Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:37:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081932.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_SRR3081932 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081932.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:37:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081932.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,703,183
Mapped reads	2,461,358 / 91.05%
Unmapped reads	241,825 / 8.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,563 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	114,862 / 4.25%
Duplication rate	3.1%
Clipped reads	875,541 / 32.39%

2.2. ACGT Content

Number/percentage of A's	48,512,953 / 28.63%
Number/percentage of C's	31,839,365 / 18.79%
Number/percentage of T's	52,731,359 / 31.12%
Number/percentage of G's	36,355,167 / 21.45%
Number/percentage of N's	21,618 / 0.01%
GC Percentage	40.24%

2.3. Coverage

Mean	0.0548

Standard Deviation	0.6124

2.4. Mapping Quality

Mean Mapping Quality	45.06

2.5. Mismatches and indels

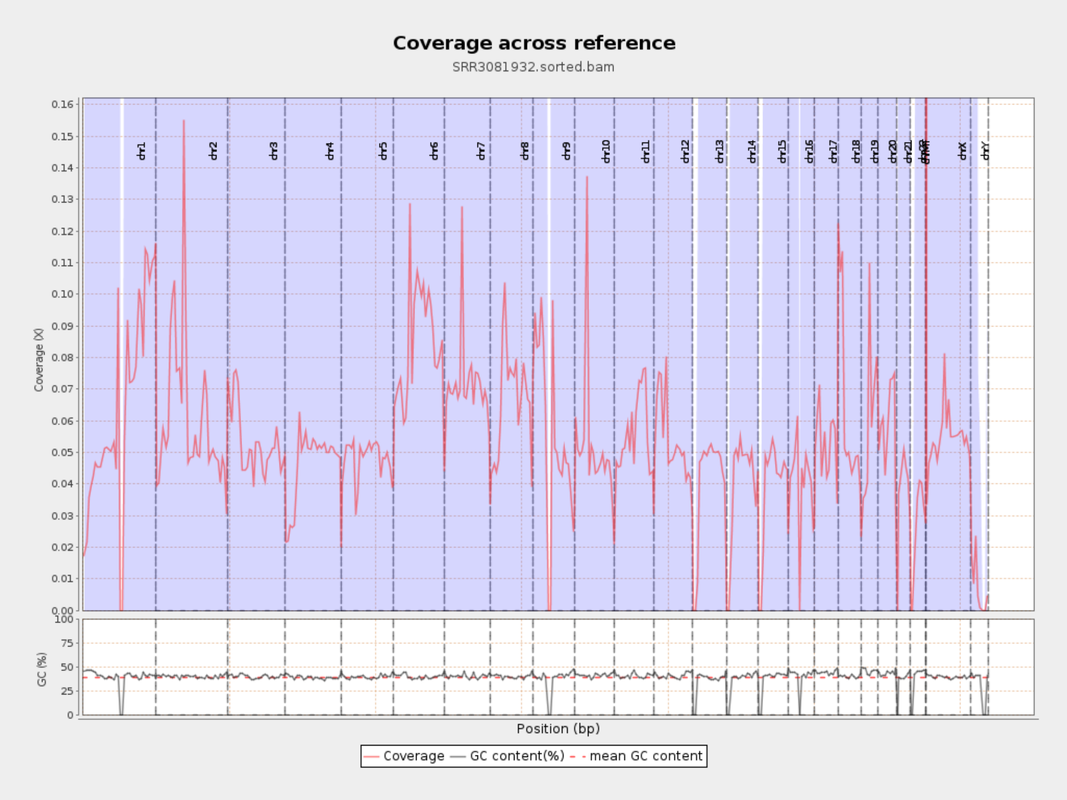
General error rate	0.82%
Mismatches	1,365,154
Insertions	13,386
Mapped reads with at least one insertion	0.54%
Deletions	35,853
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.07%

2.6. Chromosome stats

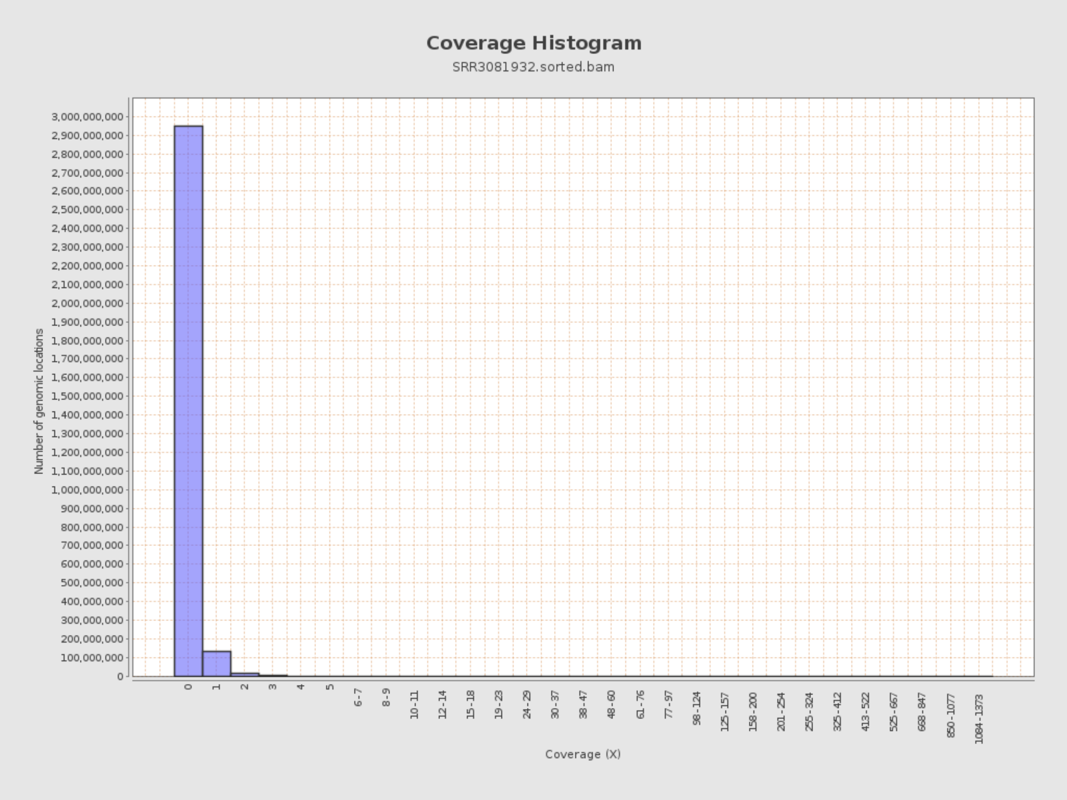
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15822491	0.0635	1.1657
chr2	243199373	15023471	0.0618	0.7909
chr3	198022430	10570912	0.0534	0.263
chr4	191154276	8915246	0.0466	0.2891
chr5	180915260	8622261	0.0477	0.2492
chr6	171115067	14600332	0.0853	0.4963
chr7	159138663	11371767	0.0715	0.9236

chr8	146364022	9759484	0.0667	0.7966
chr9	141213431	7898856	0.0559	0.6357
chr10	135534747	7148397	0.0527	0.6676
chr11	135006516	7511195	0.0556	0.4209
chr12	133851895	7214094	0.0539	0.2782
chr13	115169878	4616191	0.0401	0.2207
chr14	107349540	4273716	0.0398	0.2746
chr15	102531392	3905255	0.0381	0.2194
chr16	90354753	3549809	0.0393	0.3092
chr17	81195210	4362939	0.0537	0.3165
chr18	78077248	4943146	0.0633	1.1144
chr19	59128983	3538922	0.0599	0.8489
chr20	63025520	3782030	0.06	0.2862
chr21	48129895	1822761	0.0379	0.278
chr22	51304566	1335637	0.026	0.1767
chrMT	16571	41866	2.5265	2.0584
chrX	155270560	8481306	0.0546	0.339
chrY	59373566	412479	0.0069	0.2038

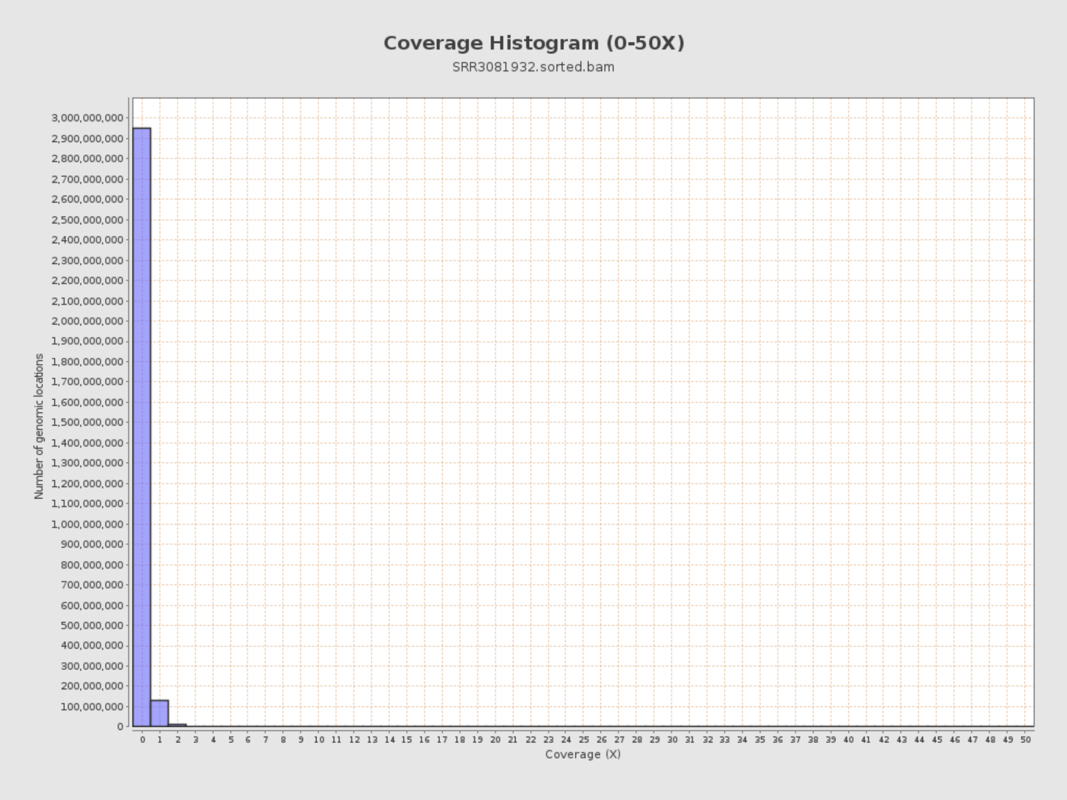
3. Results : Coverage across reference



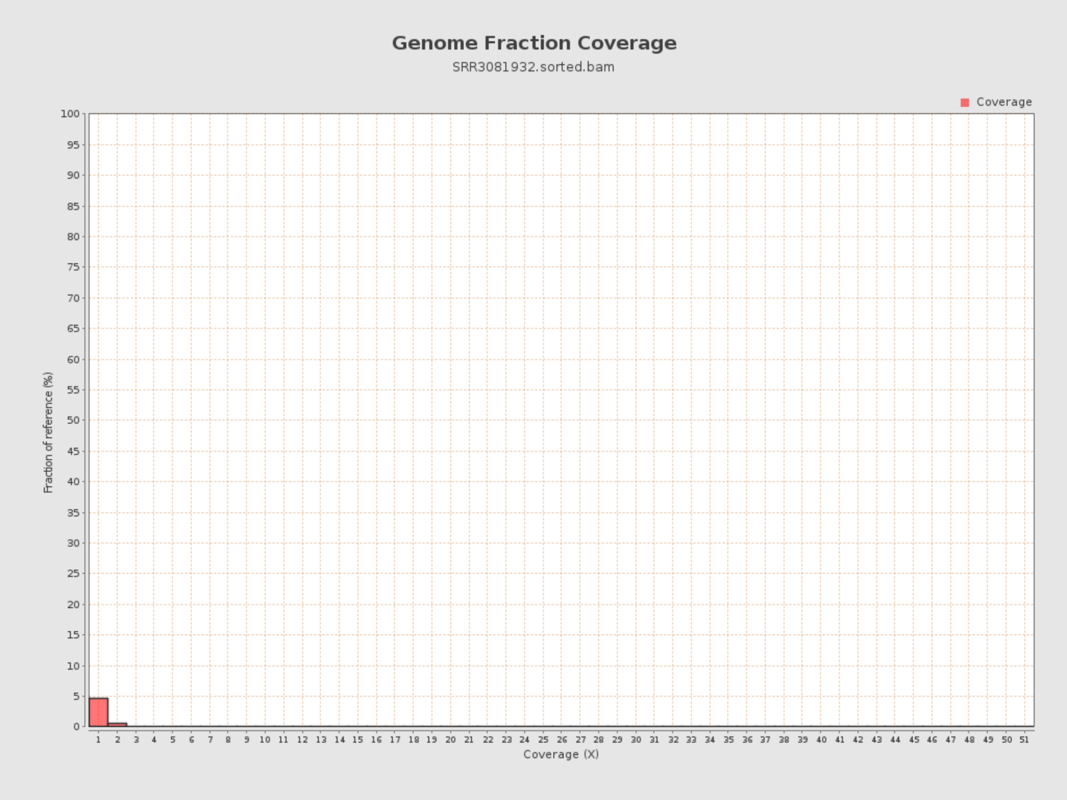
4. Results : Coverage Histogram



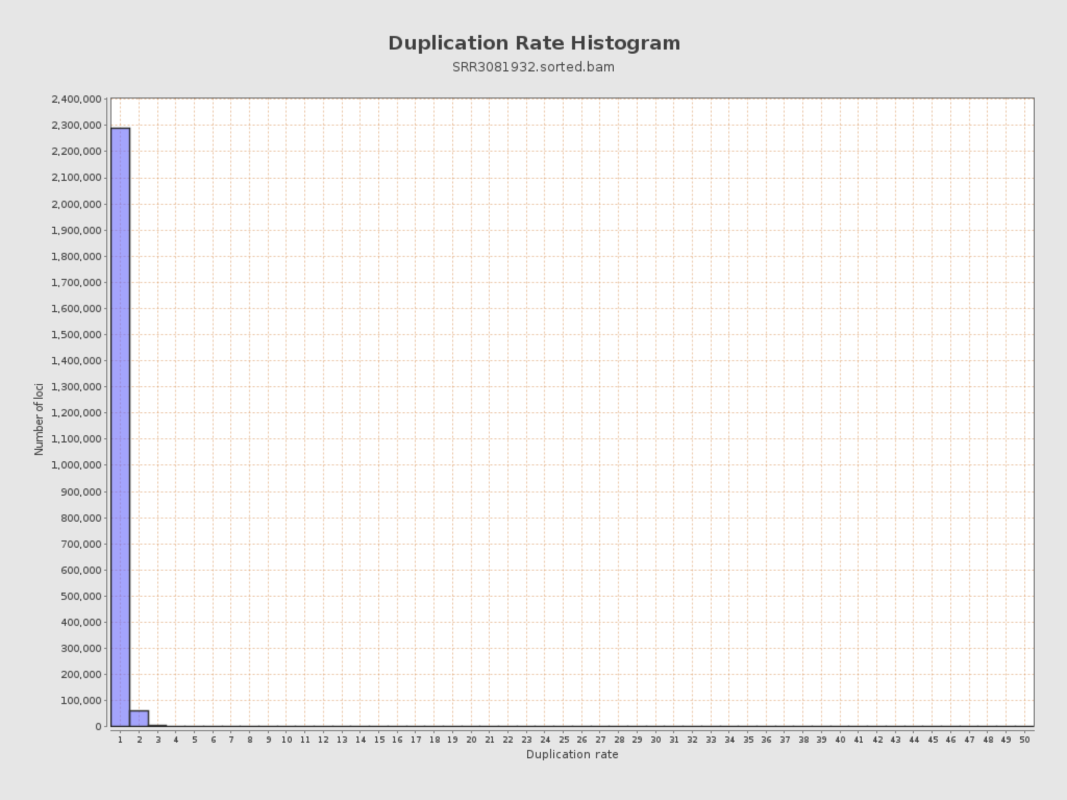
5. Results : Coverage Histogram (0-50X)



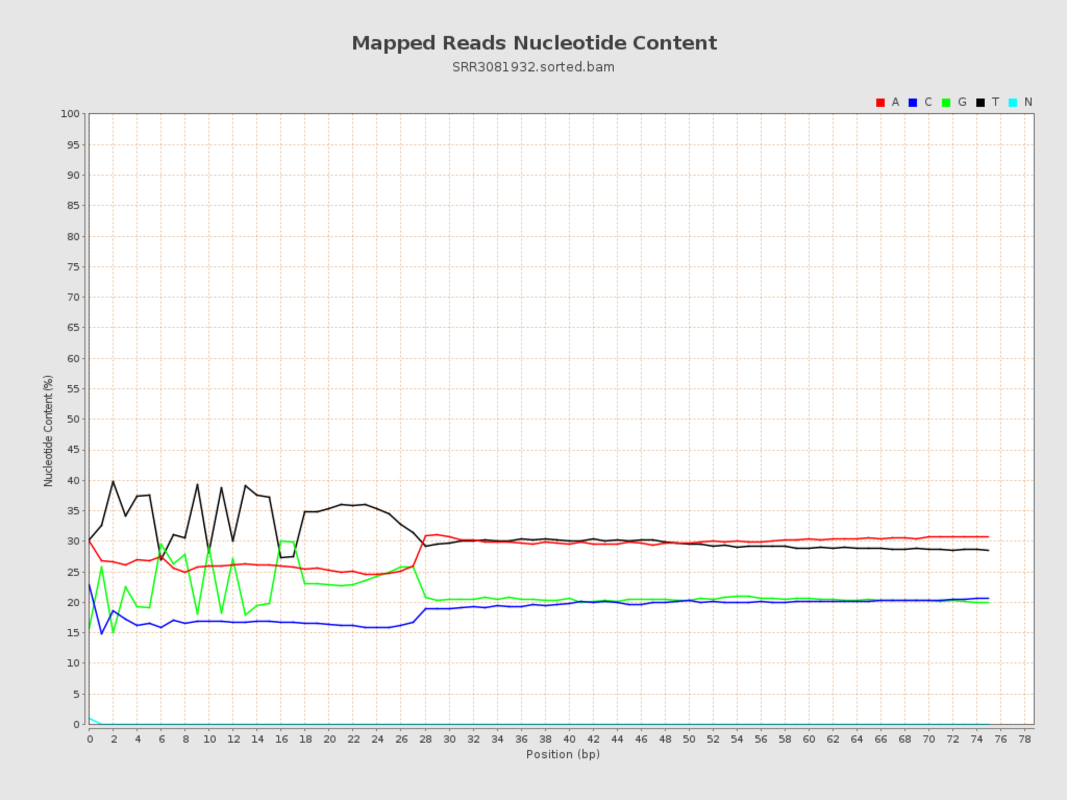
6. Results : Genome Fraction Coverage



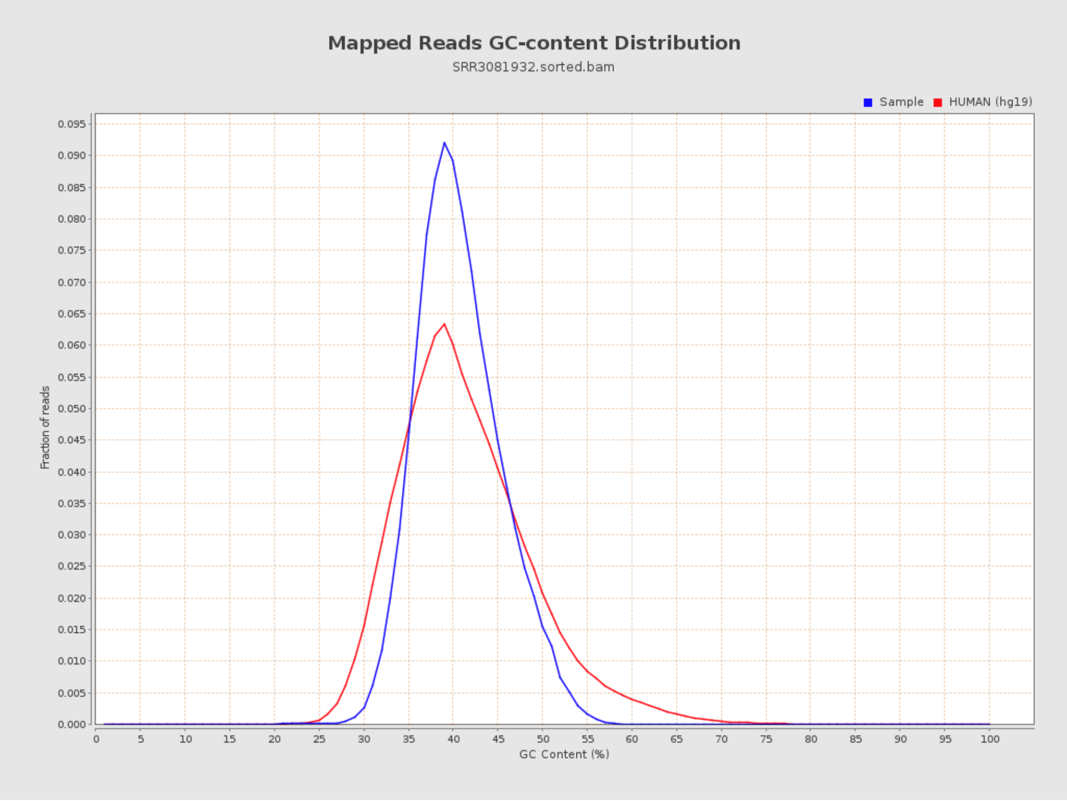
7. Results : Duplication Rate Histogram



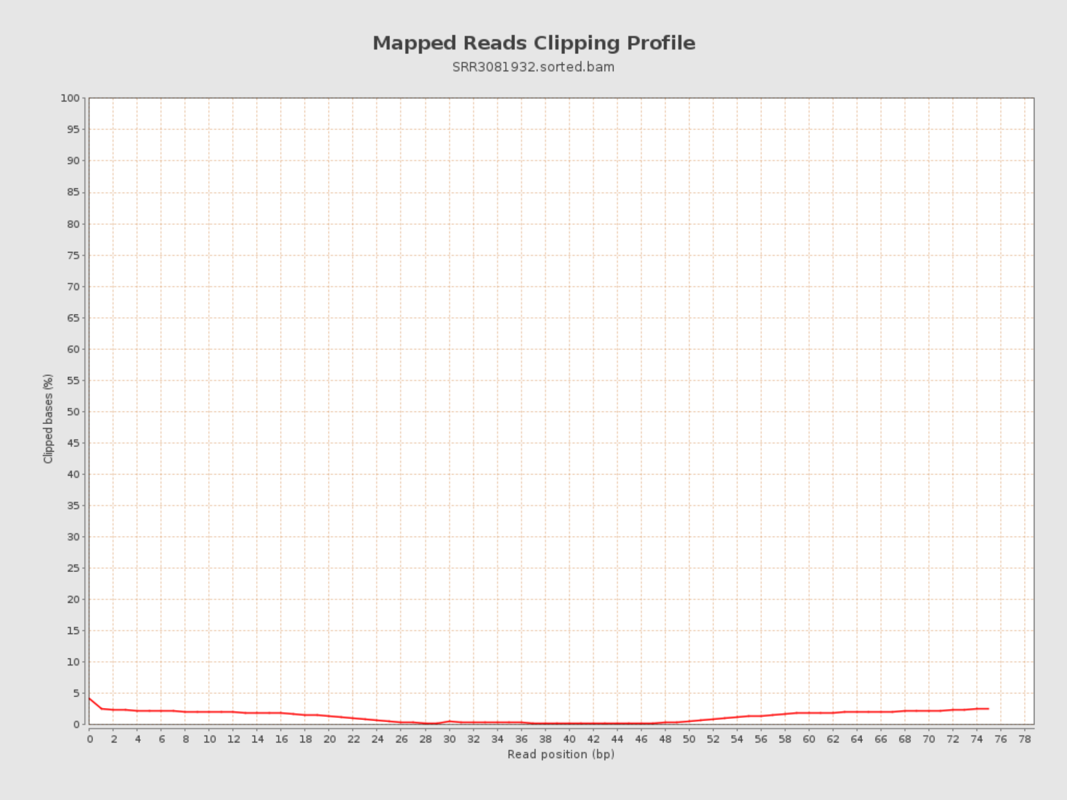
8. Results : Mapped Reads Nucleotide Content



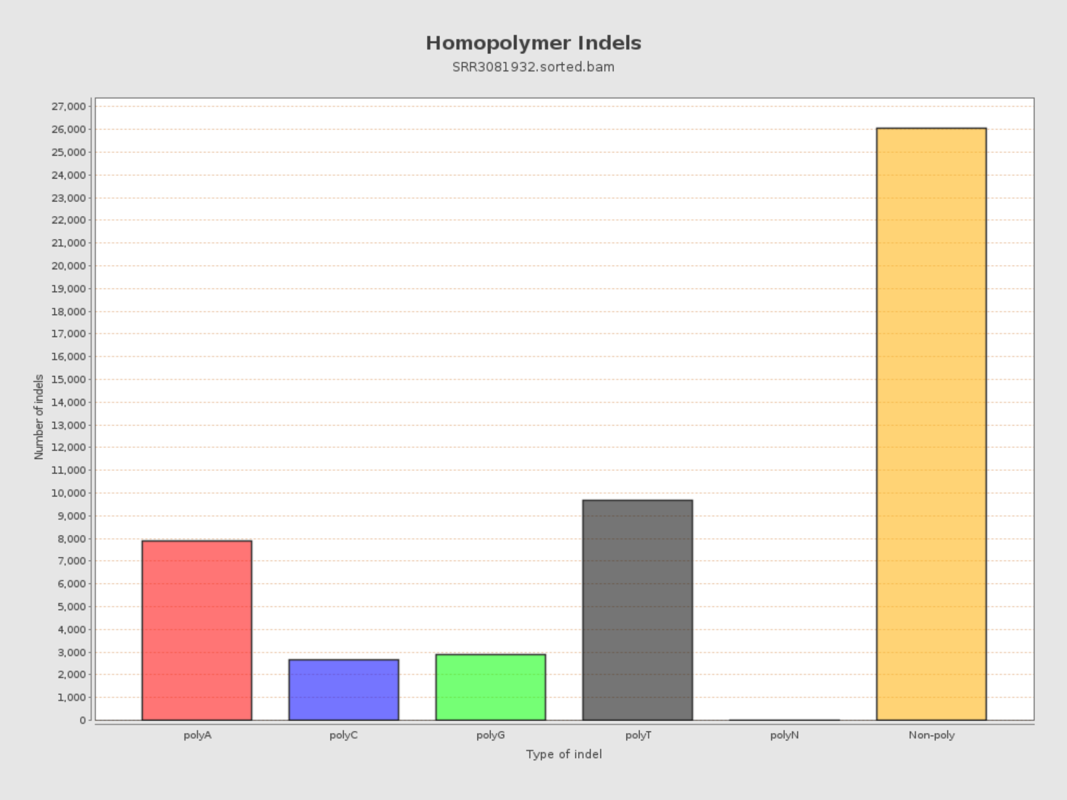
9. Results : Mapped Reads GC-content Distribution



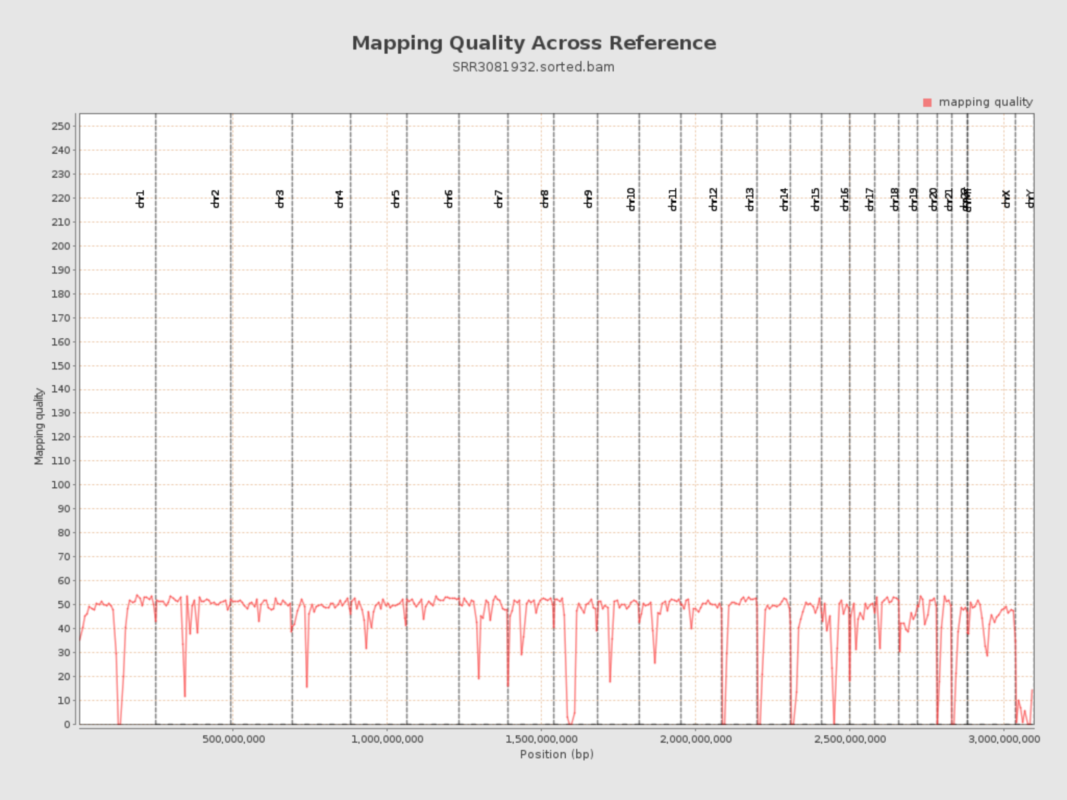
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram