Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:23:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081032.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_SRR3081032 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081032.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:23:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081032.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,712,602
Mapped reads	2,003,526 / 73.86%
Unmapped reads	709,076 / 26.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,055 / 0.33%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	67,145 / 2.48%
Duplication rate	2.6%
Clipped reads	1,160,073 / 42.77%

2.2. ACGT Content

Number/percentage of A's	35,318,068 / 28.08%
Number/percentage of C's	25,388,892 / 20.19%
Number/percentage of T's	36,378,527 / 28.92%
Number/percentage of G's	28,682,748 / 22.81%
Number/percentage of N's	1,591 / 0%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0406

Standard Deviation	0.3204

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

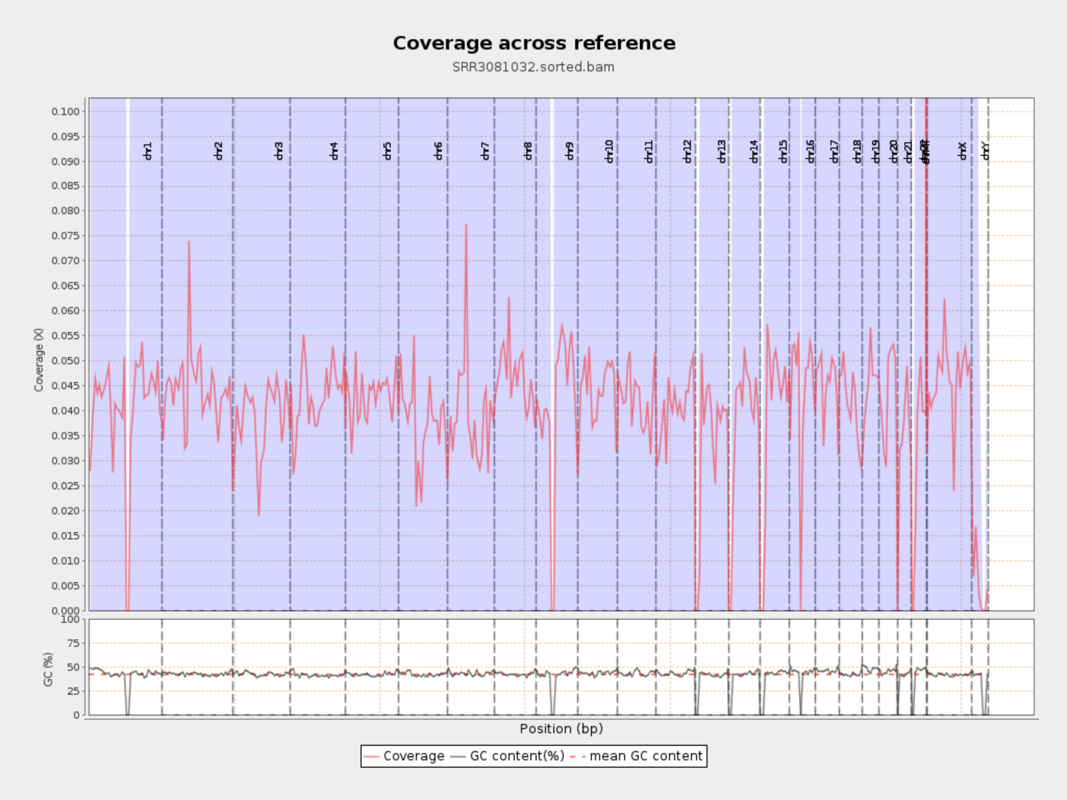
General error rate	0.78%
Mismatches	960,070
Insertions	8,428
Mapped reads with at least one insertion	0.42%
Deletions	24,928
Mapped reads with at least one deletion	1.23%
Homopolymer indels	45.77%

2.6. Chromosome stats

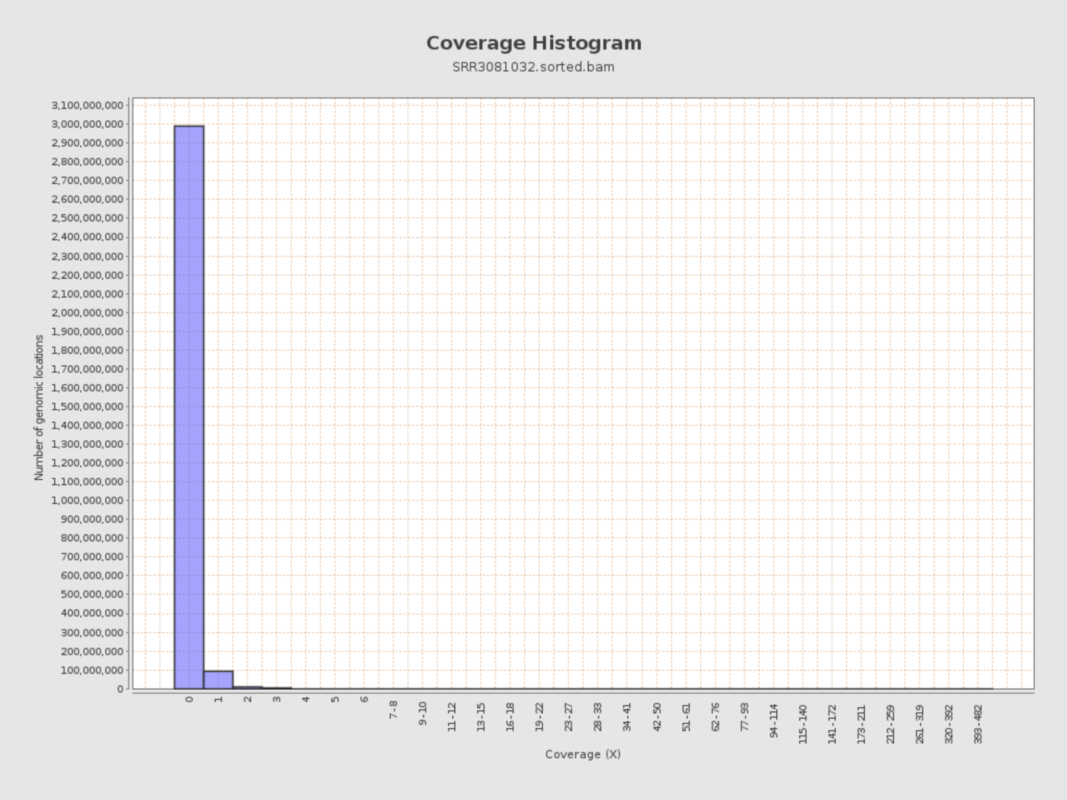
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10085289	0.0405	0.4451
chr2	243199373	10832662	0.0445	0.36
chr3	198022430	7640412	0.0386	0.2226
chr4	191154276	8200633	0.0429	0.2522
chr5	180915260	7817557	0.0432	0.2367
chr6	171115067	6531406	0.0382	0.2604
chr7	159138663	6263234	0.0394	0.532

chr8	146364022	6824738	0.0466	0.3172
chr9	141213431	5769845	0.0409	0.3213
chr10	135534747	5985070	0.0442	0.3018
chr11	135006516	5731635	0.0425	0.3043
chr12	133851895	5392241	0.0403	0.2311
chr13	115169878	3816462	0.0331	0.2069
chr14	107349540	3971389	0.037	0.2355
chr15	102531392	3983709	0.0389	0.2439
chr16	90354753	3977136	0.044	0.259
chr17	81195210	3659363	0.0451	0.2633
chr18	78077248	3276068	0.042	0.6127
chr19	59128983	2680629	0.0453	0.345
chr20	63025520	2705900	0.0429	0.2435
chr21	48129895	1620287	0.0337	0.2362
chr22	51304566	1513337	0.0295	0.1957
chrMT	16571	43057	2.5983	2.1673
chrX	155270560	7173953	0.0462	0.2793
chrY	59373566	317570	0.0053	0.1298

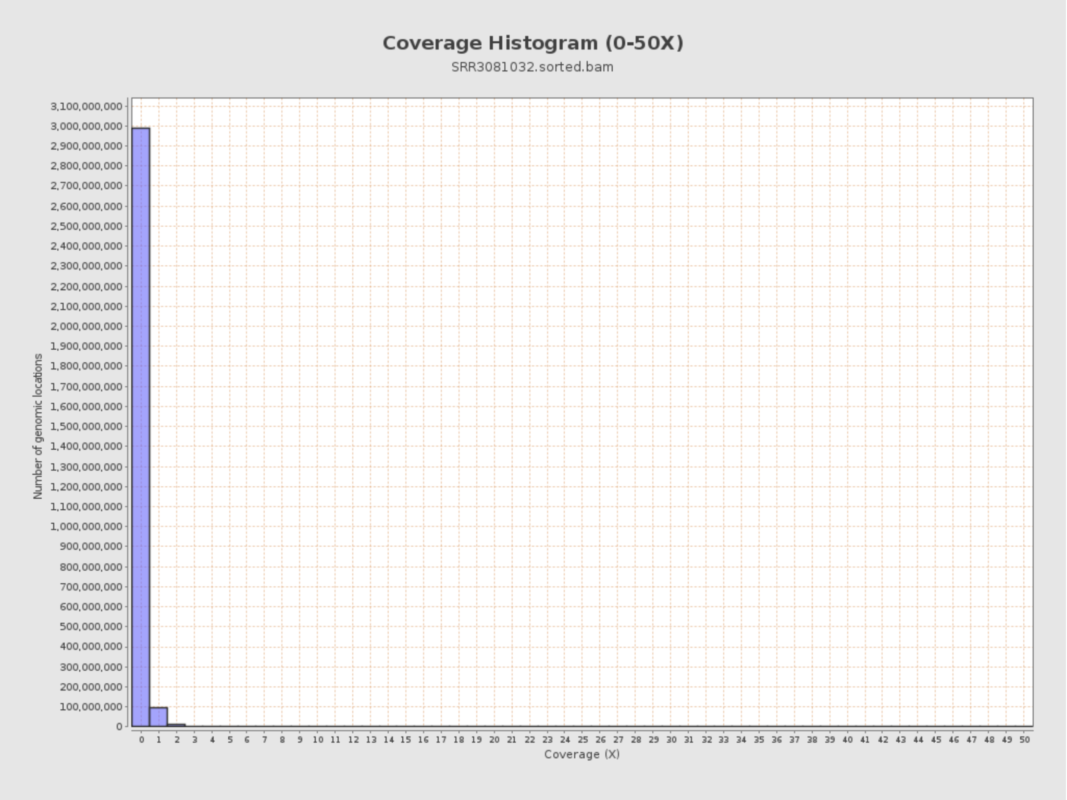
3. Results : Coverage across reference



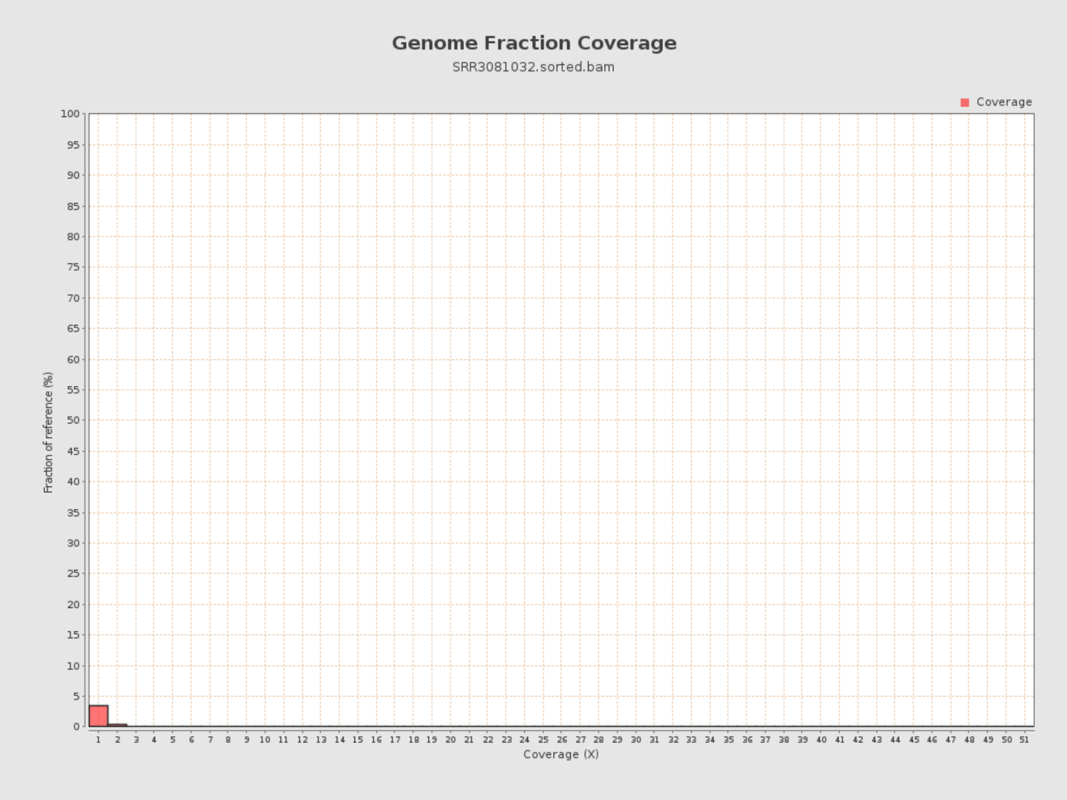
4. Results : Coverage Histogram



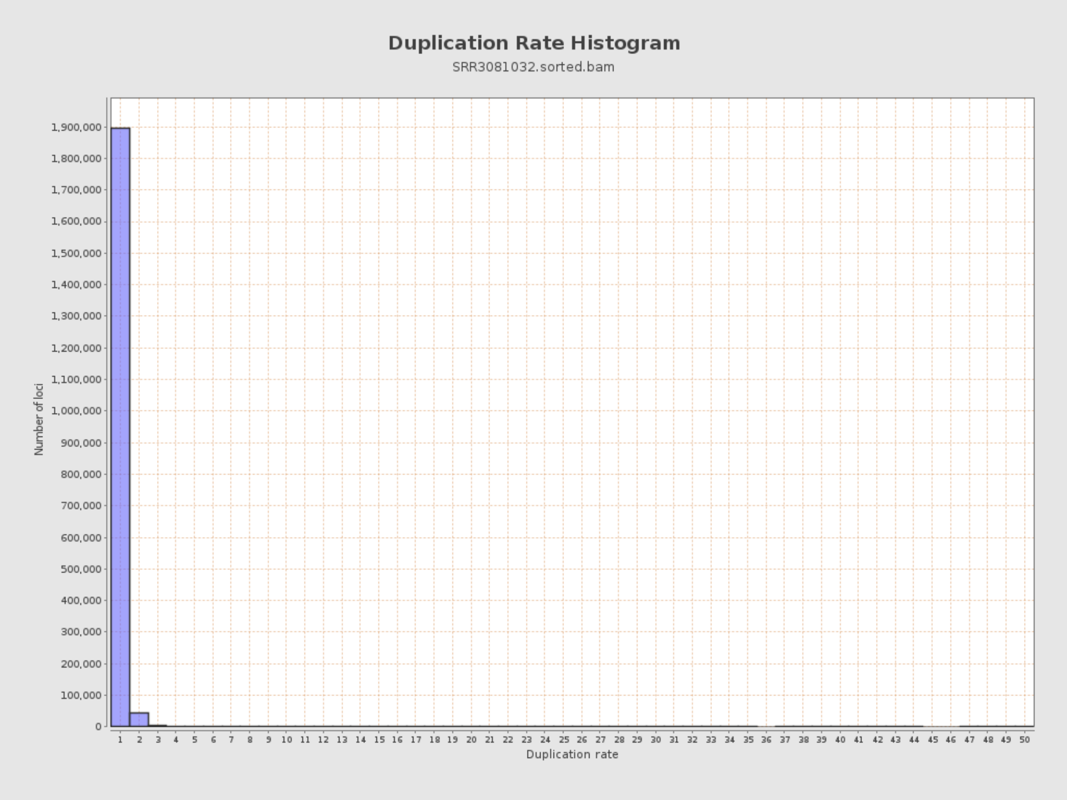
5. Results : Coverage Histogram (0-50X)



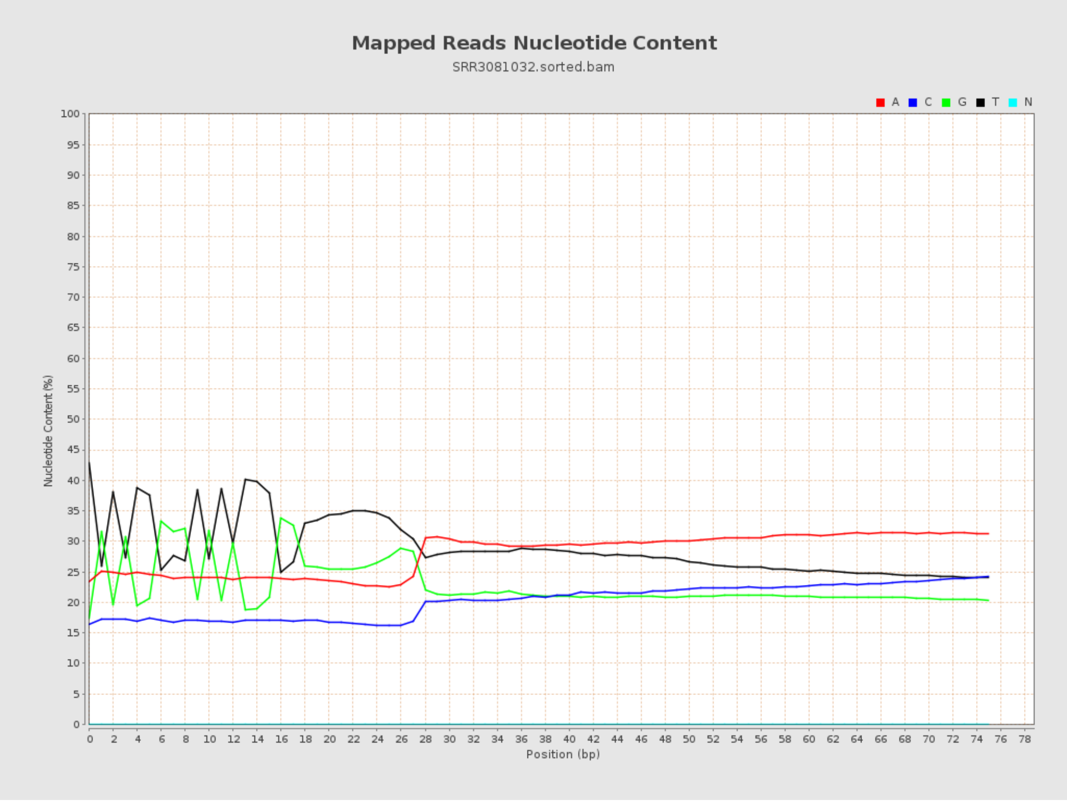
6. Results : Genome Fraction Coverage



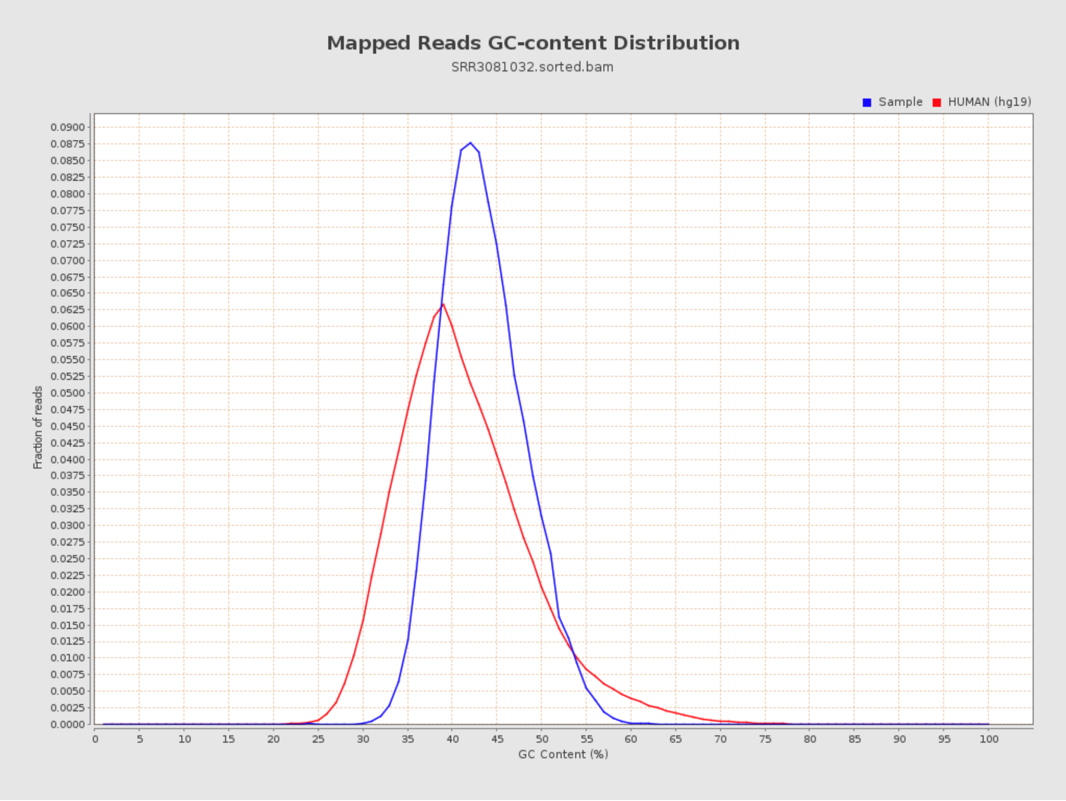
7. Results : Duplication Rate Histogram



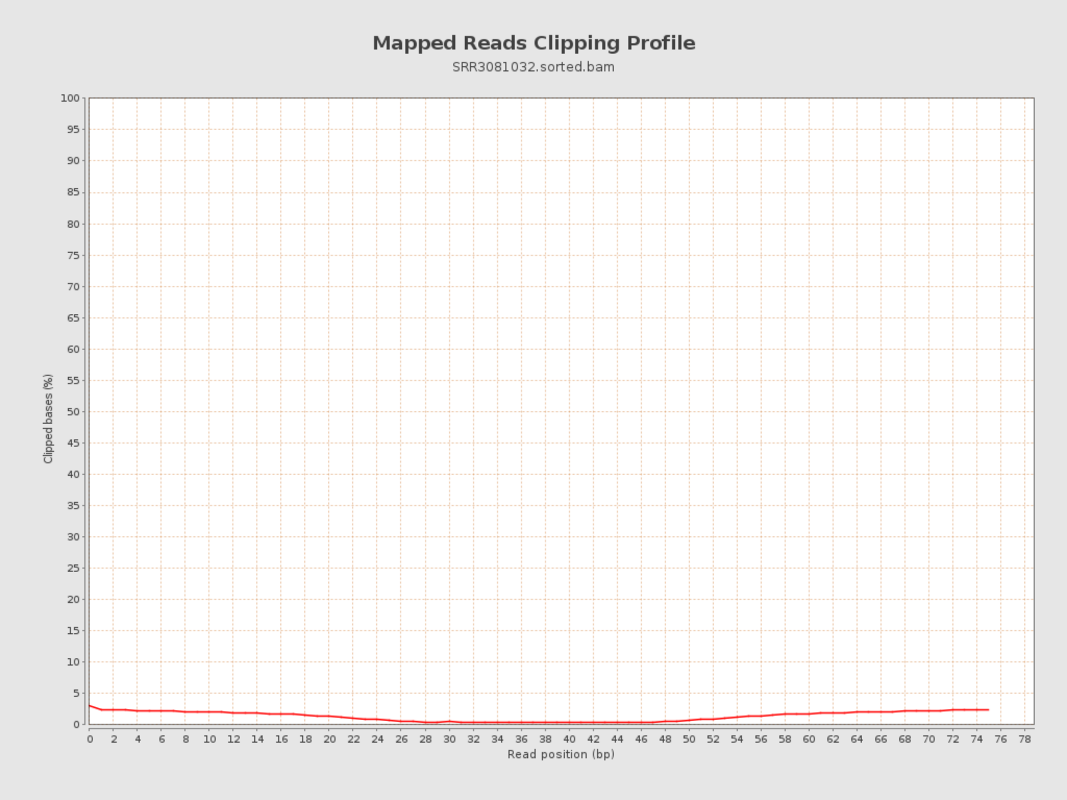
8. Results : Mapped Reads Nucleotide Content



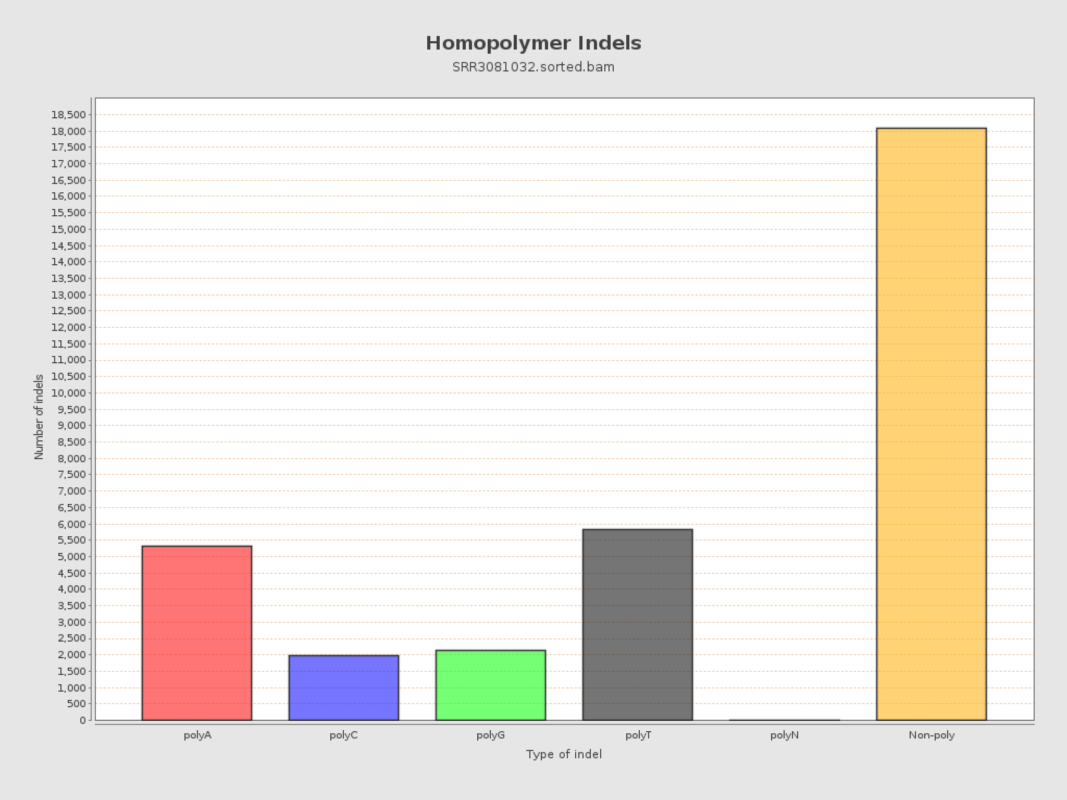
9. Results : Mapped Reads GC-content Distribution



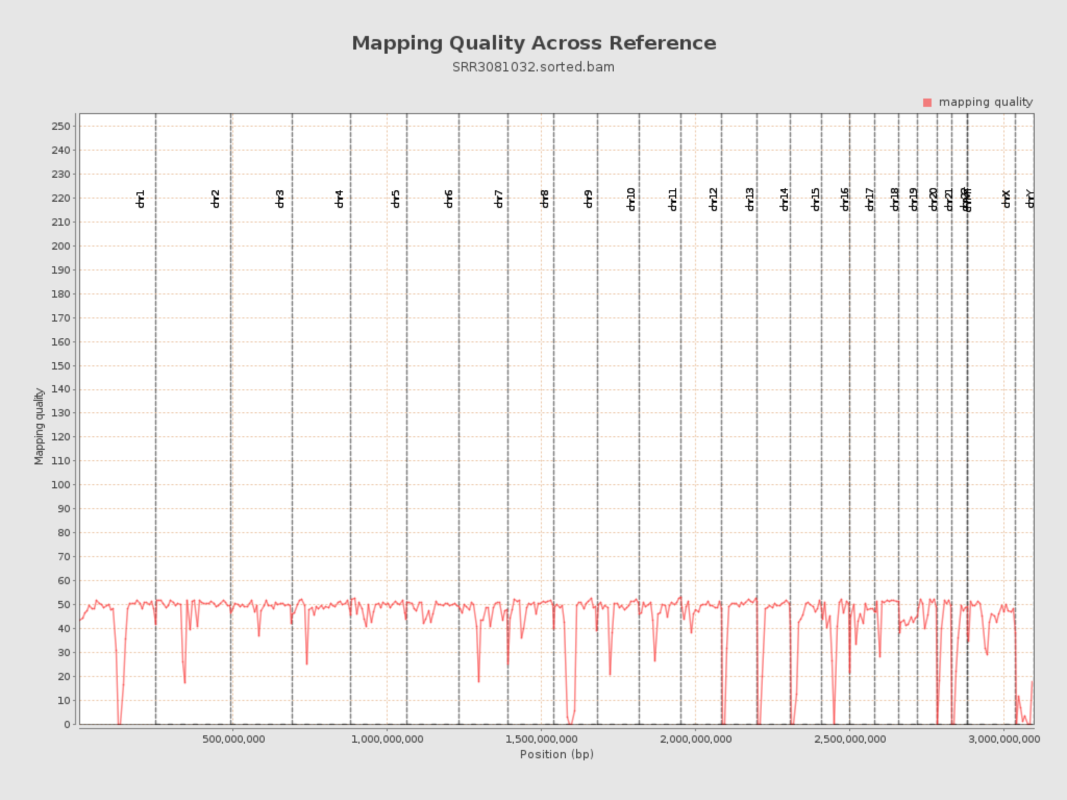
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram