Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:36:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708641.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_SRR1708641 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708641.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:36:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708641.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,445,670
Mapped reads	6,220,112 / 96.5%
Unmapped reads	225,558 / 3.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	169 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	31,747 / 0.49%
Duplication rate	0.5%
Clipped reads	82,016 / 1.27%

2.2. ACGT Content

Number/percentage of A's	95,822,179 / 30.89%
Number/percentage of C's	58,979,674 / 19.01%
Number/percentage of T's	95,851,783 / 30.9%
Number/percentage of G's	59,559,428 / 19.2%
Number/percentage of N's	8,942 / 0%
GC Percentage	38.21%

2.3. Coverage

Mean	0.1002

Standard Deviation	0.3358

2.4. Mapping Quality

Mean Mapping Quality	46.37

2.5. Mismatches and indels

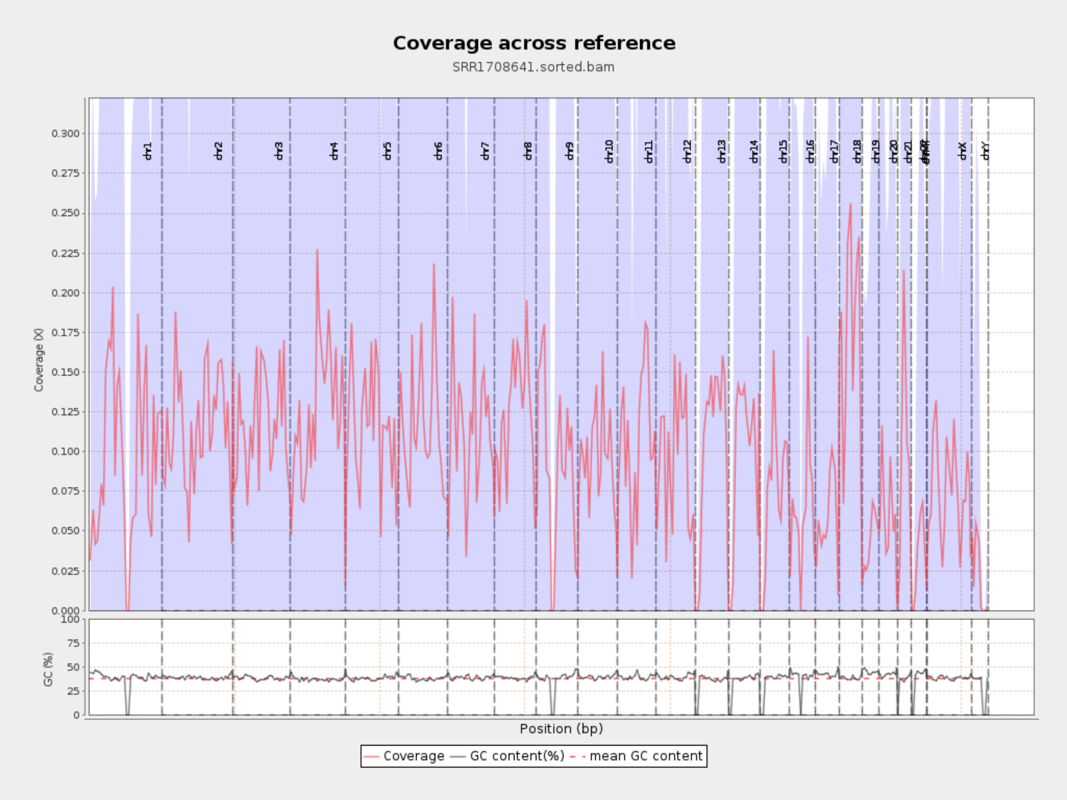
General error rate	0.17%
Mismatches	505,349
Insertions	20,828
Mapped reads with at least one insertion	0.33%
Deletions	17,484
Mapped reads with at least one deletion	0.28%
Homopolymer indels	49.2%

2.6. Chromosome stats

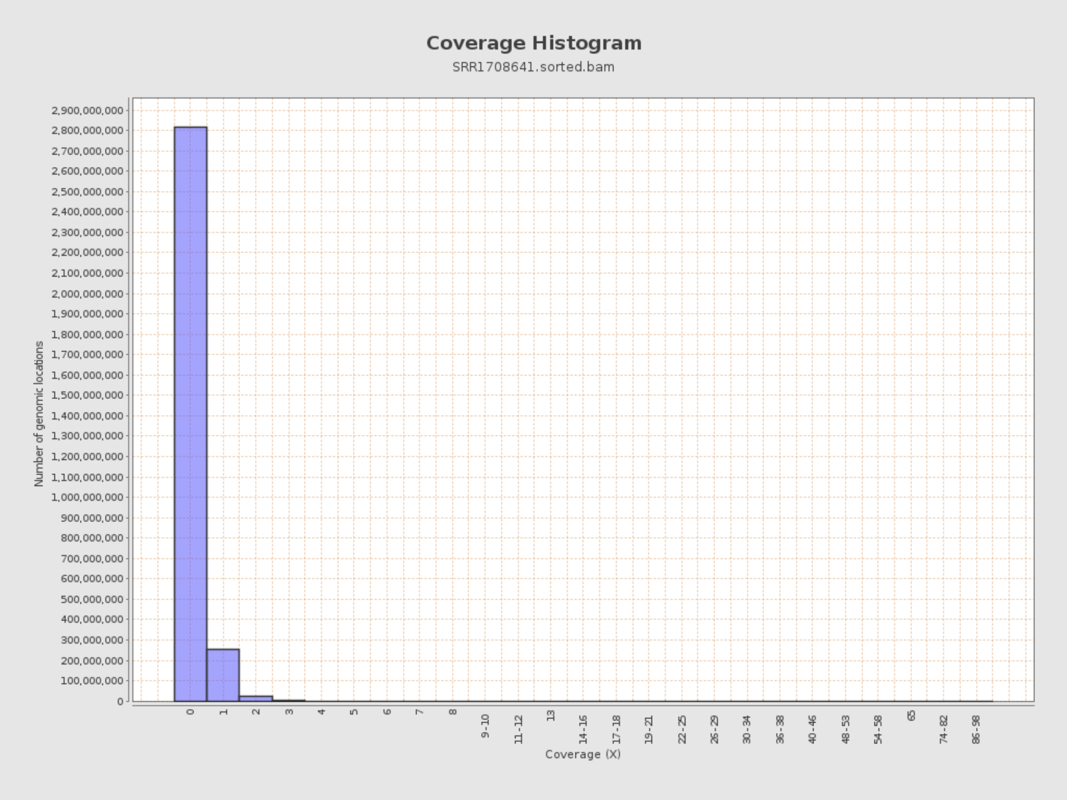
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23946594	0.0961	0.3314
chr2	243199373	27744203	0.1141	0.3564
chr3	198022430	23375186	0.118	0.3616
chr4	191154276	24182750	0.1265	0.375
chr5	180915260	20758981	0.1147	0.357
chr6	171115067	19681236	0.115	0.3577
chr7	159138663	18508091	0.1163	0.3608

chr8	146364022	18350657	0.1254	0.3727
chr9	141213431	13478397	0.0954	0.3278
chr10	135534747	13371163	0.0987	0.3299
chr11	135006516	14485446	0.1073	0.348
chr12	133851895	12543543	0.0937	0.3235
chr13	115169878	11985919	0.1041	0.3421
chr14	107349540	10314215	0.0961	0.3293
chr15	102531392	7755960	0.0756	0.2919
chr16	90354753	5839471	0.0646	0.2693
chr17	81195210	4642362	0.0572	0.2507
chr18	78077248	13731471	0.1759	0.4478
chr19	59128983	2603014	0.044	0.219
chr20	63025520	3941033	0.0625	0.2626
chr21	48129895	4452661	0.0925	0.328
chr22	51304566	1750540	0.0341	0.1922
chrMT	16571	233	0.0141	0.1177
chrX	155270560	11655225	0.0751	0.2873
chrY	59373566	1153350	0.0194	0.1474

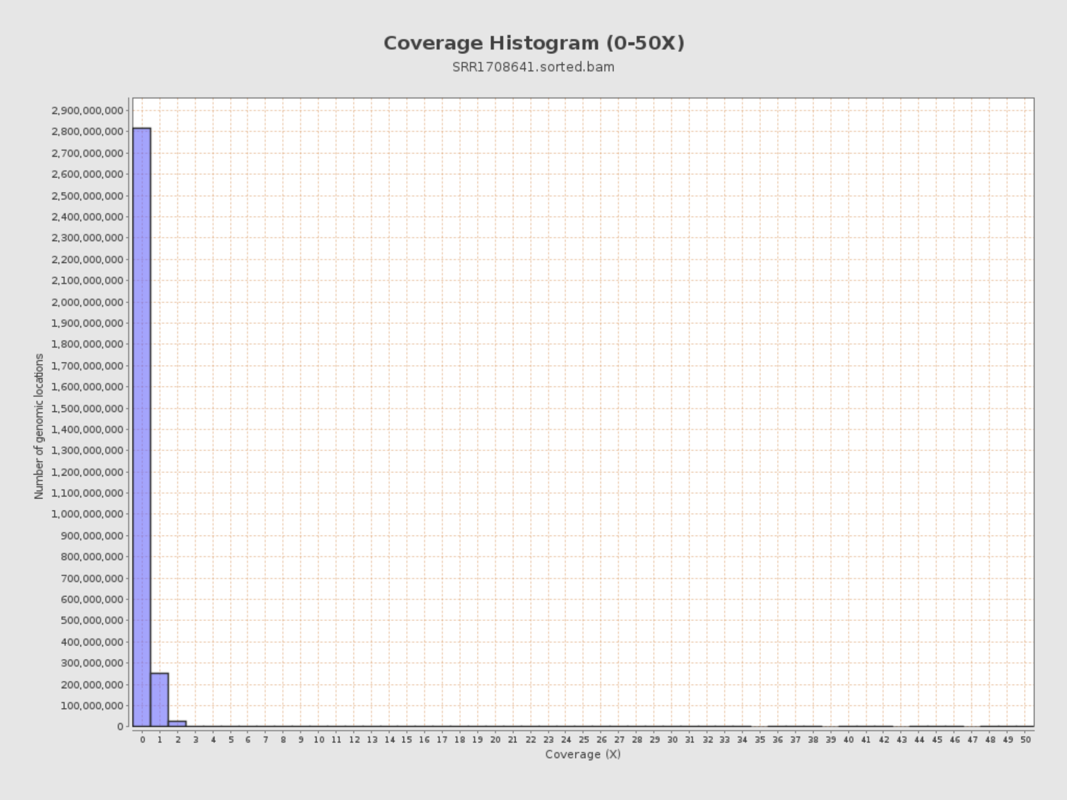
3. Results : Coverage across reference



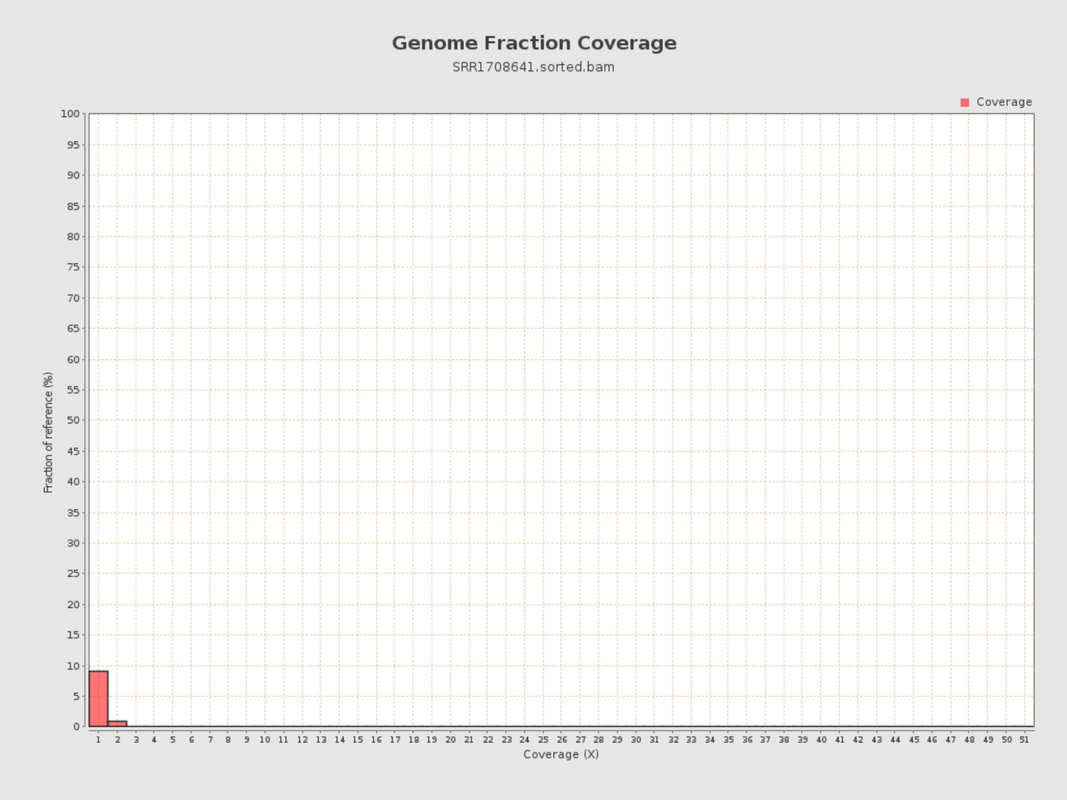
4. Results : Coverage Histogram



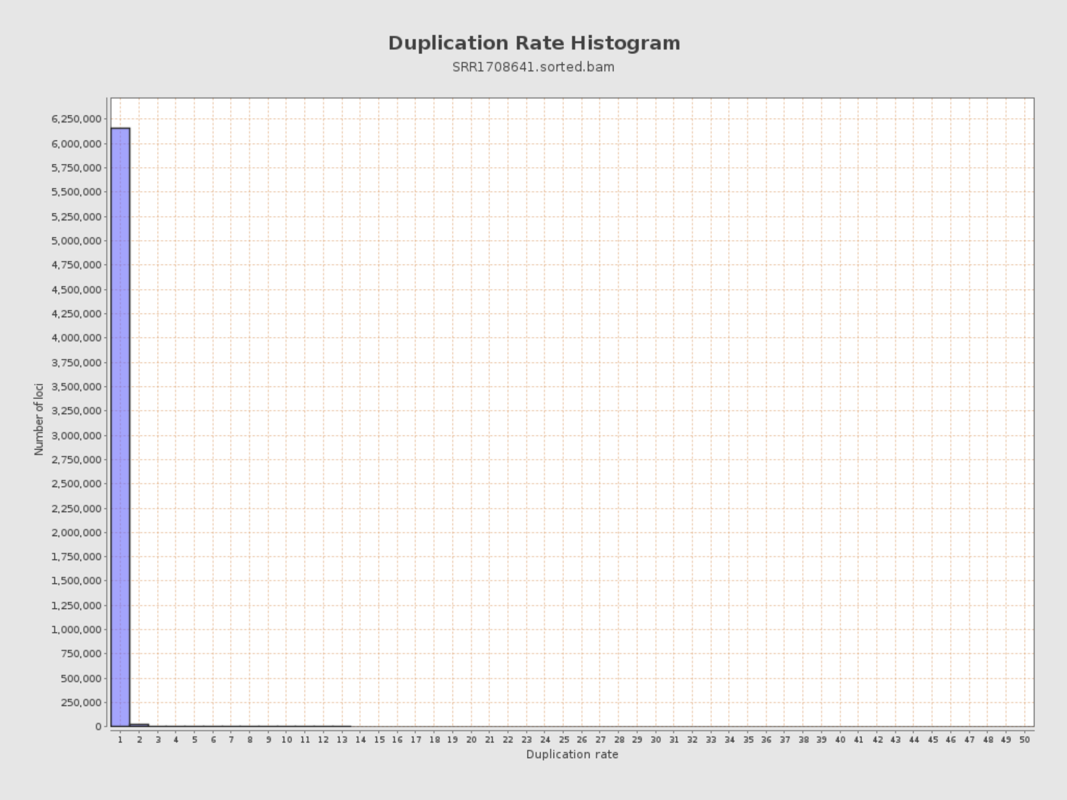
5. Results : Coverage Histogram (0-50X)



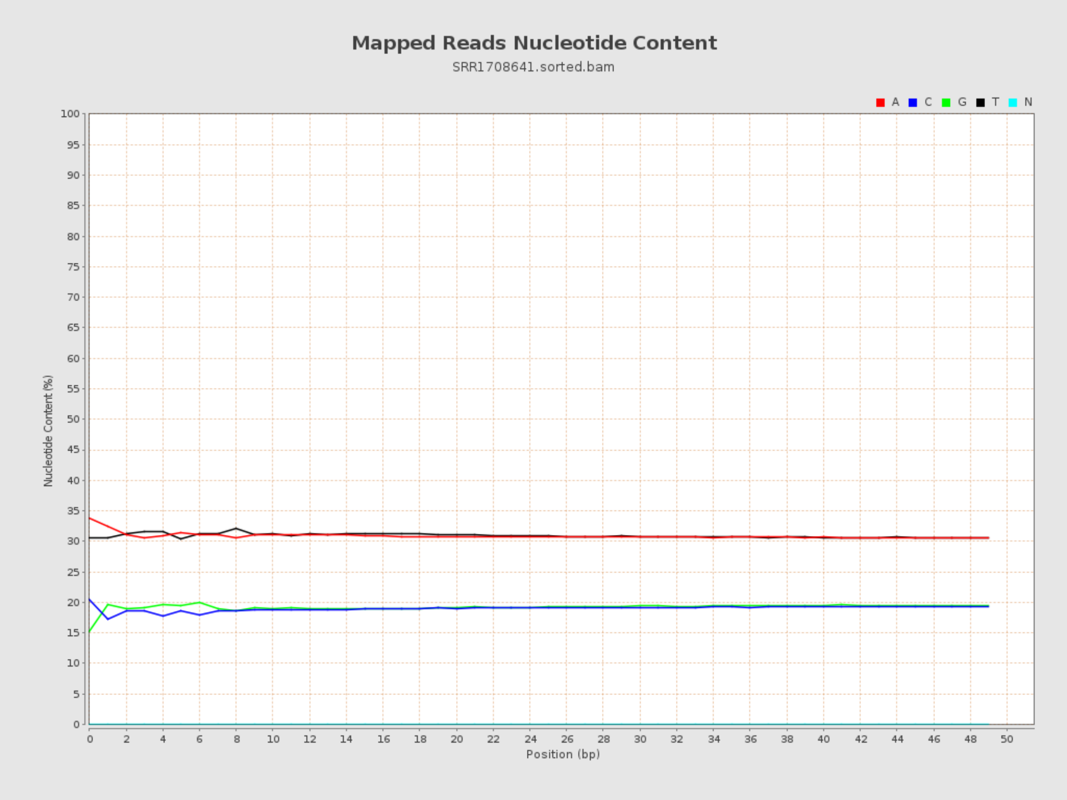
6. Results : Genome Fraction Coverage



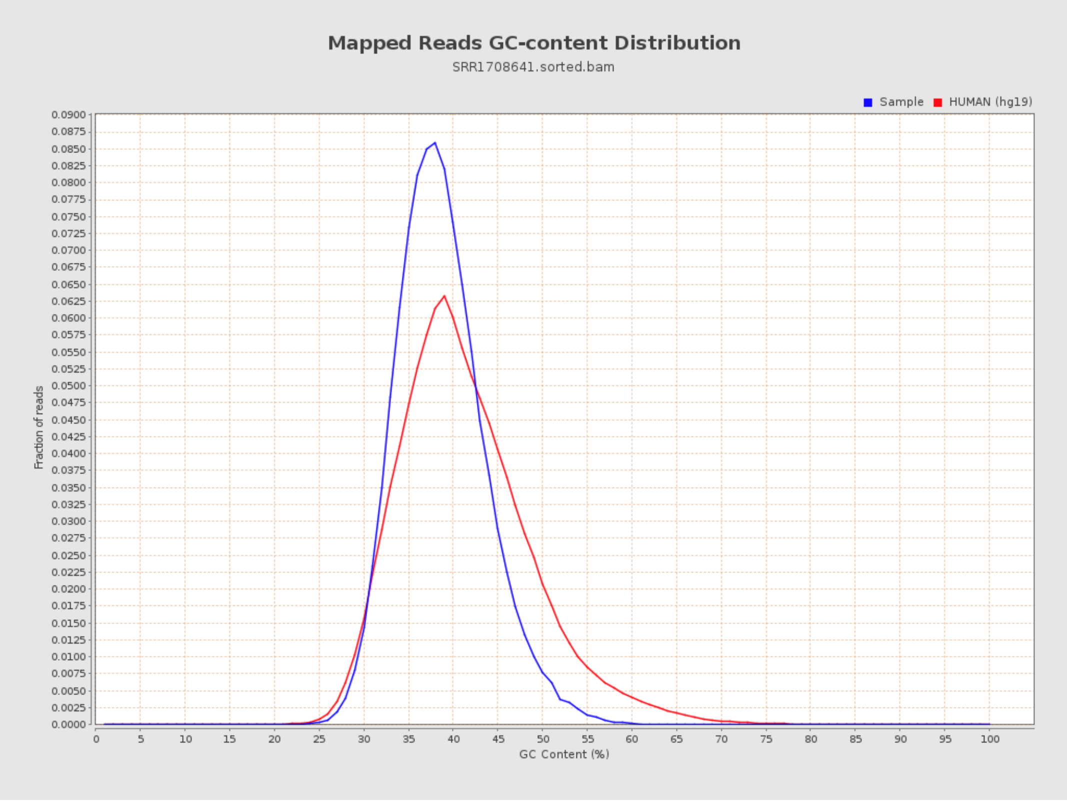
7. Results : Duplication Rate Histogram



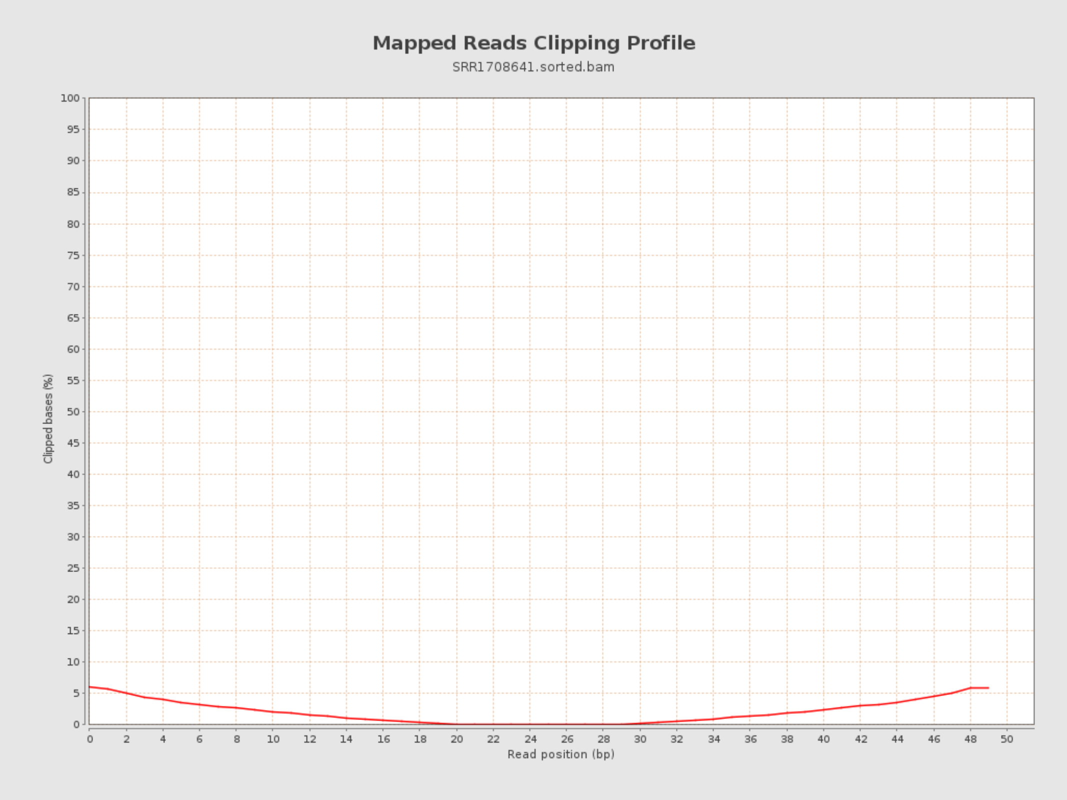
8. Results : Mapped Reads Nucleotide Content



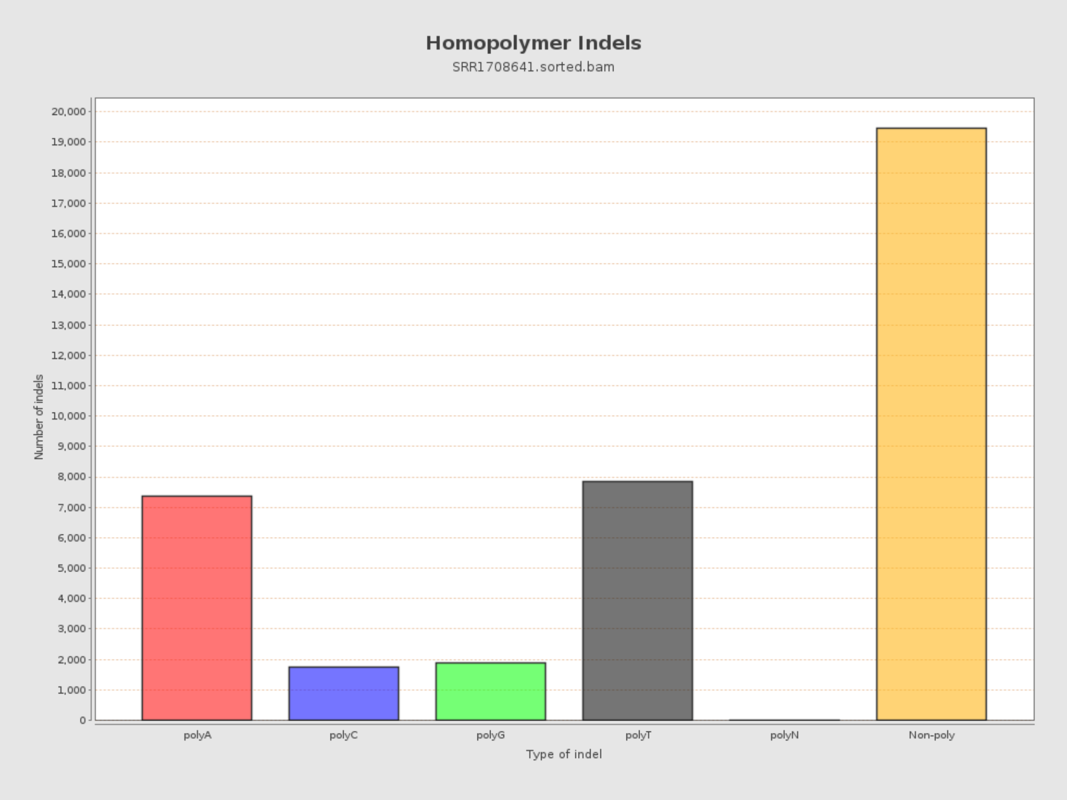
9. Results : Mapped Reads GC-content Distribution



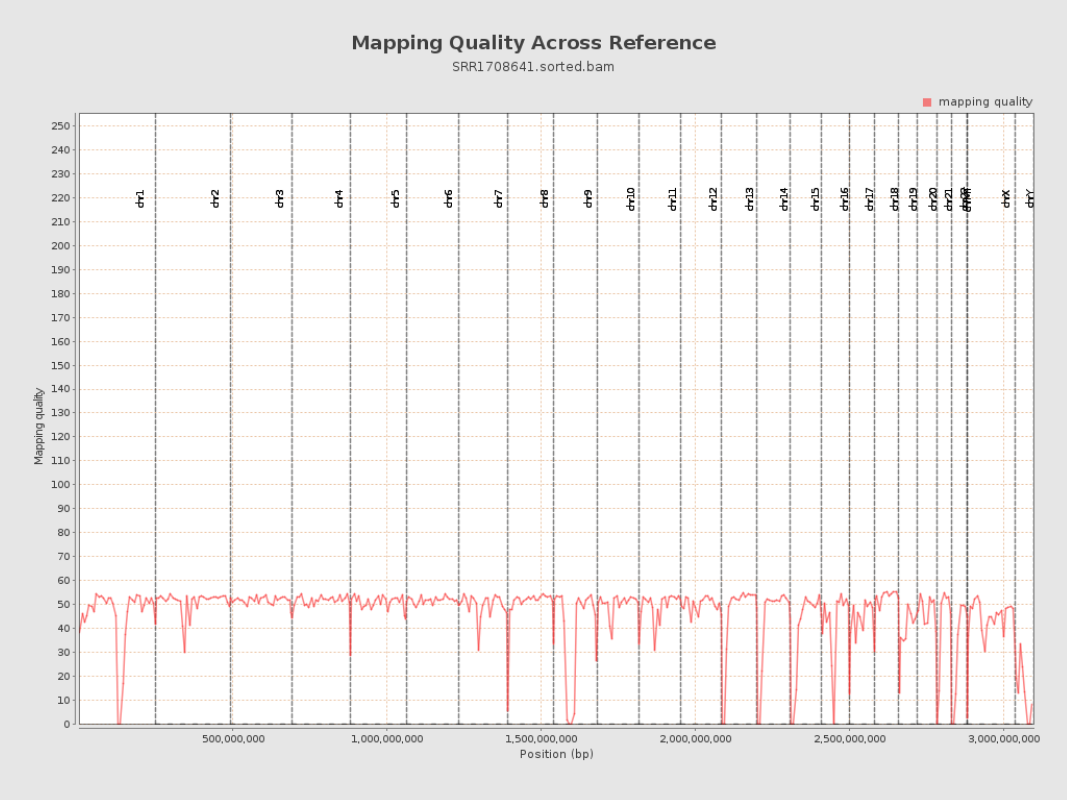
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram