Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:23:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081056.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_SRR3081056 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081056.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:23:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,179,337
Mapped reads	1,998,976 / 91.72%
Unmapped reads	180,361 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,493 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	82,231 / 3.77%
Duplication rate	3.34%
Clipped reads	886,982 / 40.7%

2.2. ACGT Content

Number/percentage of A's	37,140,441 / 27.71%
Number/percentage of C's	25,236,487 / 18.83%
Number/percentage of T's	41,883,102 / 31.24%
Number/percentage of G's	29,795,175 / 22.23%
Number/percentage of N's	1,450 / 0%
GC Percentage	41.05%

2.3. Coverage

Mean	0.0433

Standard Deviation	0.3306

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

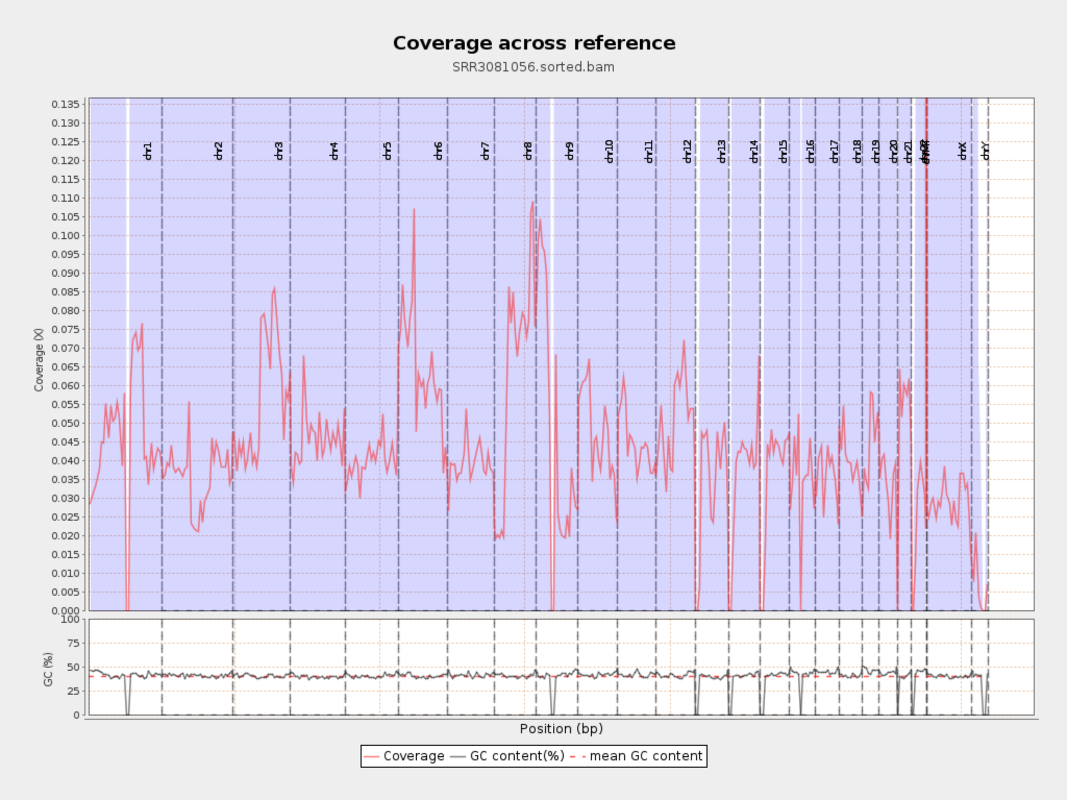
General error rate	0.9%
Mismatches	1,189,218
Insertions	10,280
Mapped reads with at least one insertion	0.51%
Deletions	29,636
Mapped reads with at least one deletion	1.47%
Homopolymer indels	46.99%

2.6. Chromosome stats

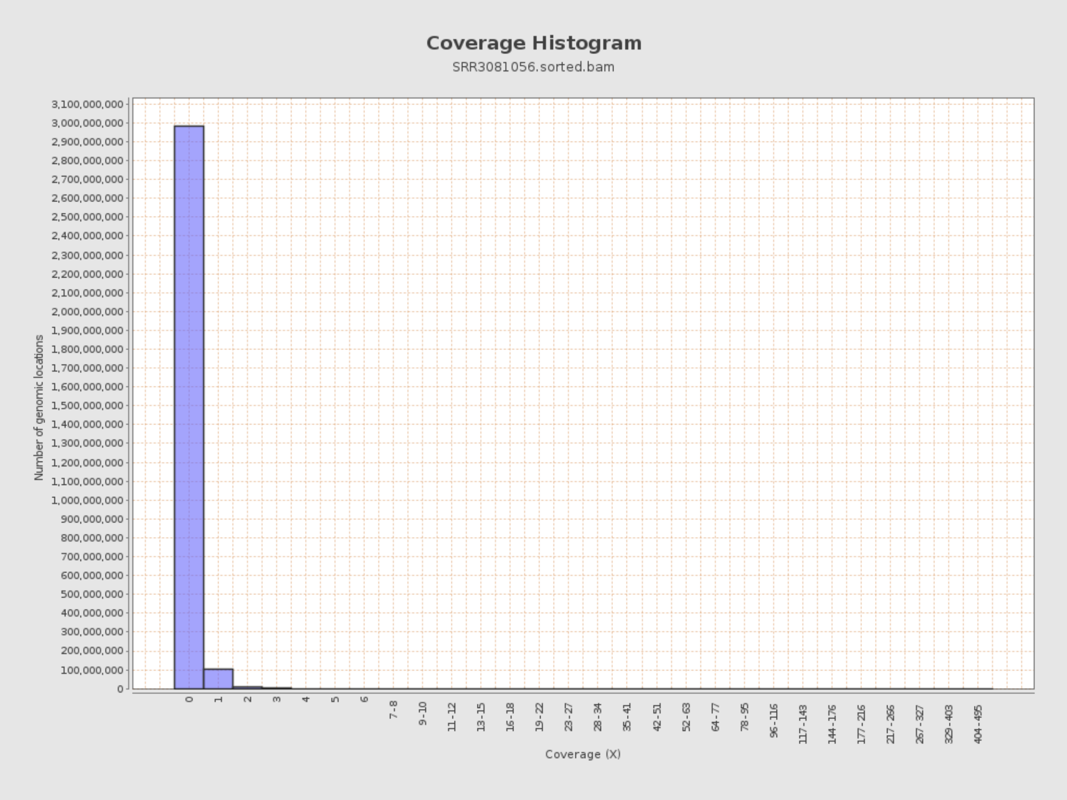
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11405847	0.0458	0.4517
chr2	243199373	8718743	0.0359	0.3583
chr3	198022430	11169294	0.0564	0.2675
chr4	191154276	8723874	0.0456	0.2591
chr5	180915260	7230649	0.04	0.2272
chr6	171115067	11105456	0.0649	0.4217
chr7	159138663	6287248	0.0395	0.2963

chr8	146364022	9394087	0.0642	0.4104
chr9	141213431	6585892	0.0466	0.3815
chr10	135534747	6501682	0.048	0.3417
chr11	135006516	6021934	0.0446	0.3121
chr12	133851895	6848906	0.0512	0.2647
chr13	115169878	3843504	0.0334	0.2053
chr14	107349540	3860945	0.036	0.2709
chr15	102531392	3645509	0.0356	0.215
chr16	90354753	3122786	0.0346	0.2613
chr17	81195210	2896529	0.0357	0.2216
chr18	78077248	3138636	0.0402	0.6502
chr19	59128983	2644357	0.0447	0.3887
chr20	63025520	2134729	0.0339	0.221
chr21	48129895	2510219	0.0522	0.2968
chr22	51304566	1209238	0.0236	0.1706
chrMT	16571	241989	14.6032	7.3693
chrX	155270560	4504891	0.029	0.2196
chrY	59373566	358305	0.006	0.1439

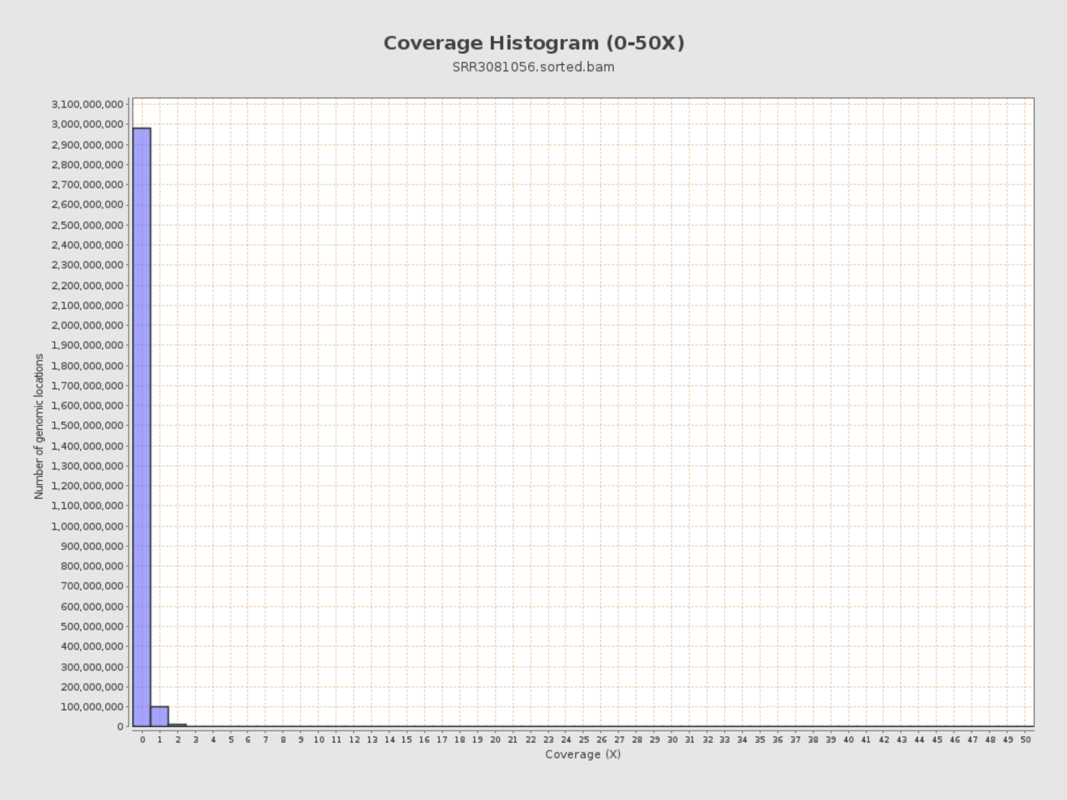
3. Results : Coverage across reference



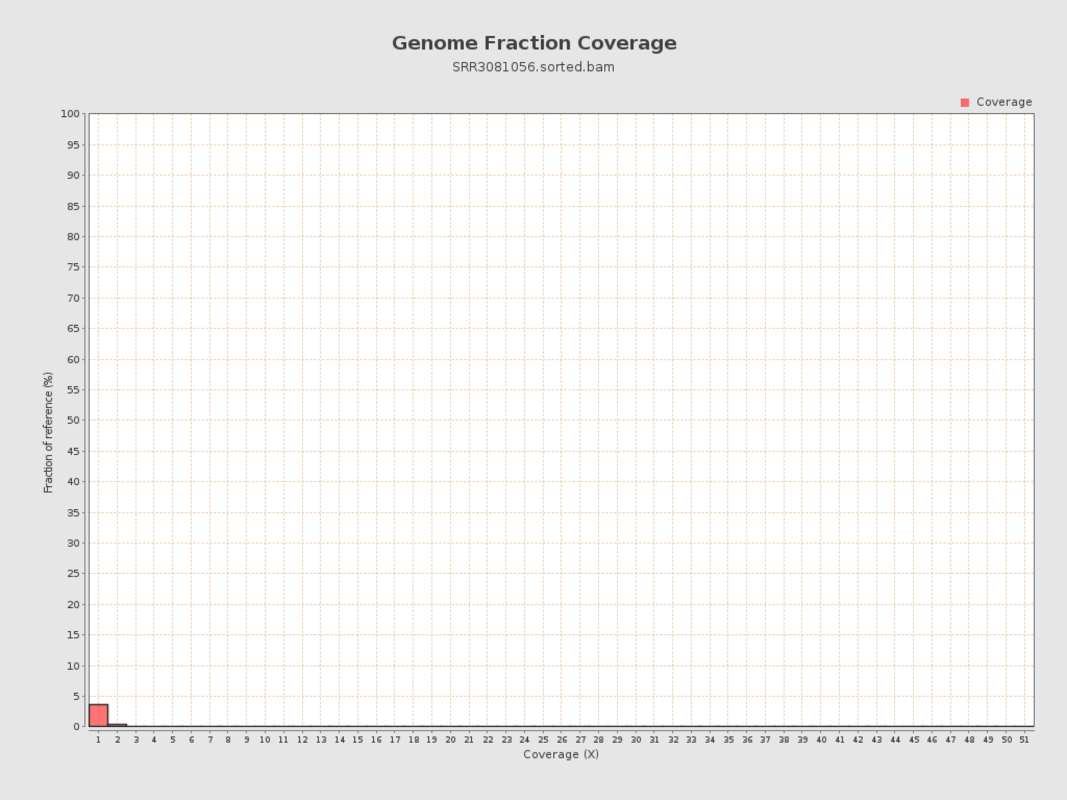
4. Results : Coverage Histogram



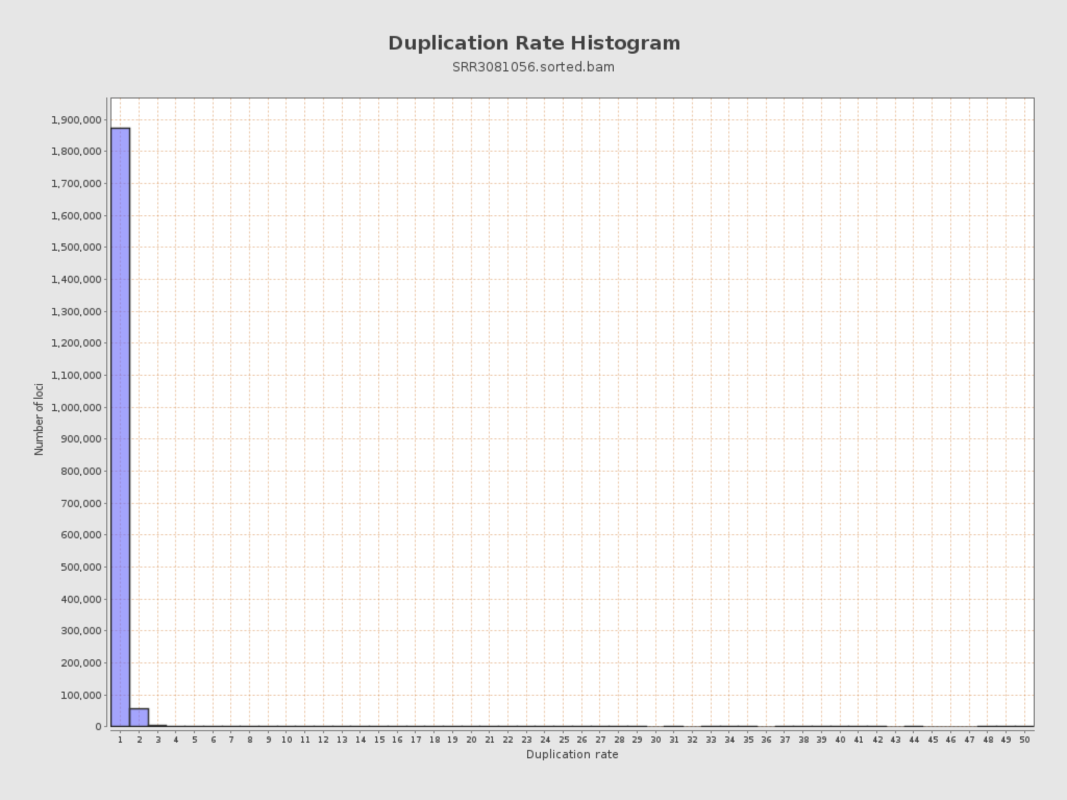
5. Results : Coverage Histogram (0-50X)



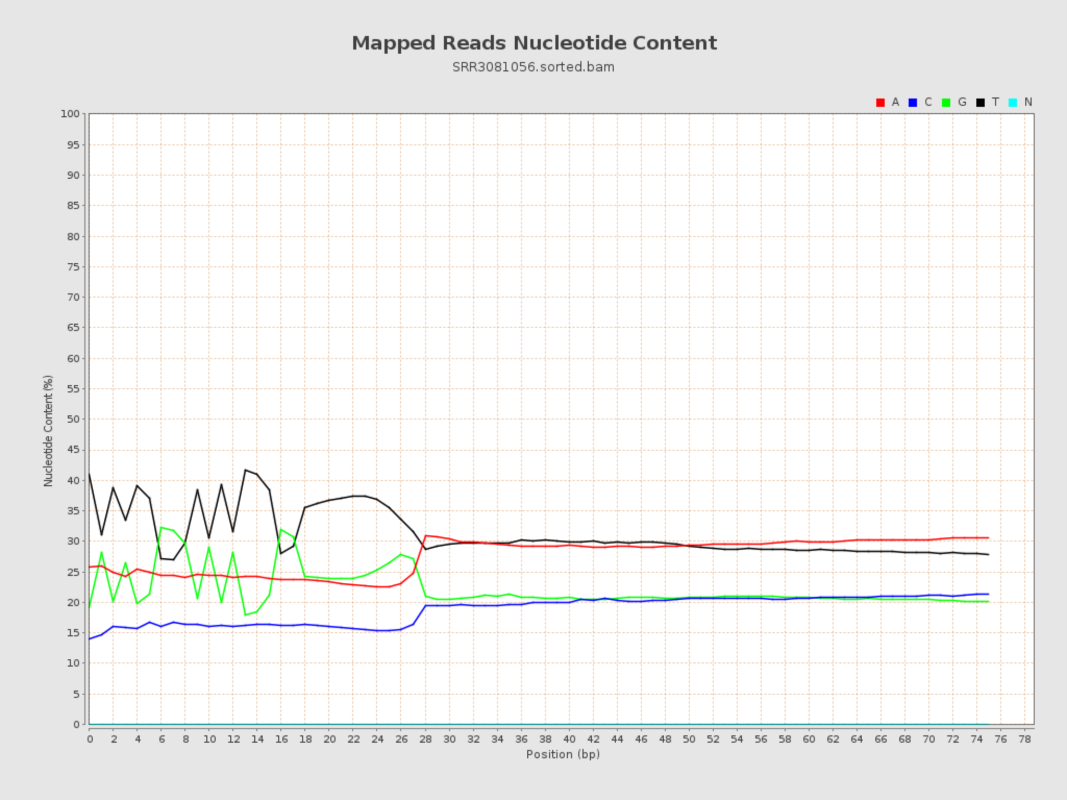
6. Results : Genome Fraction Coverage



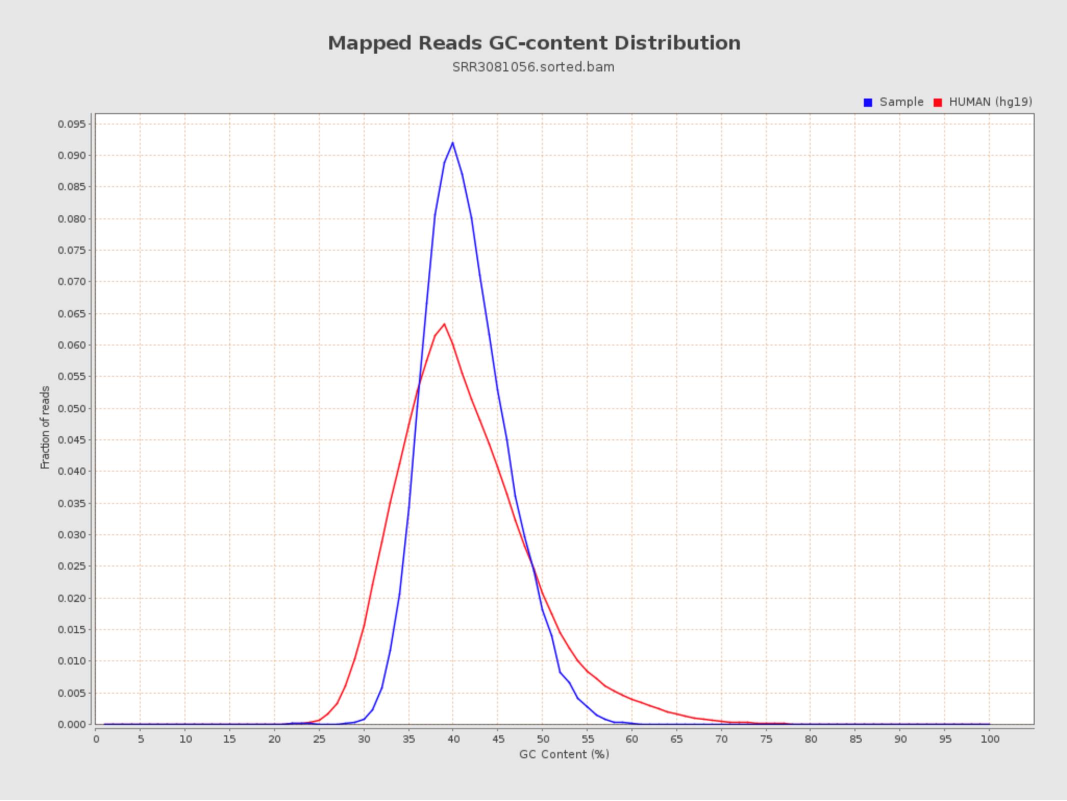
7. Results : Duplication Rate Histogram



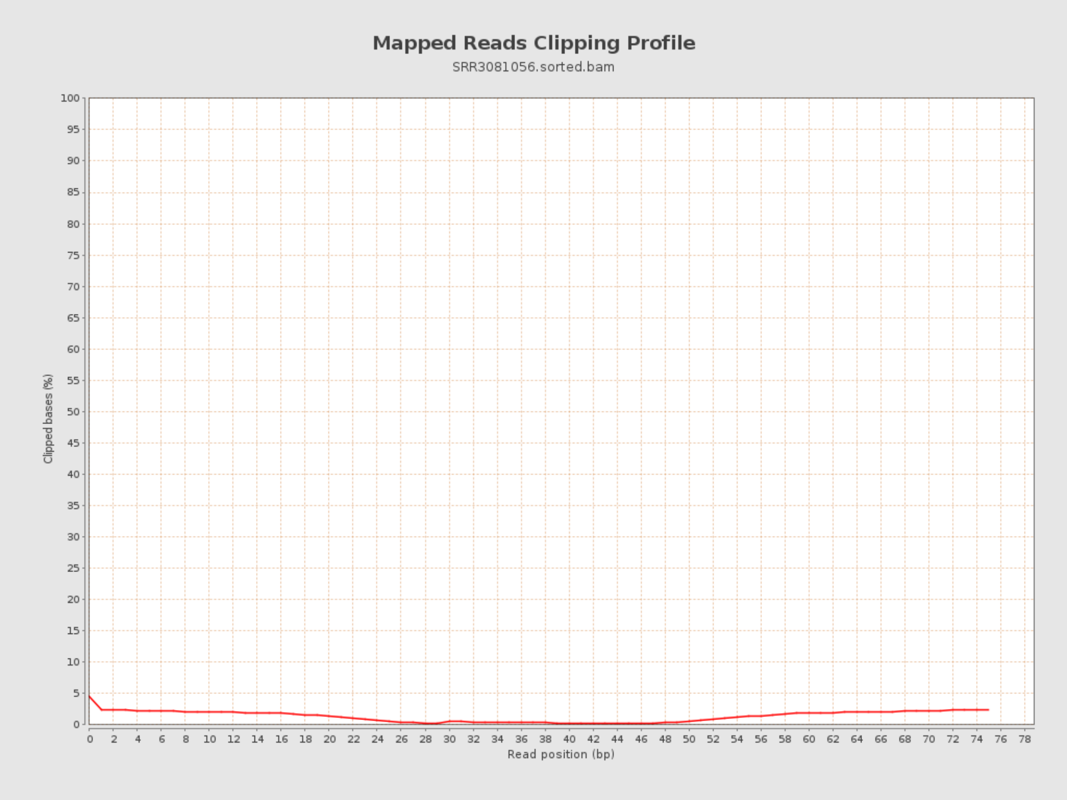
8. Results : Mapped Reads Nucleotide Content



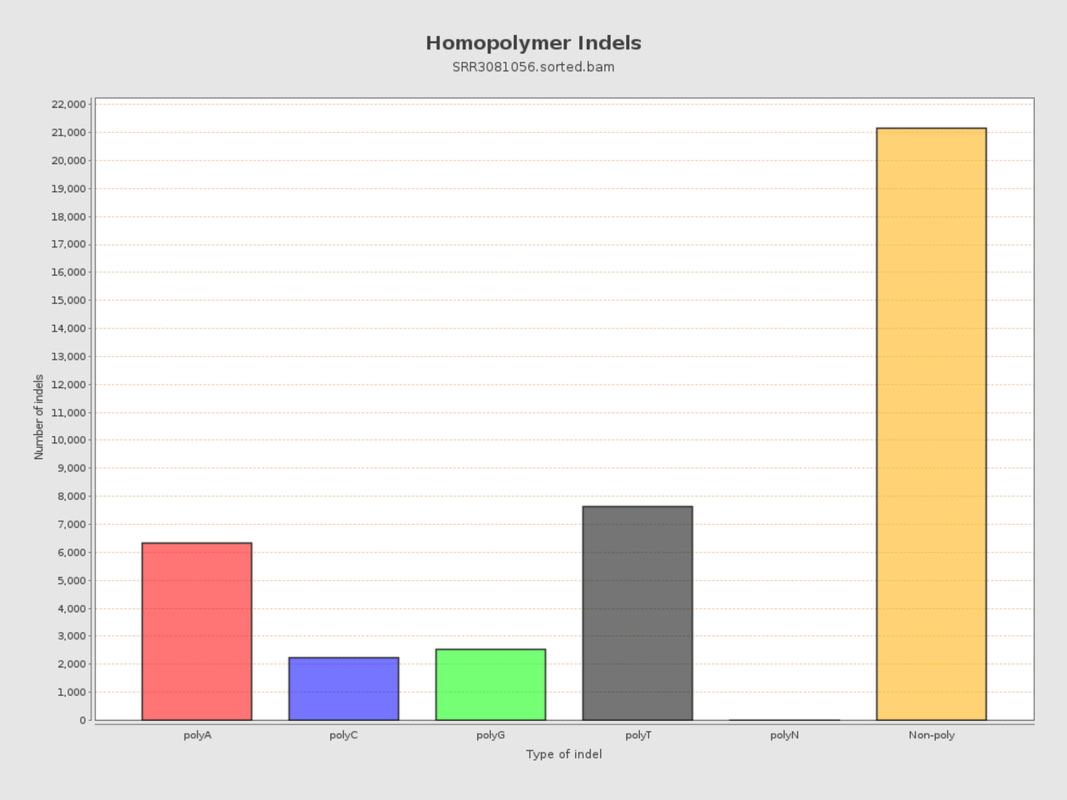
9. Results : Mapped Reads GC-content Distribution



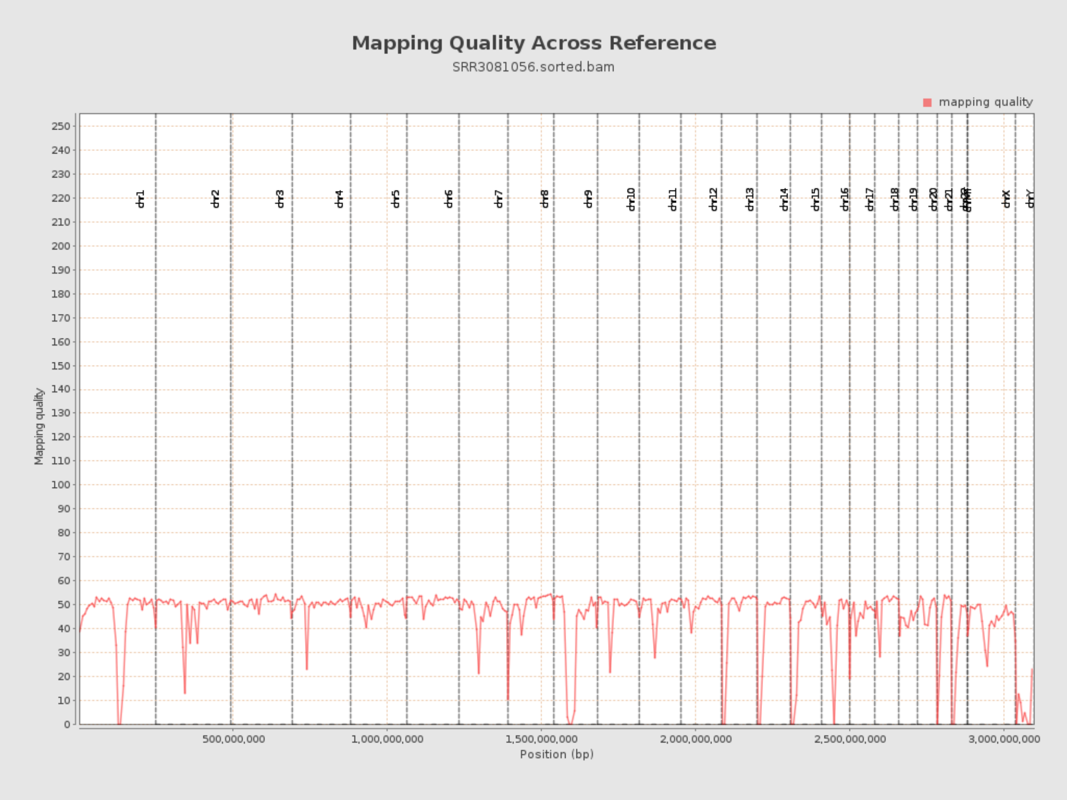
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram