Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:33:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080718.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_SRR3080718 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080718.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:33:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080718.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,392,970
Mapped reads	2,196,255 / 91.78%
Unmapped reads	196,715 / 8.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,088 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	118,860 / 4.97%
Duplication rate	4.62%
Clipped reads	864,826 / 36.14%

2.2. ACGT Content

Number/percentage of A's	42,008,478 / 28.17%
Number/percentage of C's	27,630,406 / 18.53%
Number/percentage of T's	47,376,485 / 31.77%
Number/percentage of G's	32,093,542 / 21.52%
Number/percentage of N's	2,256 / 0%
GC Percentage	40.05%

2.3. Coverage

Mean	0.0482

Standard Deviation	0.3786

2.4. Mapping Quality

Mean Mapping Quality	46.34

2.5. Mismatches and indels

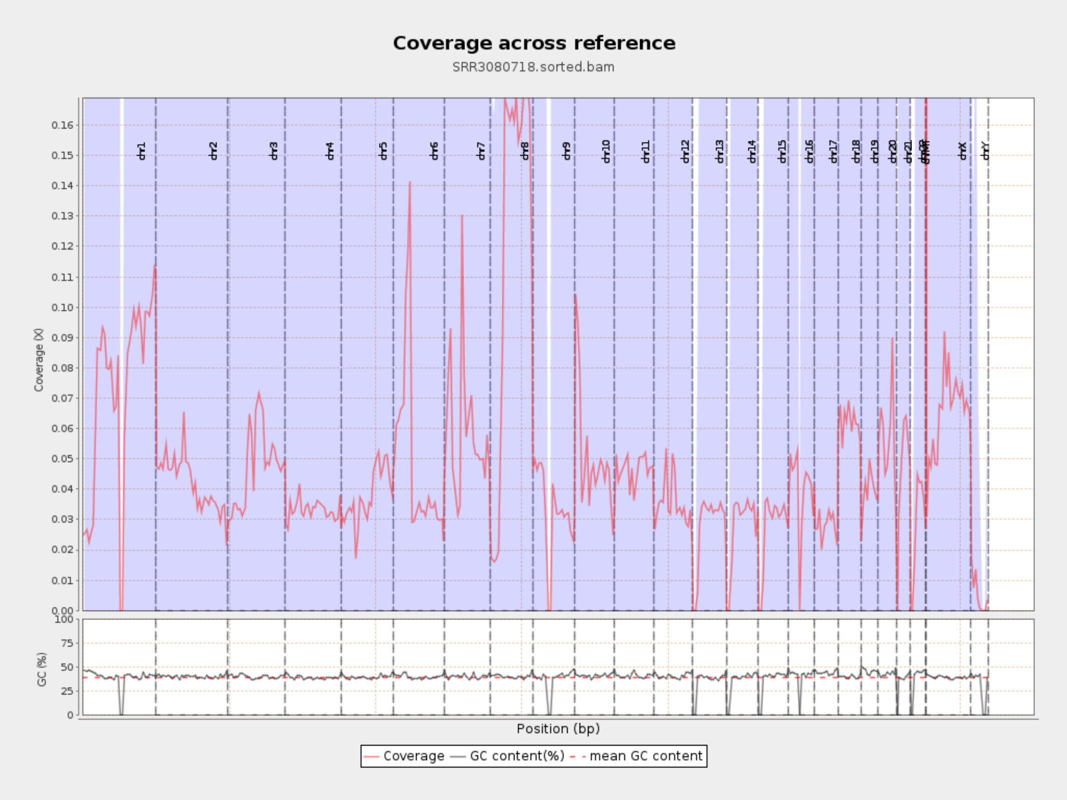
General error rate	0.83%
Mismatches	1,215,369
Insertions	10,715
Mapped reads with at least one insertion	0.48%
Deletions	31,289
Mapped reads with at least one deletion	1.41%
Homopolymer indels	48.26%

2.6. Chromosome stats

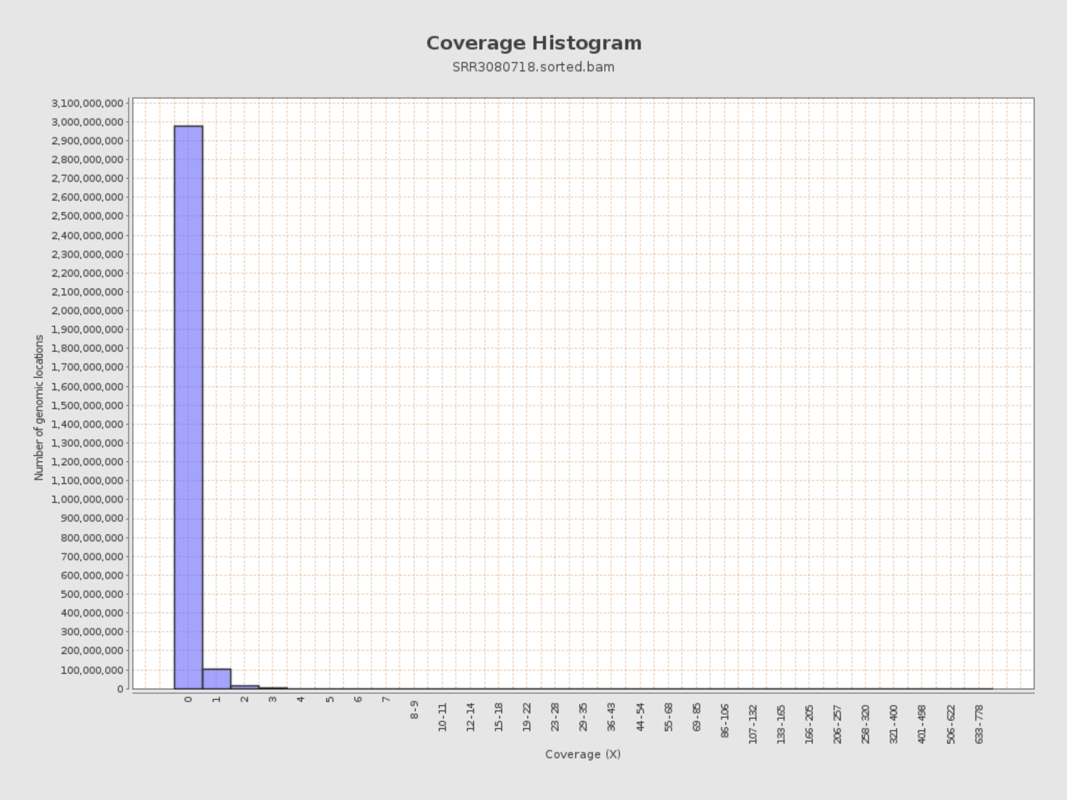
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18021161	0.0723	0.4864
chr2	243199373	10257002	0.0422	0.38
chr3	198022430	9407588	0.0475	0.2569
chr4	191154276	6363126	0.0333	0.2192
chr5	180915260	6810359	0.0376	0.2268
chr6	171115067	8676919	0.0507	0.3627
chr7	159138663	9427332	0.0592	0.9397

chr8	146364022	17827129	0.1218	0.526
chr9	141213431	4658172	0.033	0.2748
chr10	135534747	6983620	0.0515	0.3314
chr11	135006516	6233601	0.0462	0.2802
chr12	133851895	4728473	0.0353	0.2216
chr13	115169878	3181858	0.0276	0.1954
chr14	107349540	2993325	0.0279	0.2075
chr15	102531392	2742863	0.0268	0.1926
chr16	90354753	3478419	0.0385	0.2463
chr17	81195210	2299420	0.0283	0.2089
chr18	78077248	4865221	0.0623	0.4313
chr19	59128983	2358050	0.0399	0.3374
chr20	63025520	3675830	0.0583	0.2881
chr21	48129895	2231163	0.0464	0.2595
chr22	51304566	1458703	0.0284	0.196
chrMT	16571	70440	4.2508	2.9177
chrX	155270560	10108366	0.0651	0.3182
chrY	59373566	308207	0.0052	0.1021

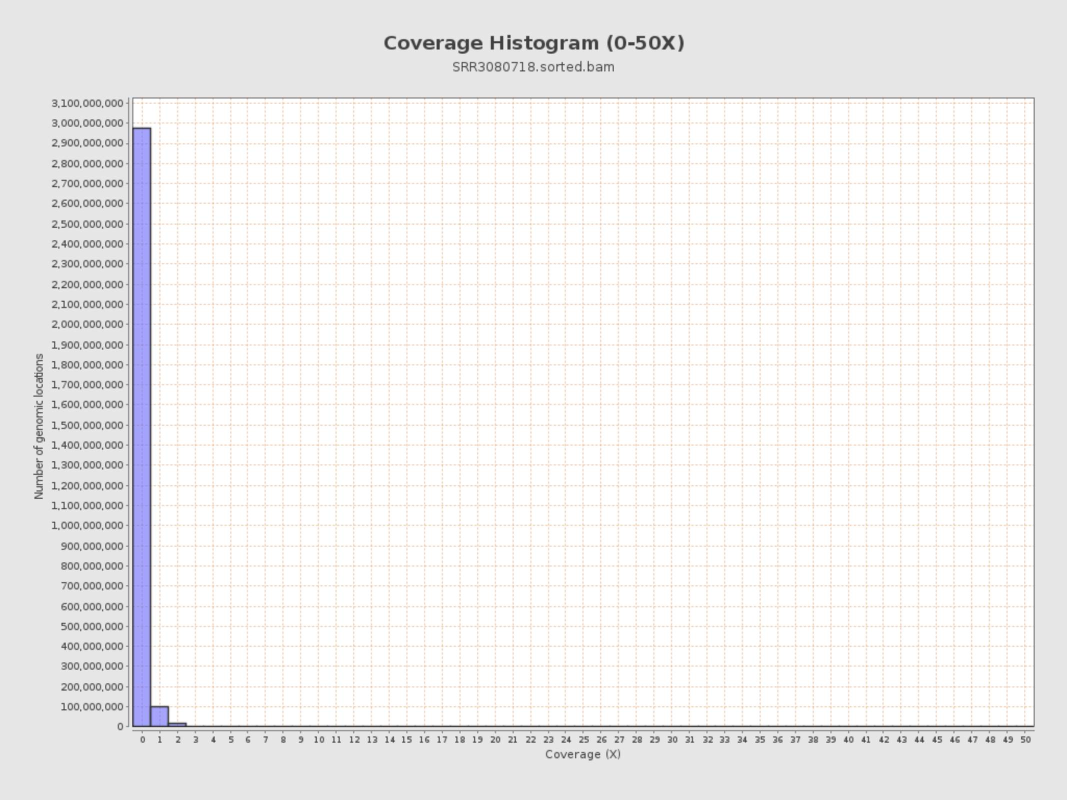
3. Results : Coverage across reference



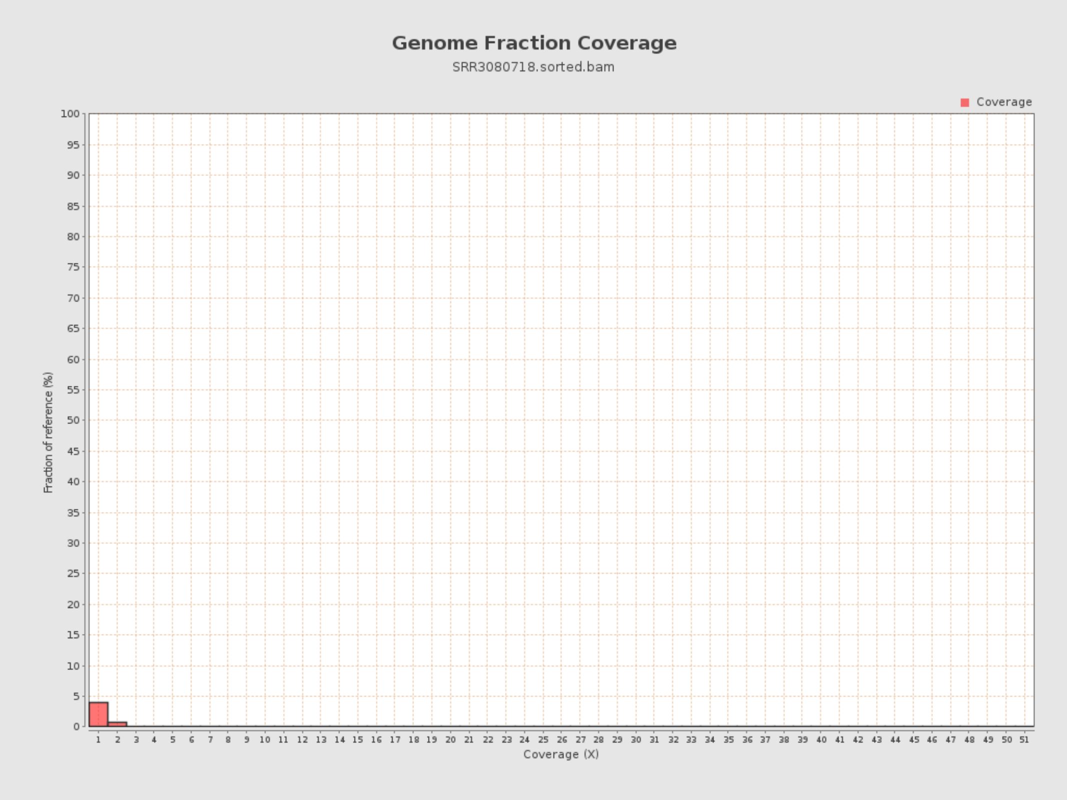
4. Results : Coverage Histogram



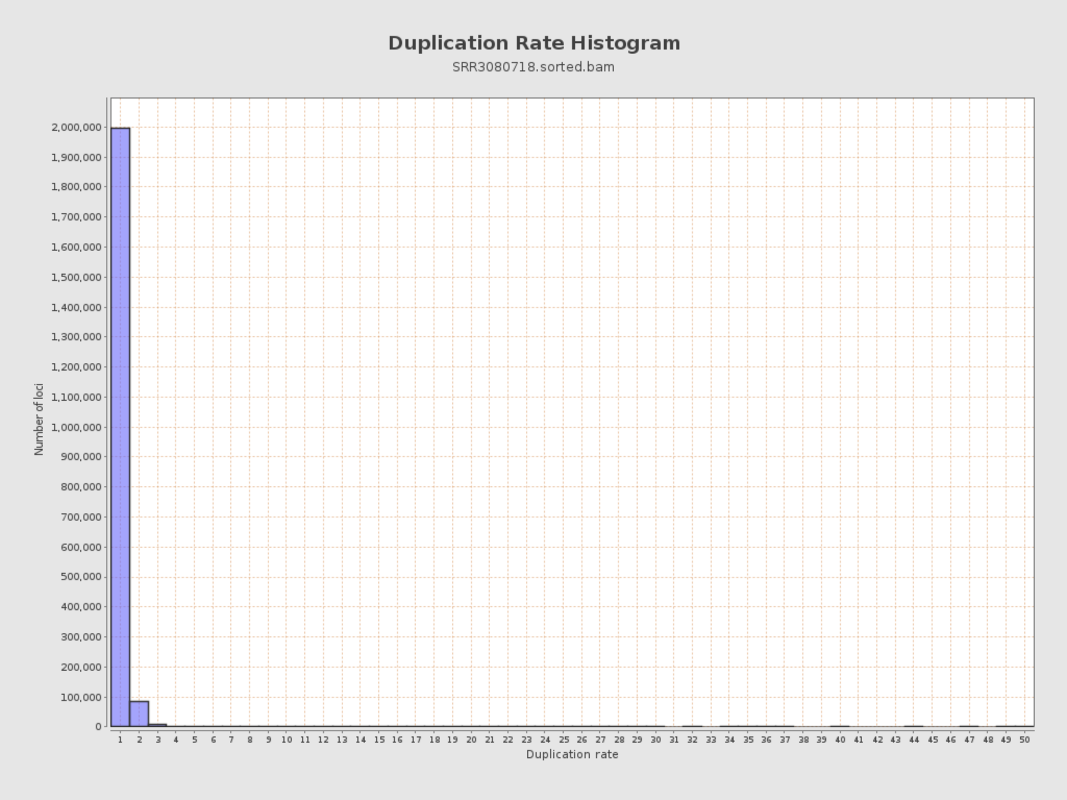
5. Results : Coverage Histogram (0-50X)



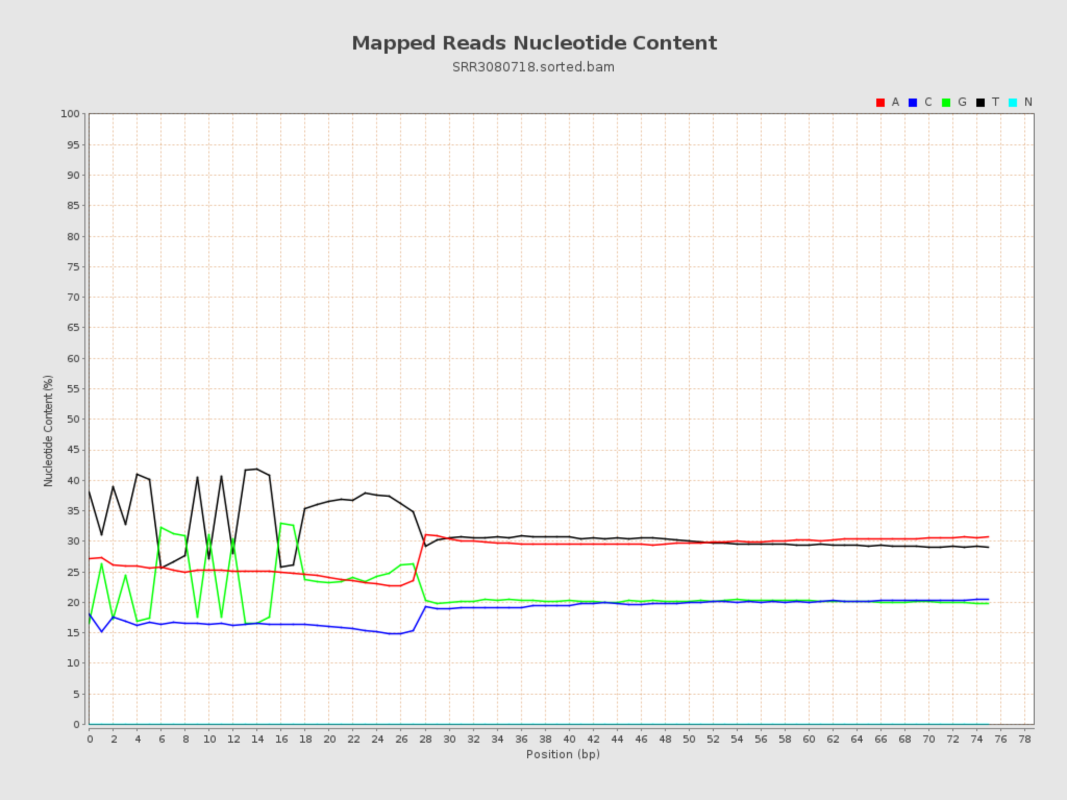
6. Results : Genome Fraction Coverage



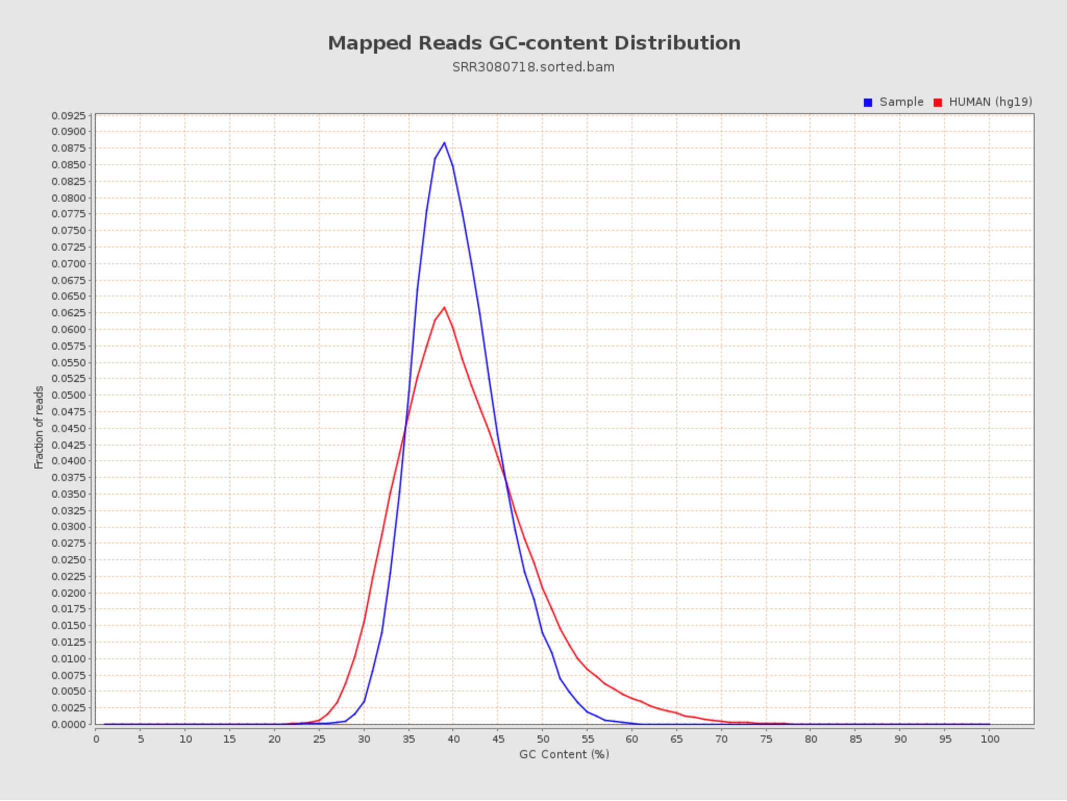
7. Results : Duplication Rate Histogram



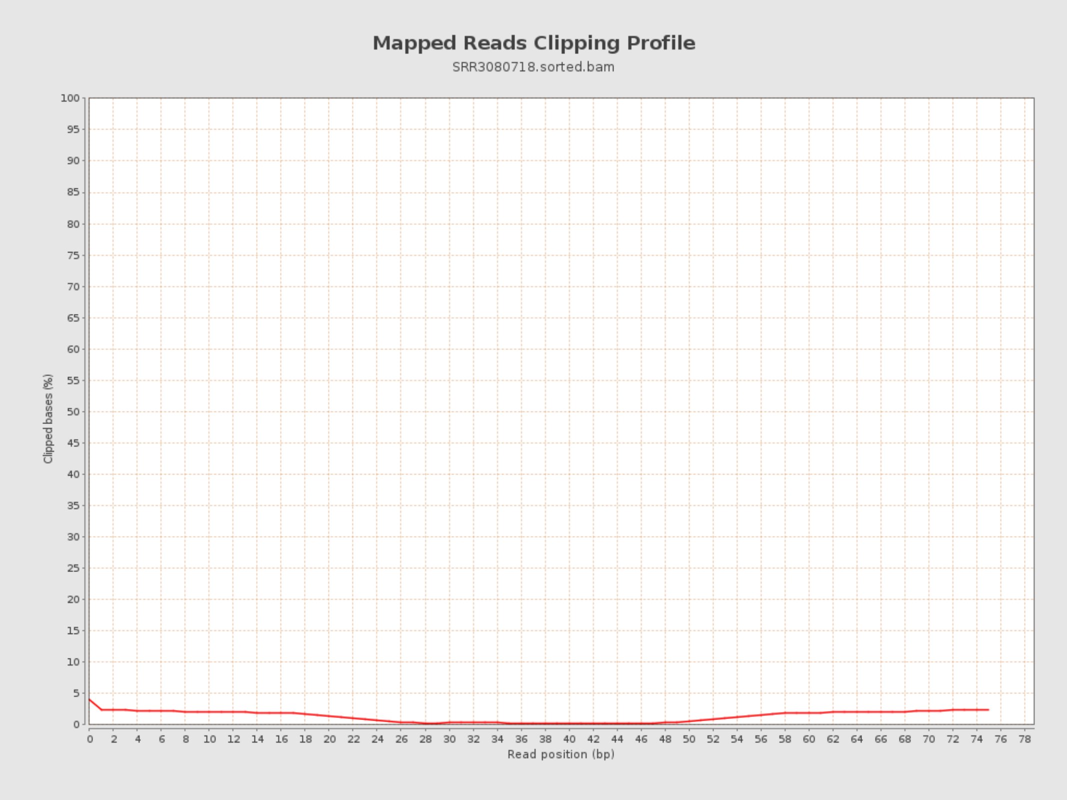
8. Results : Mapped Reads Nucleotide Content



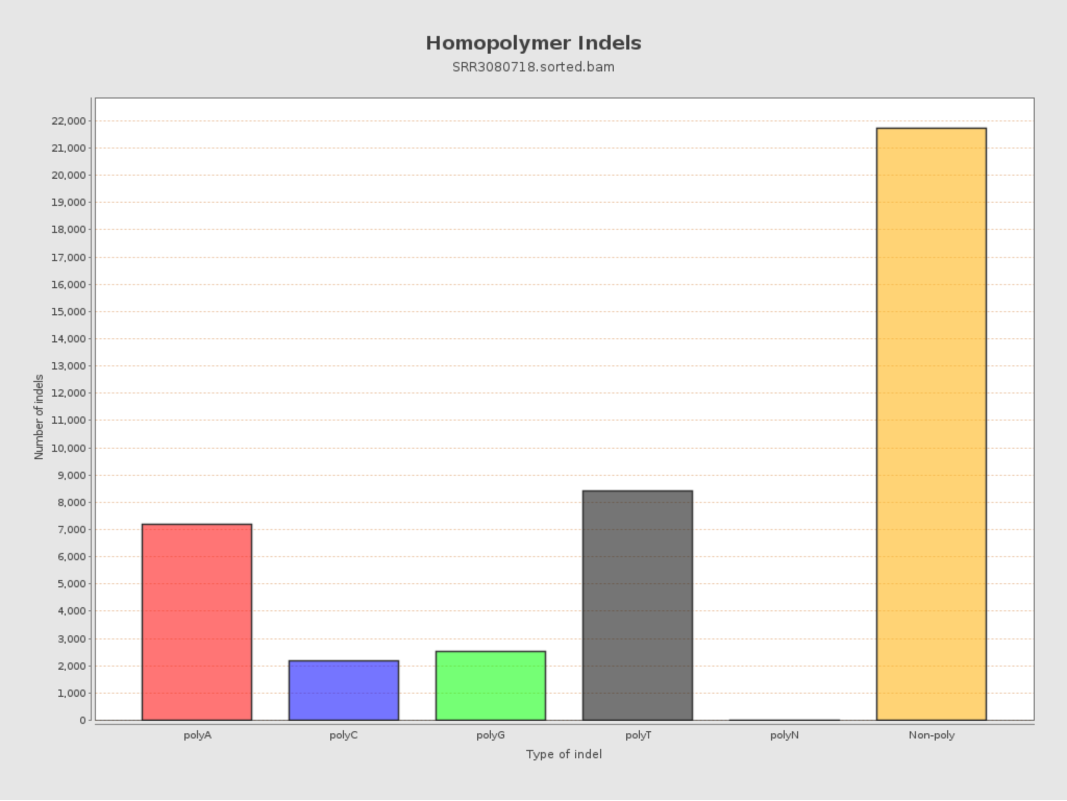
9. Results : Mapped Reads GC-content Distribution



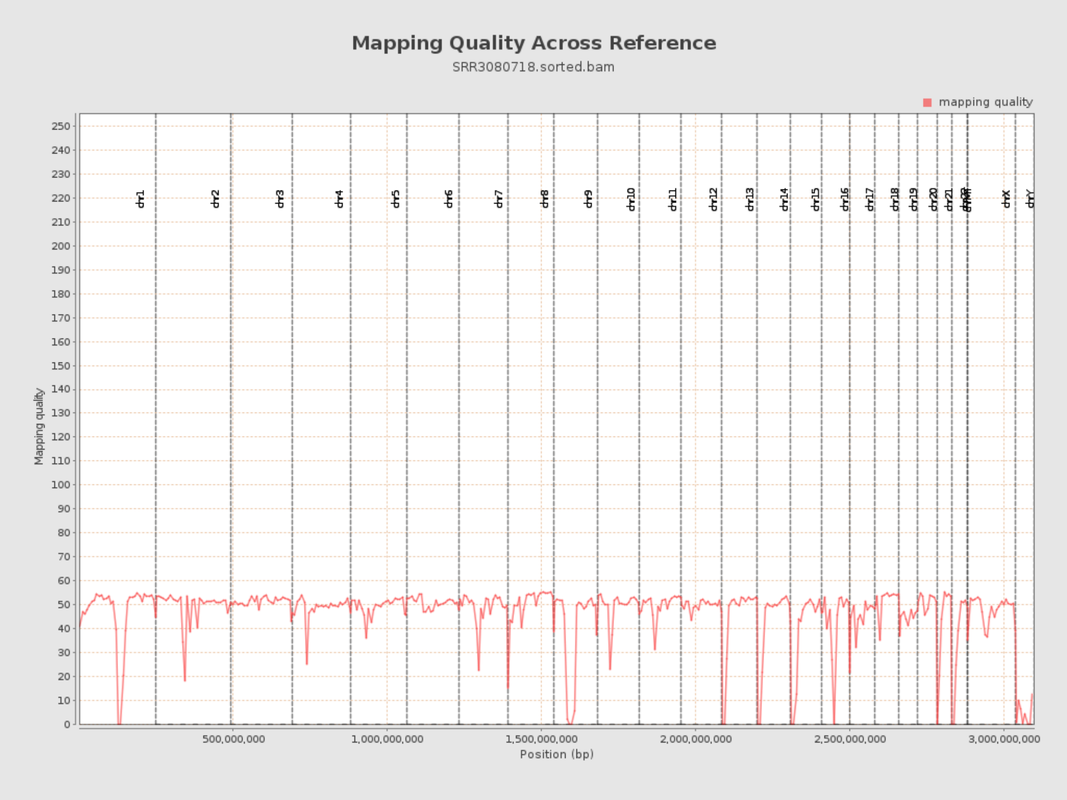
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram