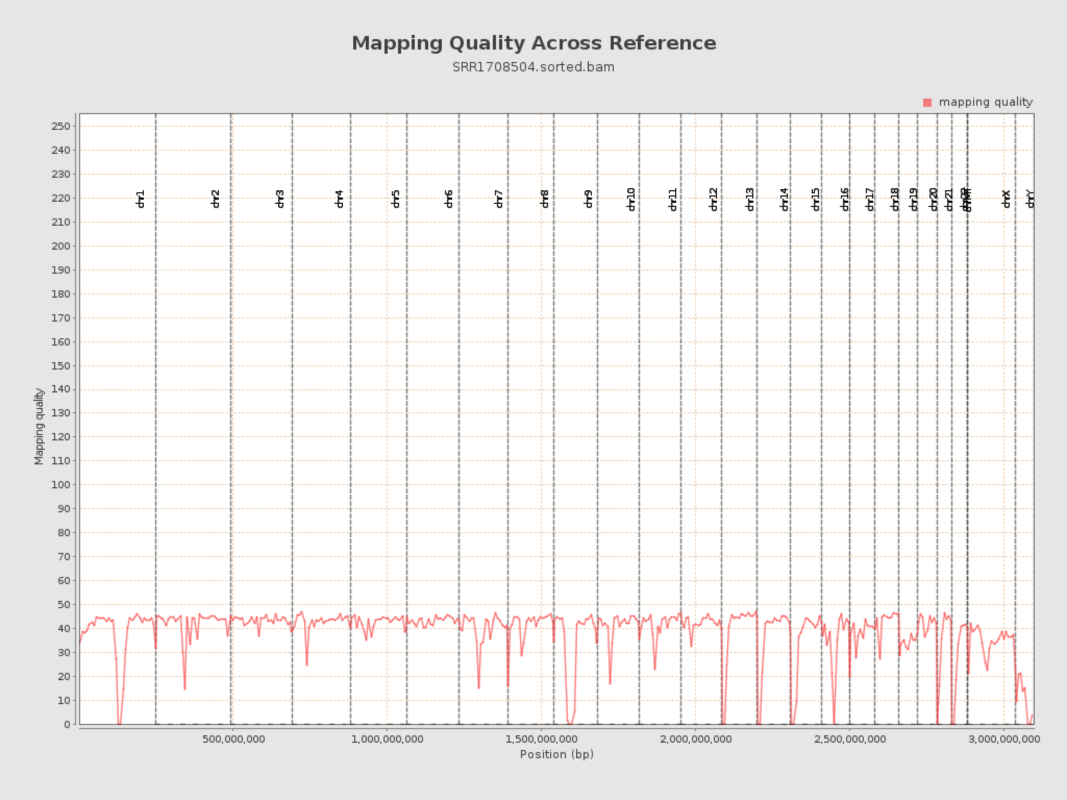
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram