Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:14:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081198.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_SRR3081198 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081198.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:14:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081198.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,286,687
Mapped reads	3,443,172 / 80.32%
Unmapped reads	843,515 / 19.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,431 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	291,858 / 6.81%
Duplication rate	6.07%
Clipped reads	1,574,310 / 36.73%

2.2. ACGT Content

Number/percentage of A's	64,258,362 / 28.11%
Number/percentage of C's	44,879,360 / 19.63%
Number/percentage of T's	68,552,646 / 29.99%
Number/percentage of G's	49,773,737 / 21.78%
Number/percentage of N's	1,113,315 / 0.49%
GC Percentage	41.41%

2.3. Coverage

Mean	0.0739

Standard Deviation	0.7976

2.4. Mapping Quality

Mean Mapping Quality	46.07

2.5. Mismatches and indels

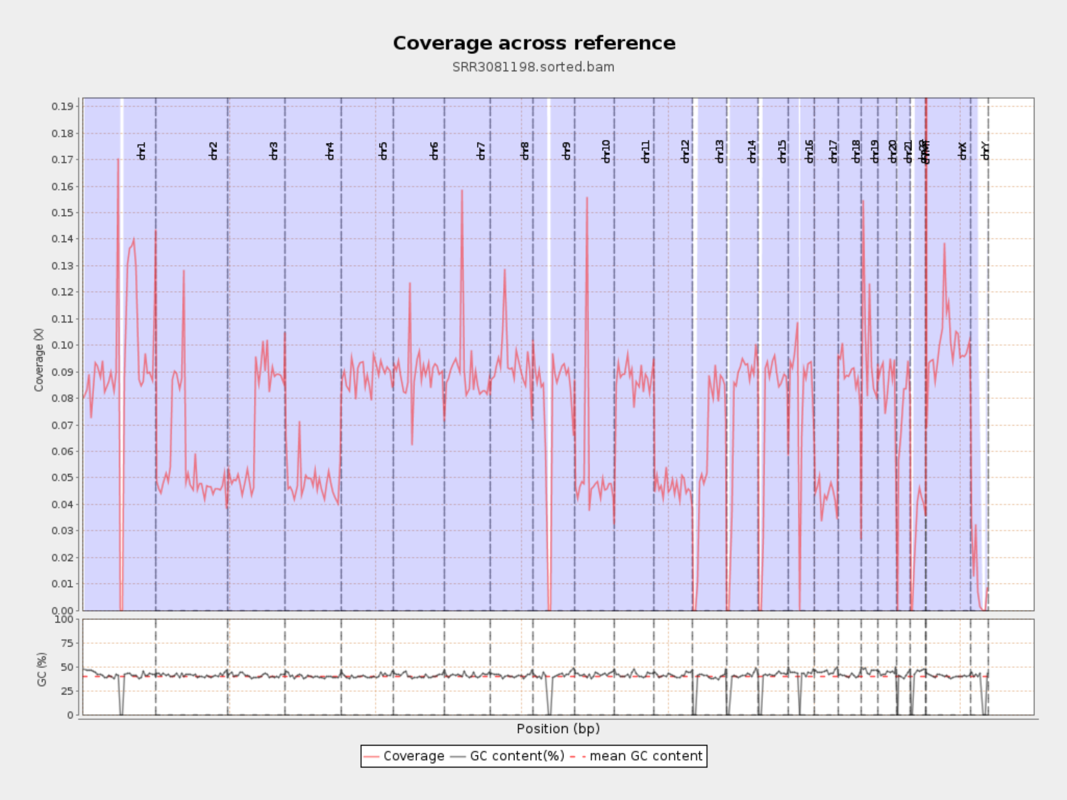
General error rate	1.36%
Mismatches	3,077,251
Insertions	16,152
Mapped reads with at least one insertion	0.47%
Deletions	49,923
Mapped reads with at least one deletion	1.43%
Homopolymer indels	46.55%

2.6. Chromosome stats

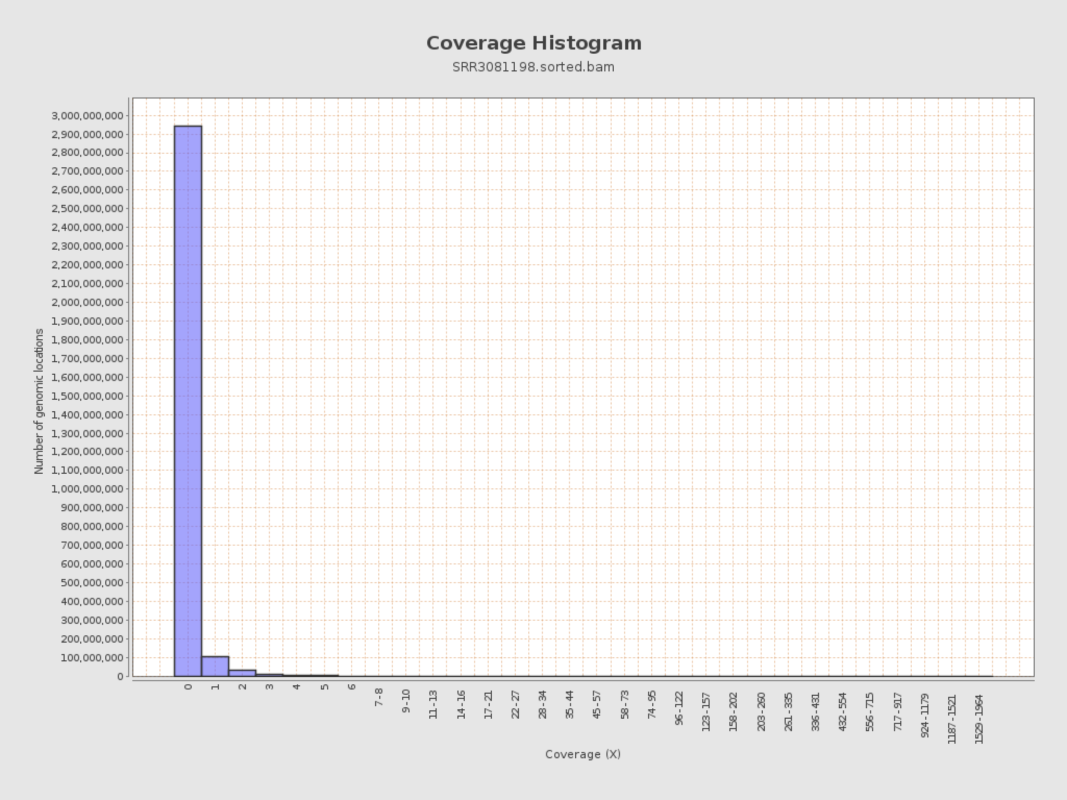
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23164578	0.0929	1.7864
chr2	243199373	13758251	0.0566	0.6522
chr3	198022430	13964717	0.0705	0.3905
chr4	191154276	9291959	0.0486	0.335
chr5	180915260	16080548	0.0889	0.4208
chr6	171115067	15382550	0.0899	0.568
chr7	159138663	14399639	0.0905	1.1218

chr8	146364022	13610354	0.093	0.8934
chr9	141213431	10826375	0.0767	0.6226
chr10	135534747	7085915	0.0523	0.8825
chr11	135006516	11701912	0.0867	0.6083
chr12	133851895	6237169	0.0466	0.3199
chr13	115169878	7078152	0.0615	0.3418
chr14	107349540	8121143	0.0757	0.931
chr15	102531392	7415269	0.0723	0.37
chr16	90354753	7239964	0.0801	0.4348
chr17	81195210	3539316	0.0436	0.345
chr18	78077248	7015465	0.0899	1.0064
chr19	59128983	5840246	0.0988	1.2113
chr20	63025520	5457744	0.0866	0.4279
chr21	48129895	3361906	0.0699	0.4019
chr22	51304566	1531916	0.0299	0.2323
chrMT	16571	399067	24.0823	13.2187
chrX	155270560	15500168	0.0998	0.4991
chrY	59373566	652679	0.011	0.2275

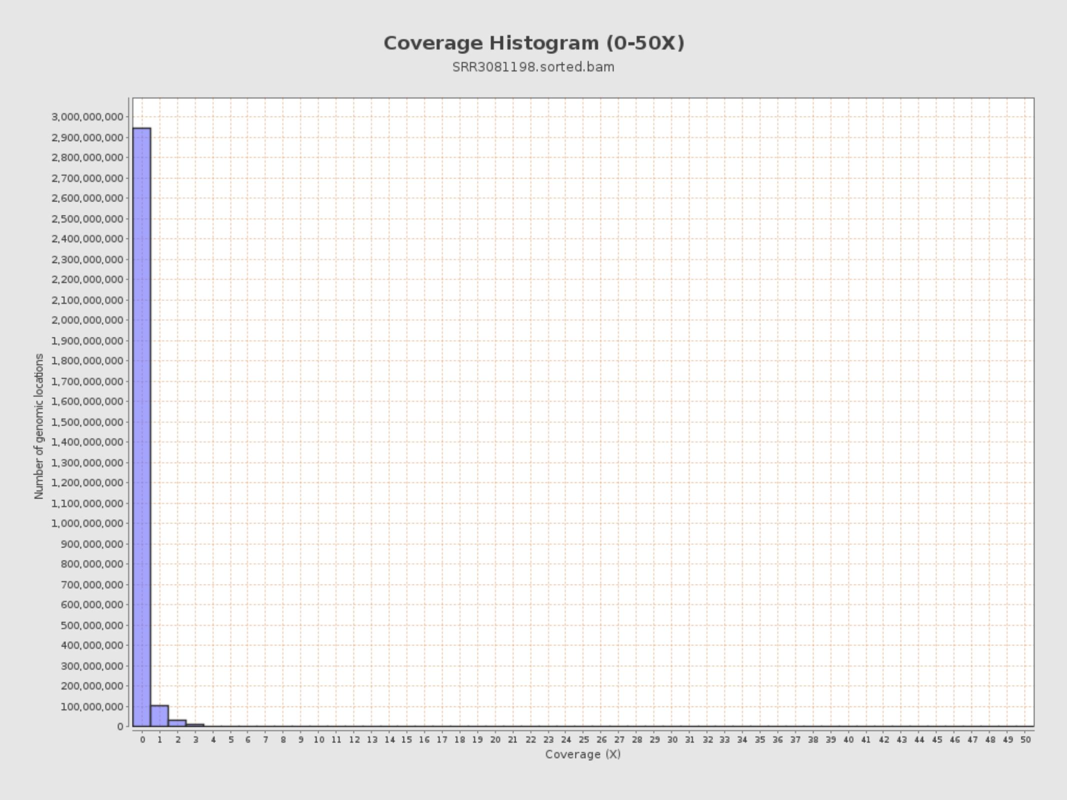
3. Results : Coverage across reference



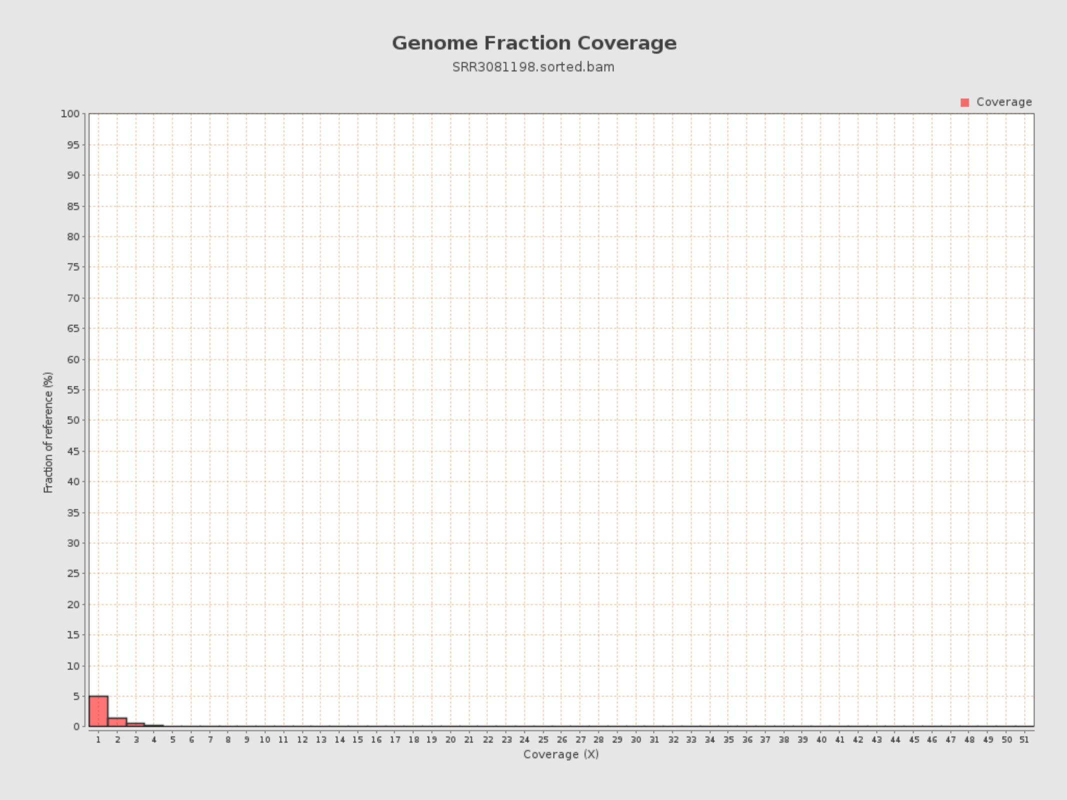
4. Results : Coverage Histogram



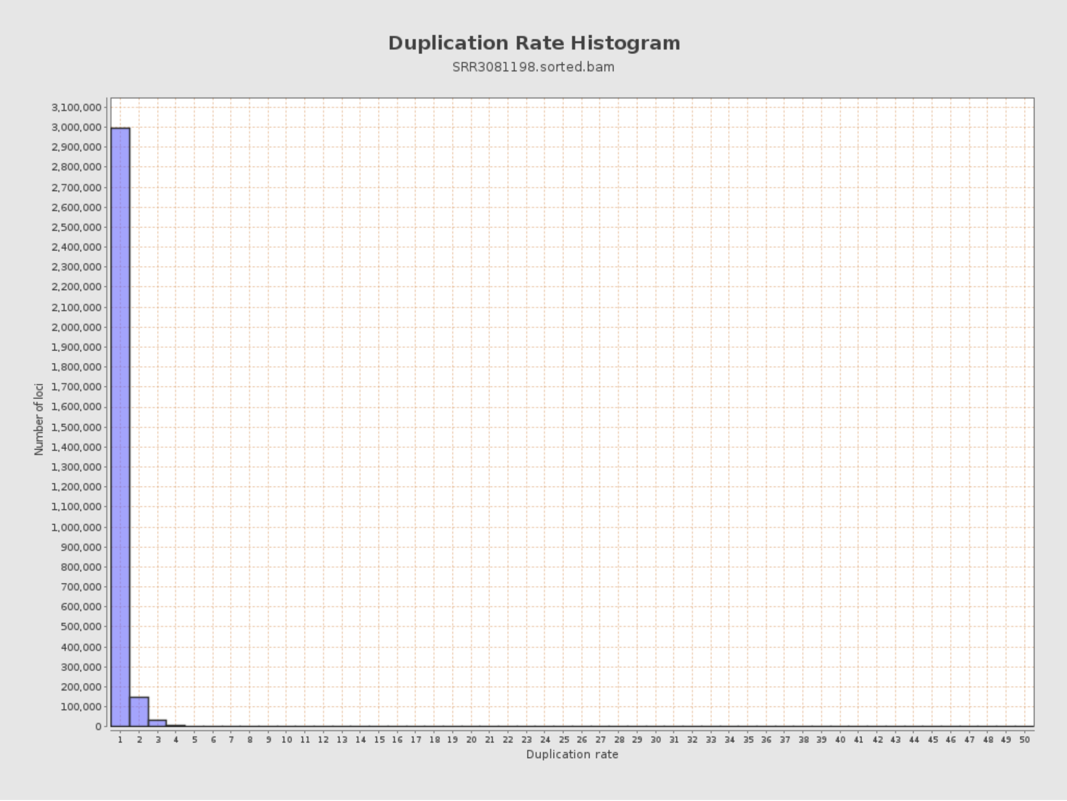
5. Results : Coverage Histogram (0-50X)



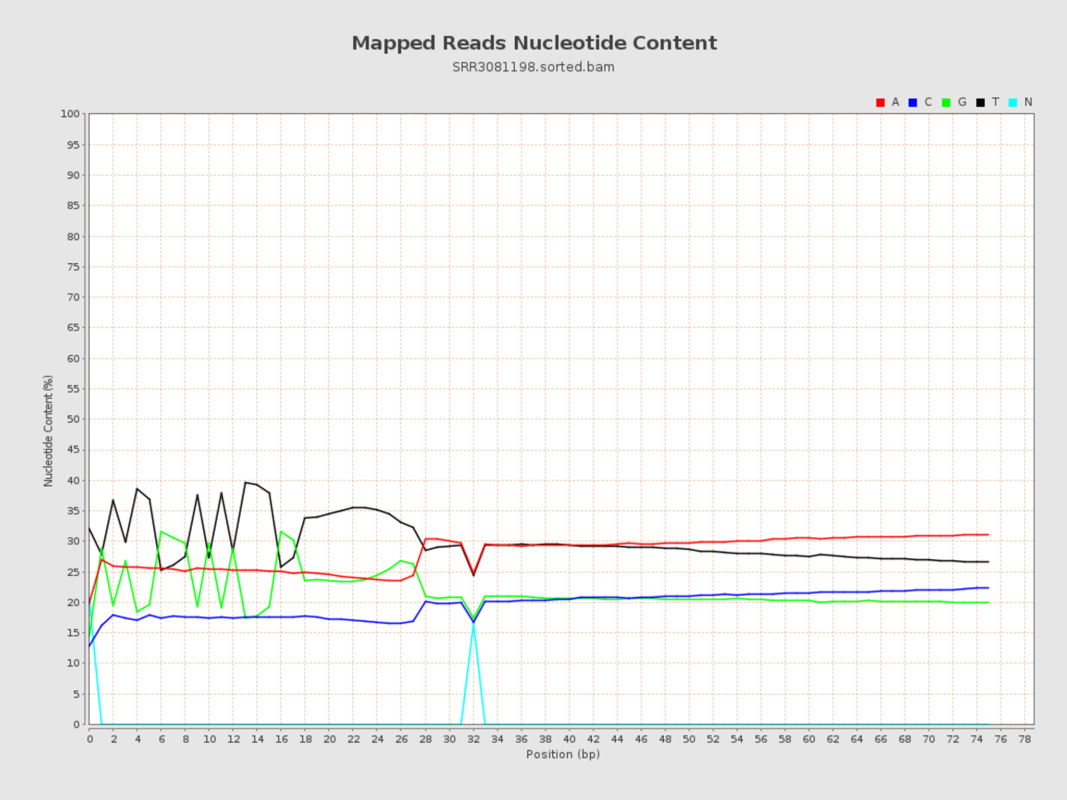
6. Results : Genome Fraction Coverage



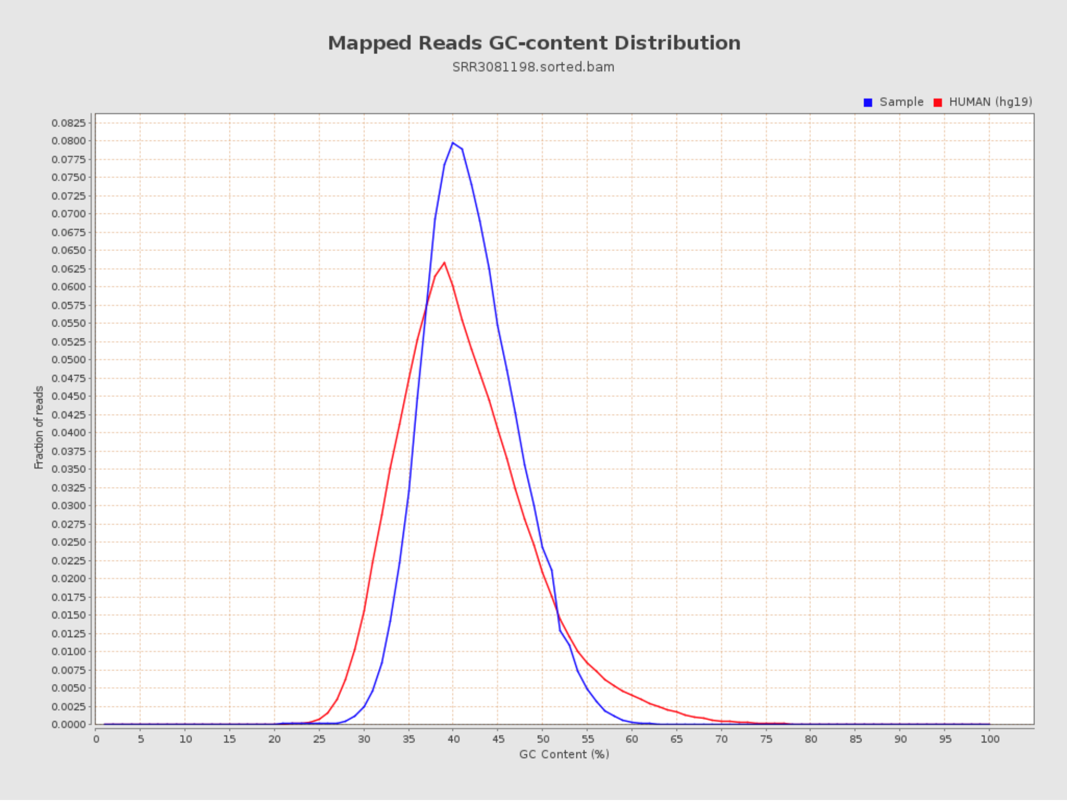
7. Results : Duplication Rate Histogram



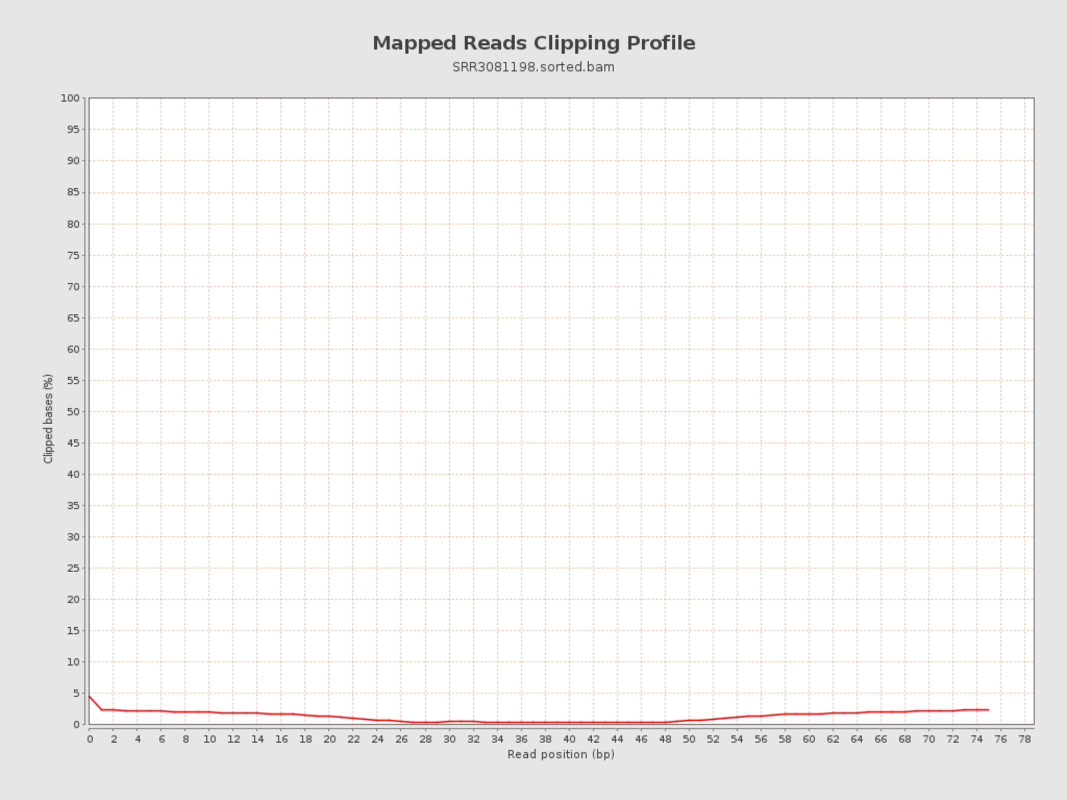
8. Results : Mapped Reads Nucleotide Content



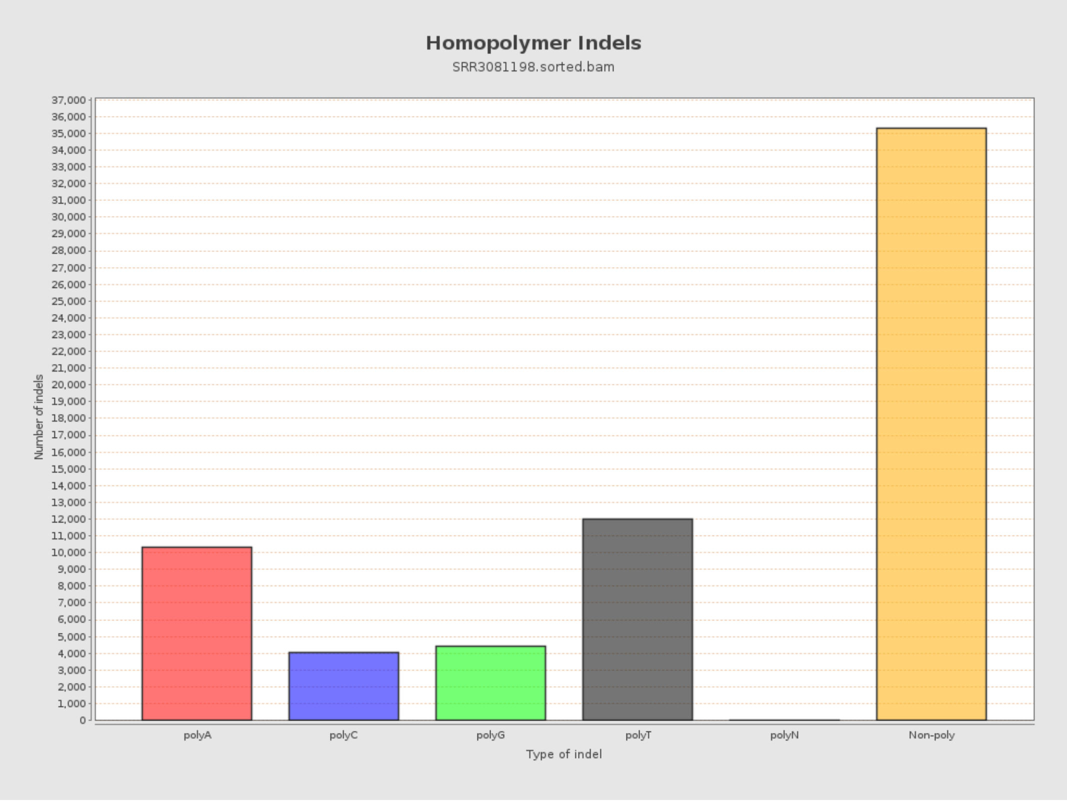
9. Results : Mapped Reads GC-content Distribution



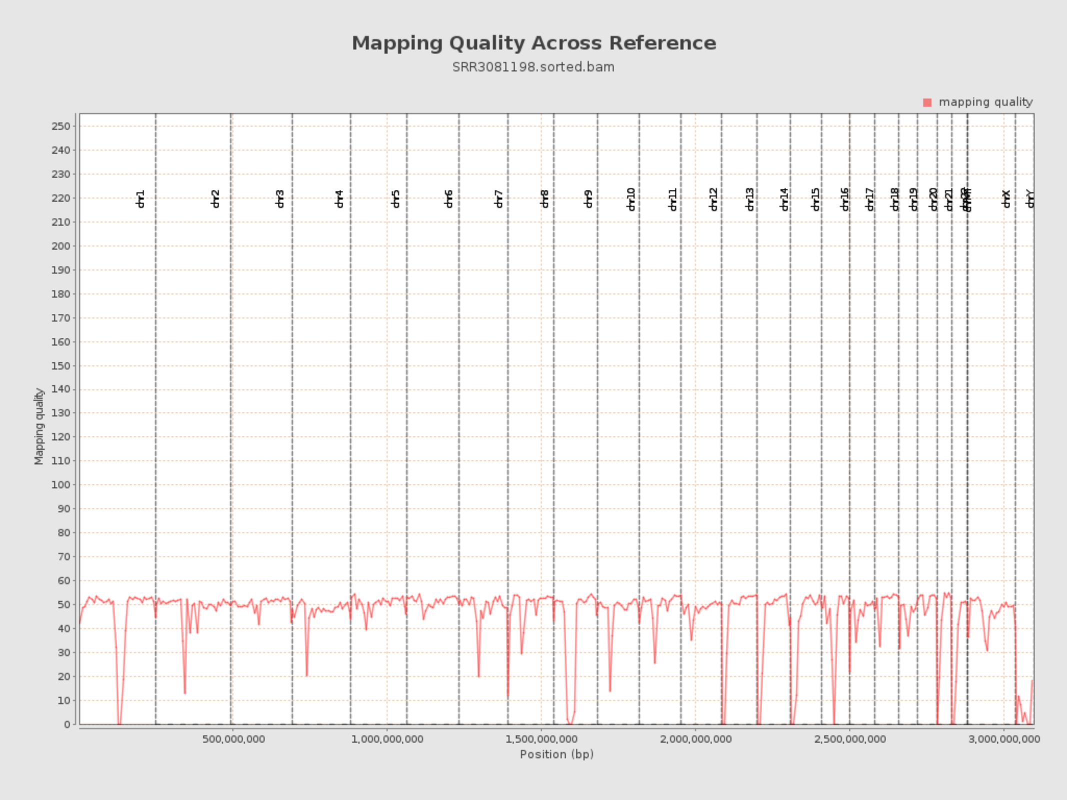
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram