Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:45:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708541.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_SRR1708541 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708541.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:45:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708541.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,174,906
Mapped reads	22,374,858 / 96.55%
Unmapped reads	800,048 / 3.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	547 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	190,491 / 0.82%
Duplication rate	0.84%
Clipped reads	349,746 / 1.51%

2.2. ACGT Content

Number/percentage of A's	344,240,109 / 30.85%
Number/percentage of C's	211,657,124 / 18.97%
Number/percentage of T's	343,979,921 / 30.83%
Number/percentage of G's	215,517,646 / 19.32%
Number/percentage of N's	380,398 / 0.03%
GC Percentage	38.29%

2.3. Coverage

Mean	0.3605

Standard Deviation	0.6659

2.4. Mapping Quality

Mean Mapping Quality	46.36

2.5. Mismatches and indels

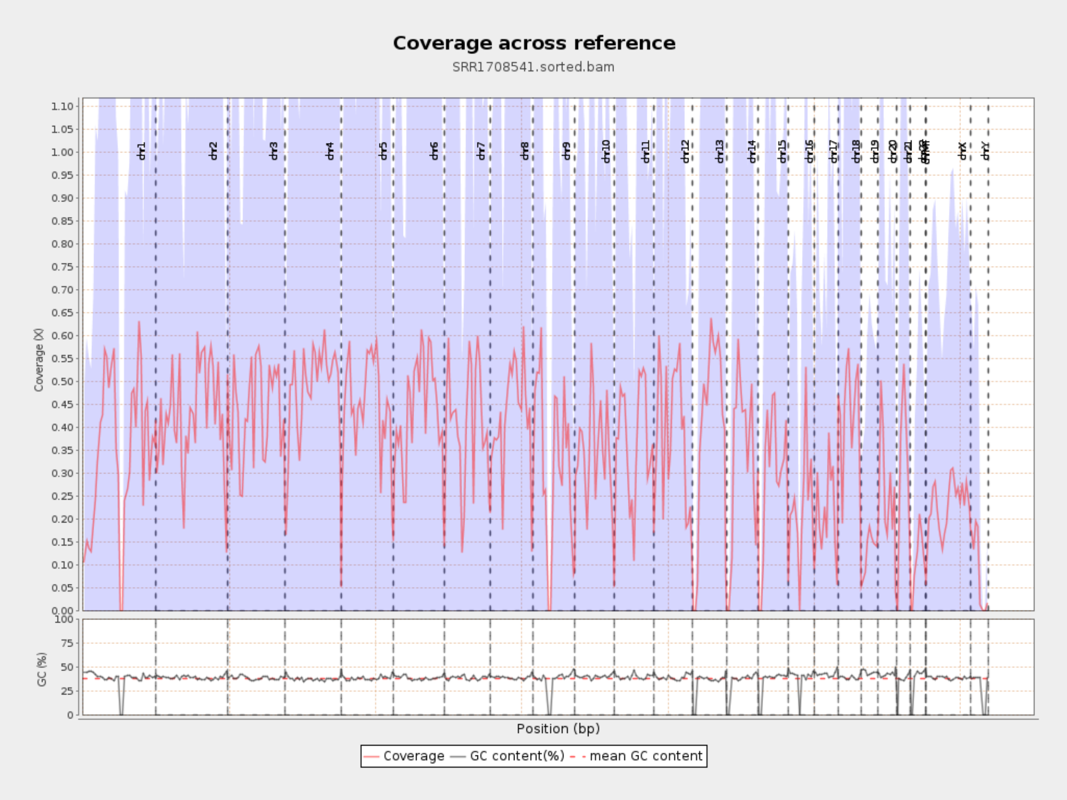
General error rate	0.34%
Mismatches	3,705,431
Insertions	58,865
Mapped reads with at least one insertion	0.26%
Deletions	56,342
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.18%

2.6. Chromosome stats

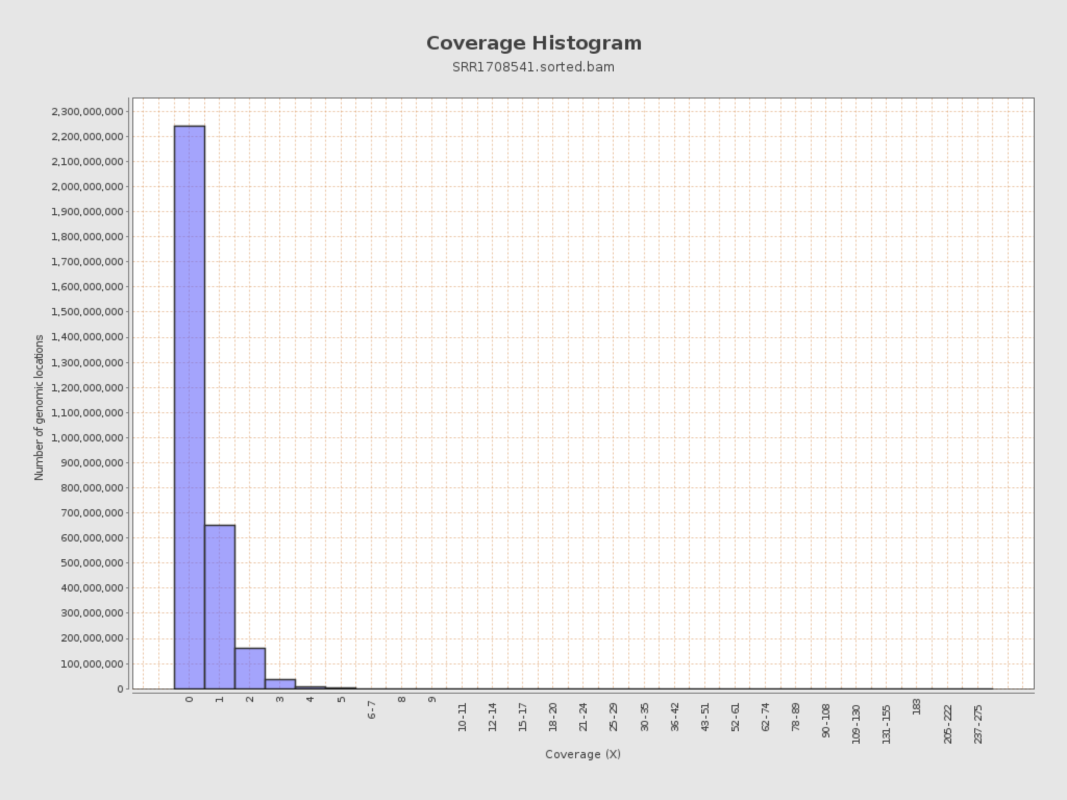
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	85547918	0.3432	0.6619
chr2	243199373	103396569	0.4252	0.7097
chr3	198022430	86376555	0.4362	0.714
chr4	191154276	92946934	0.4862	0.7522
chr5	180915260	80135056	0.4429	0.721
chr6	171115067	75874818	0.4434	0.7242
chr7	159138663	64031639	0.4024	0.6993

chr8	146364022	62409897	0.4264	0.709
chr9	141213431	46406822	0.3286	0.6434
chr10	135534747	47641427	0.3515	0.6439
chr11	135006516	49762365	0.3686	0.6728
chr12	133851895	51528447	0.385	0.6851
chr13	115169878	47085999	0.4088	0.711
chr14	107349540	35634562	0.3319	0.6471
chr15	102531392	29961433	0.2922	0.6096
chr16	90354753	20084863	0.2223	0.5235
chr17	81195210	17696189	0.2179	0.5232
chr18	78077248	33808025	0.433	0.7159
chr19	59128983	7772480	0.1314	0.3942
chr20	63025520	17011374	0.2699	0.5784
chr21	48129895	14273046	0.2966	0.6311
chr22	51304566	5625012	0.1096	0.3663
chrMT	16571	921	0.0556	0.2291
chrX	155270560	35780771	0.2304	0.5053
chrY	59373566	5075448	0.0855	0.3274

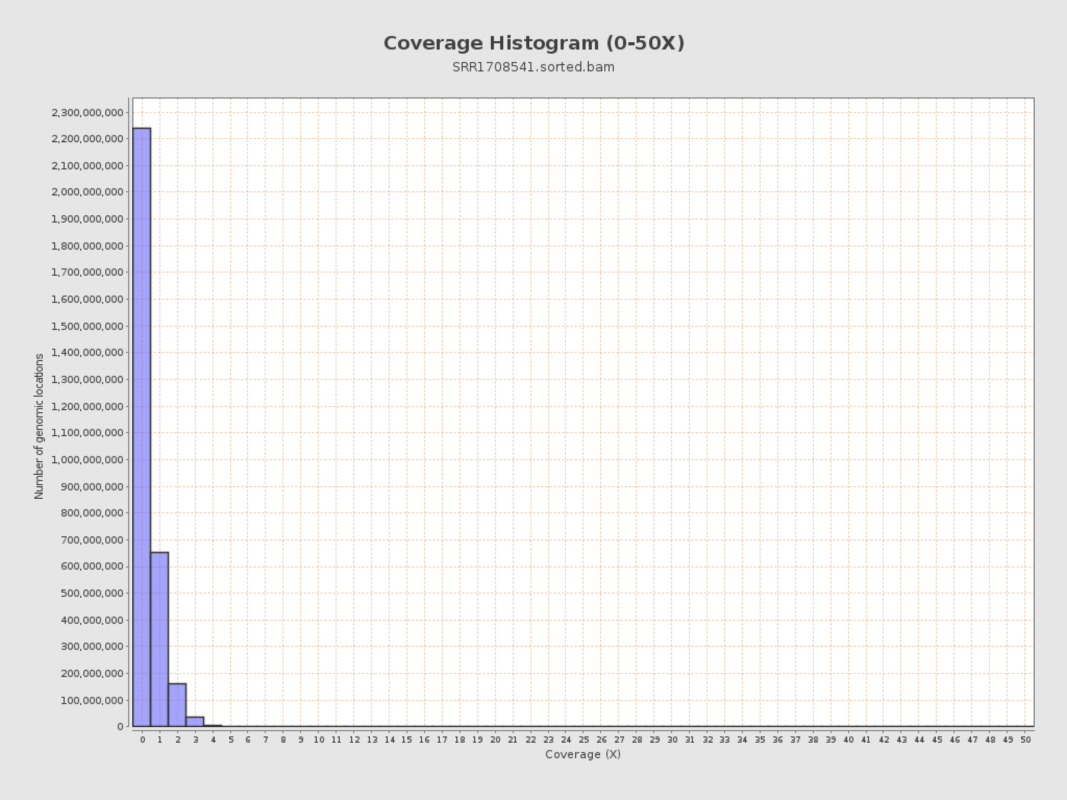
3. Results : Coverage across reference



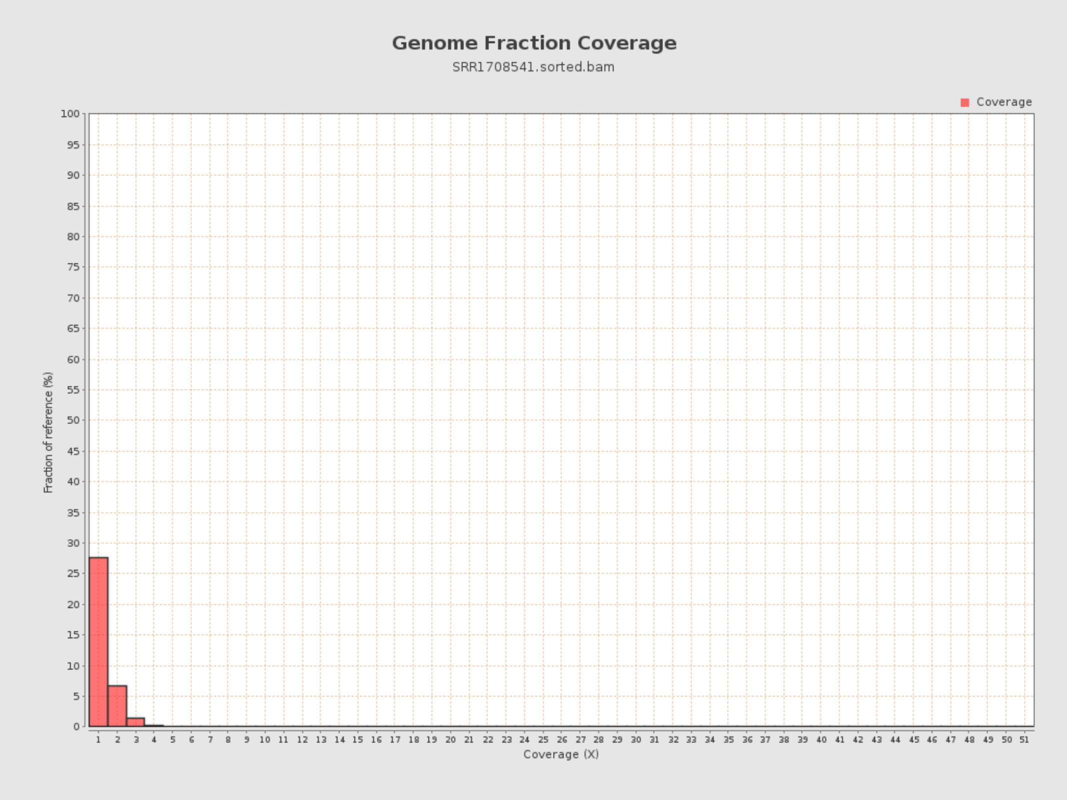
4. Results : Coverage Histogram



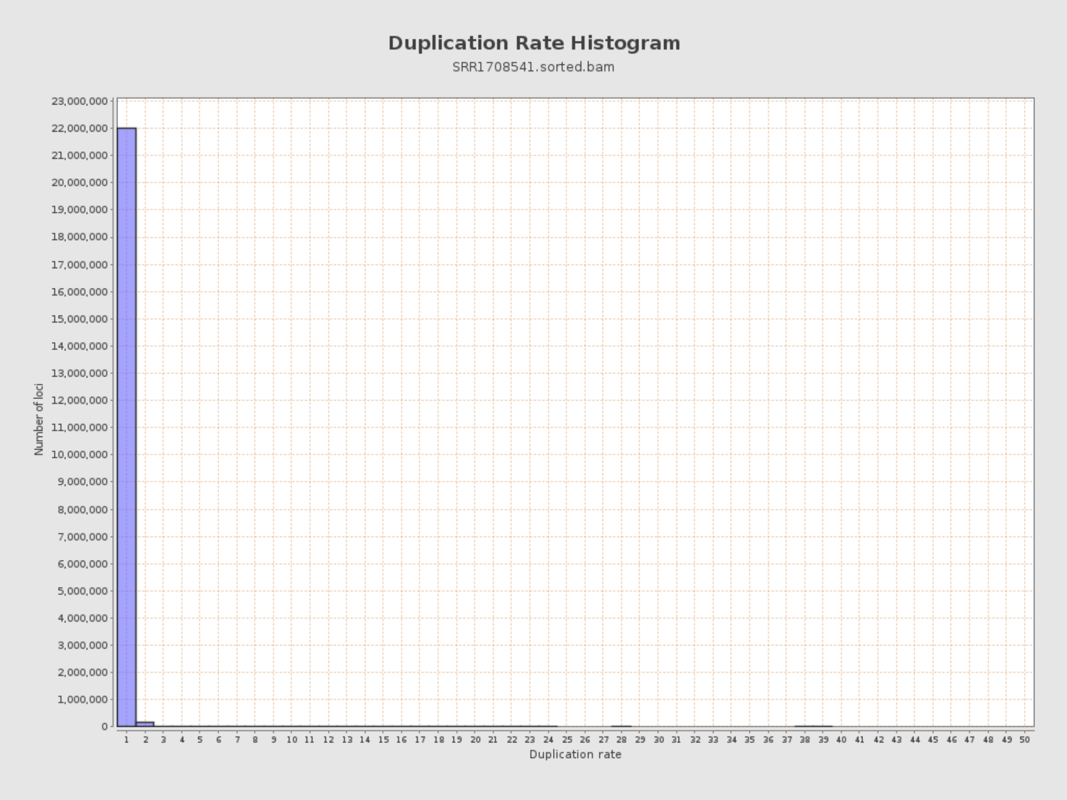
5. Results : Coverage Histogram (0-50X)



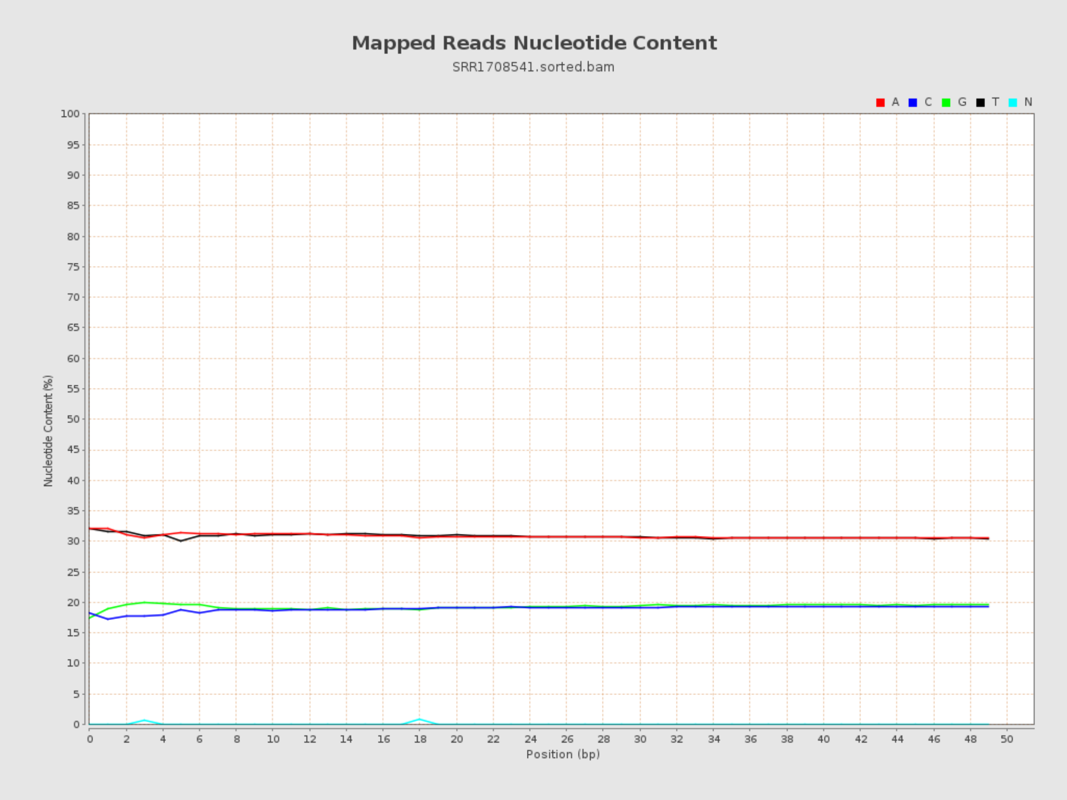
6. Results : Genome Fraction Coverage



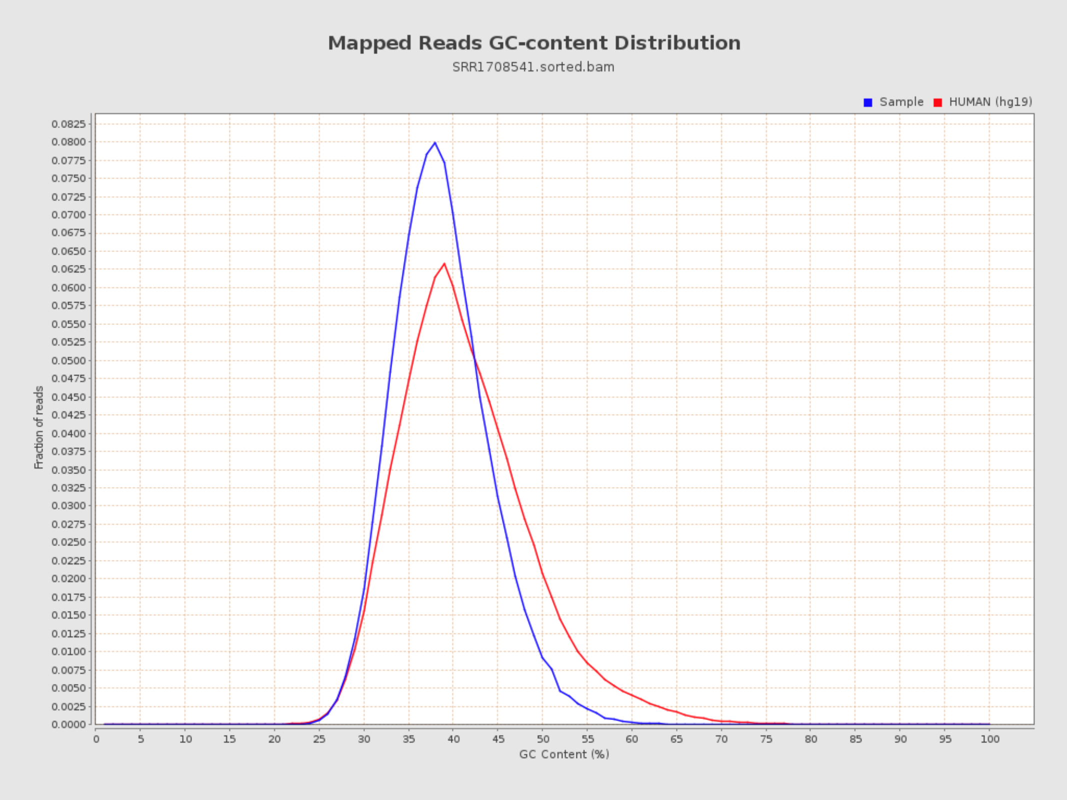
7. Results : Duplication Rate Histogram



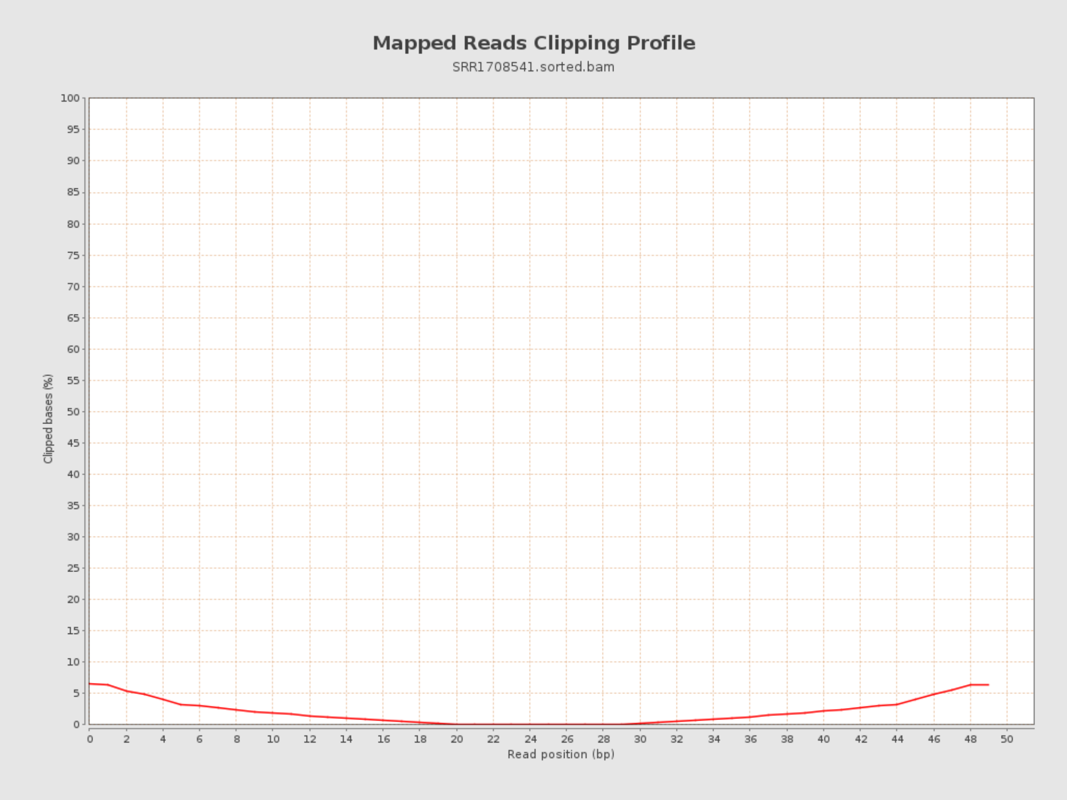
8. Results : Mapped Reads Nucleotide Content



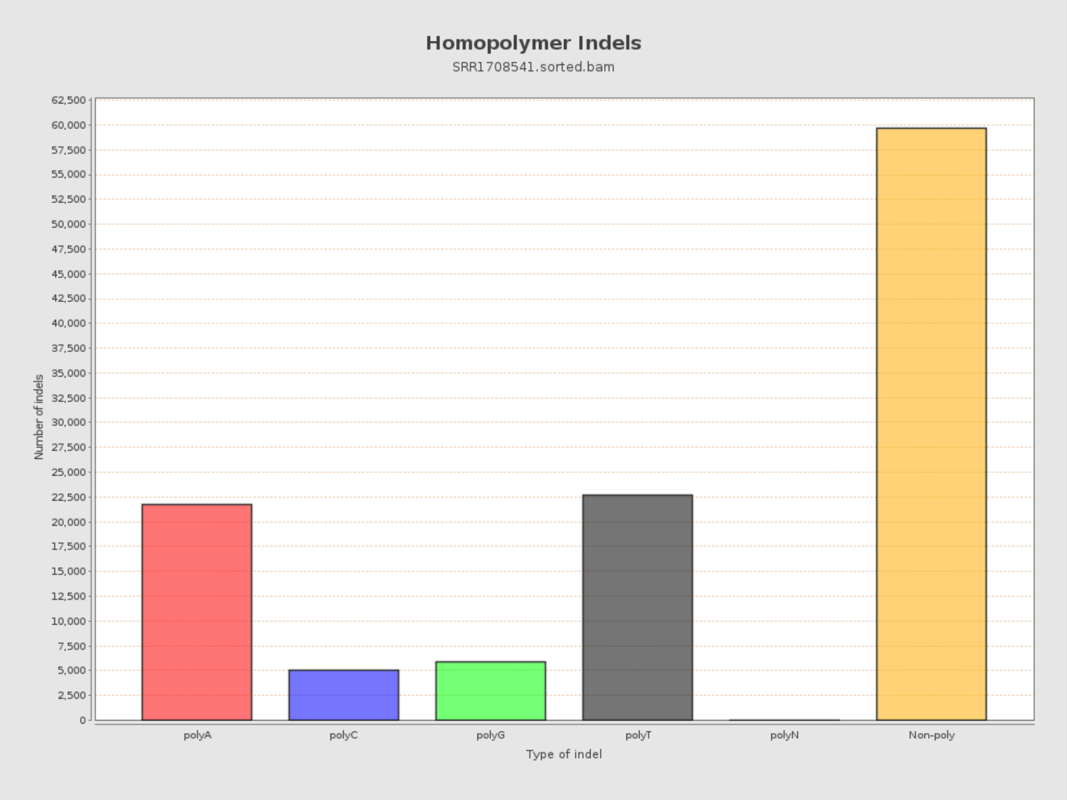
9. Results : Mapped Reads GC-content Distribution



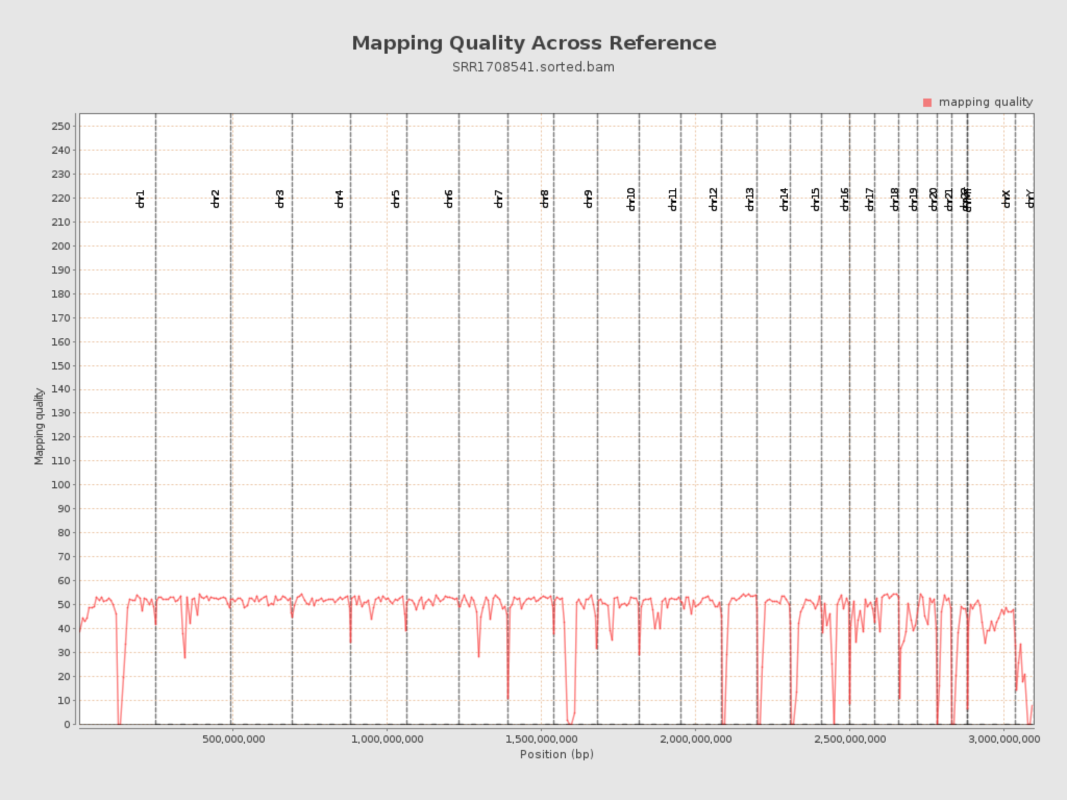
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram