Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:23:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082321.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_SRR3082321 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082321.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:23:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082321.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,122,816
Mapped reads	1,902,057 / 89.6%
Unmapped reads	220,759 / 10.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,185 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	66,786 / 3.15%
Duplication rate	2.72%
Clipped reads	839,118 / 39.53%

2.2. ACGT Content

Number/percentage of A's	35,720,038 / 27.96%
Number/percentage of C's	23,809,352 / 18.64%
Number/percentage of T's	39,917,084 / 31.25%
Number/percentage of G's	28,294,430 / 22.15%
Number/percentage of N's	2,554 / 0%
GC Percentage	40.79%

2.3. Coverage

Mean	0.0413

Standard Deviation	0.348

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

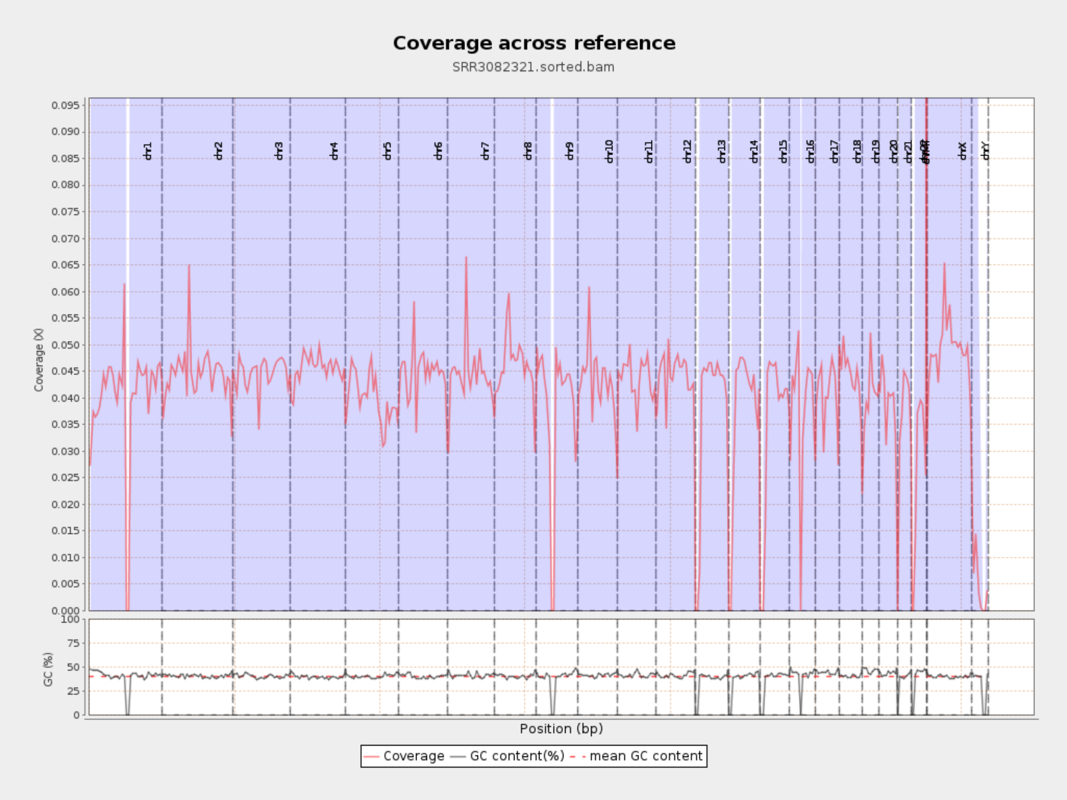
General error rate	0.84%
Mismatches	1,057,101
Insertions	10,167
Mapped reads with at least one insertion	0.53%
Deletions	28,243
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.33%

2.6. Chromosome stats

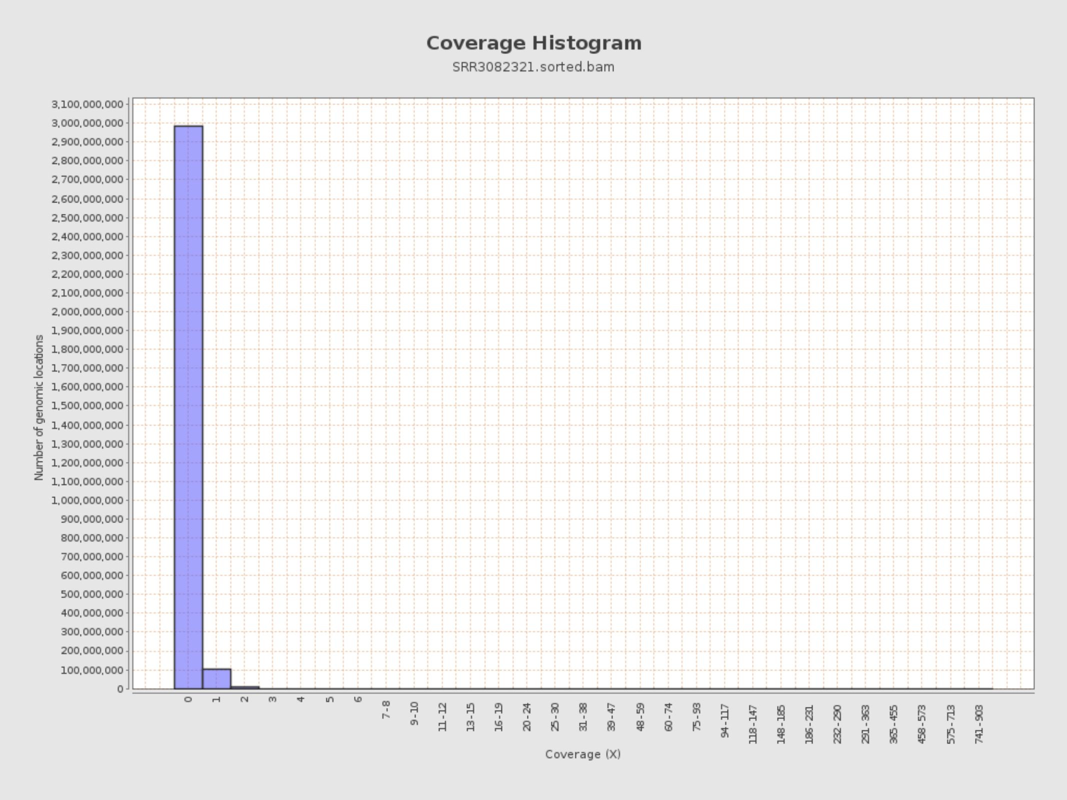
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9947423	0.0399	0.5767
chr2	243199373	10858880	0.0447	0.4222
chr3	198022430	8843064	0.0447	0.2312
chr4	191154276	8709245	0.0456	0.2394
chr5	180915260	7247883	0.0401	0.2206
chr6	171115067	7627580	0.0446	0.2758
chr7	159138663	7132453	0.0448	0.4266

chr8	146364022	6733406	0.046	0.5884
chr9	141213431	5347816	0.0379	0.3184
chr10	135534747	5888783	0.0434	0.3052
chr11	135006516	5864508	0.0434	0.294
chr12	133851895	5905689	0.0441	0.2327
chr13	115169878	4244592	0.0369	0.2103
chr14	107349540	3903803	0.0364	0.2233
chr15	102531392	3589874	0.035	0.2092
chr16	90354753	3456037	0.0382	0.2355
chr17	81195210	3266154	0.0402	0.2399
chr18	78077248	3489415	0.0447	0.5577
chr19	59128983	2376368	0.0402	0.4488
chr20	63025520	2449586	0.0389	0.2208
chr21	48129895	1692226	0.0352	0.2162
chr22	51304566	1294420	0.0252	0.1727
chrMT	16571	5330	0.3216	0.6187
chrX	155270560	7608747	0.049	0.2706
chrY	59373566	305898	0.0052	0.1047

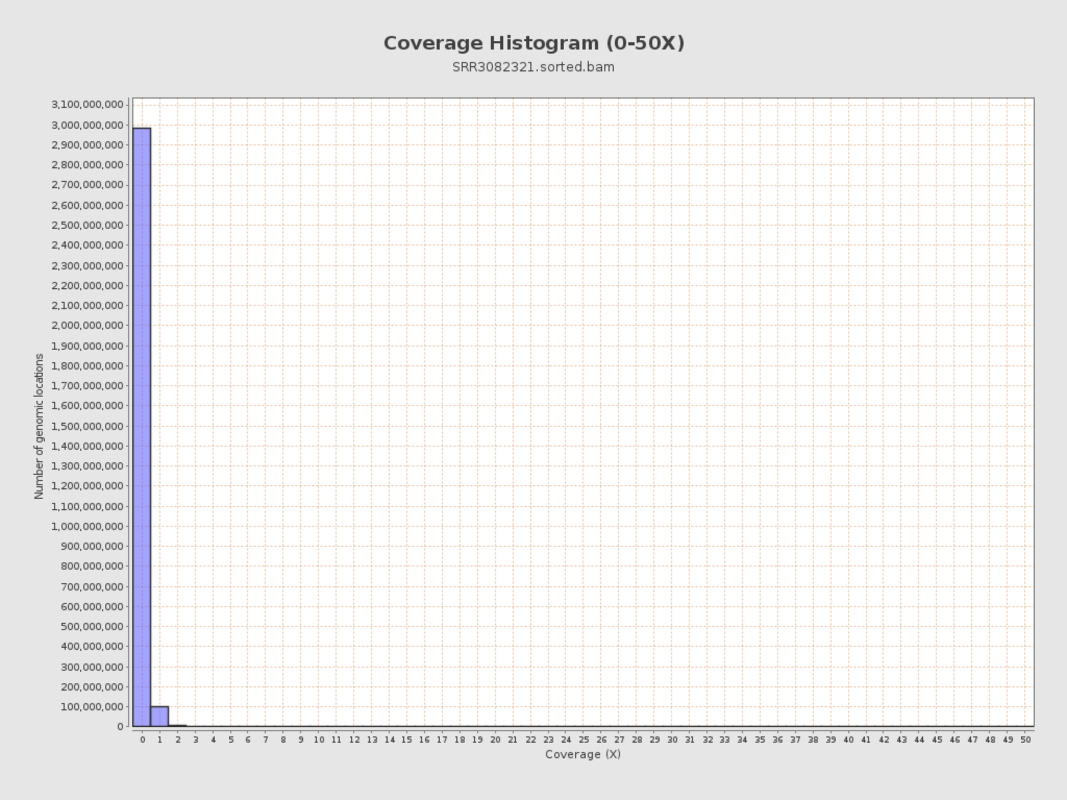
3. Results : Coverage across reference



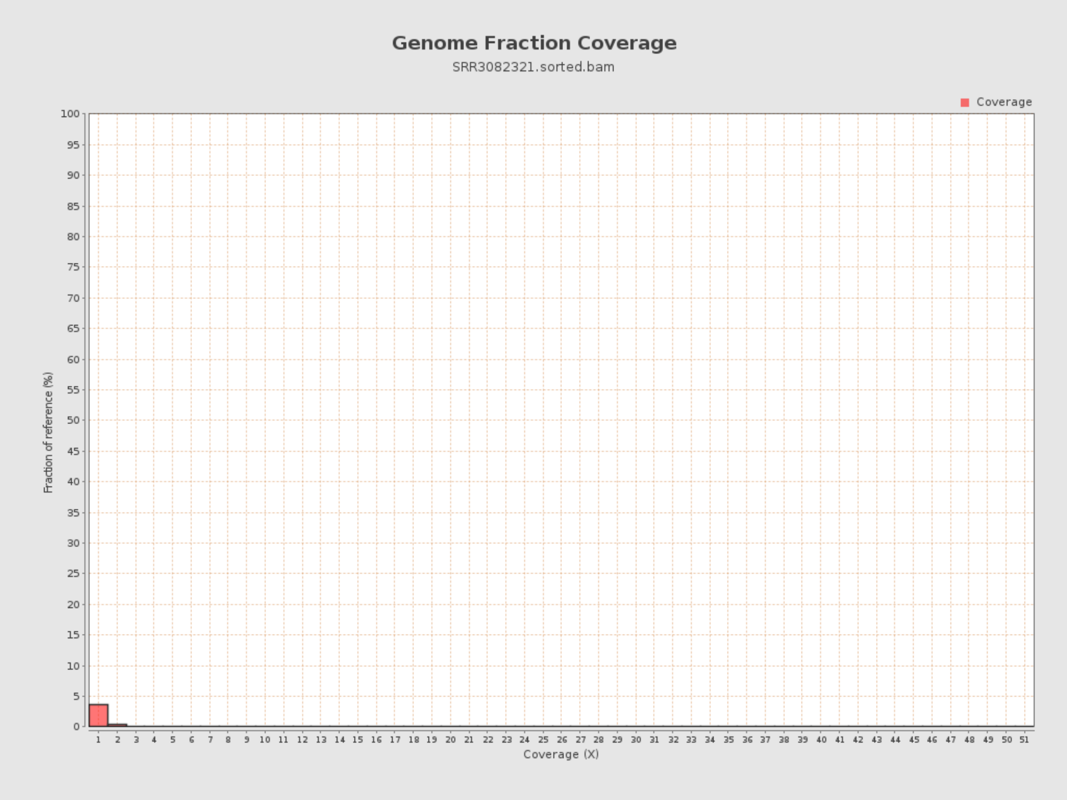
4. Results : Coverage Histogram



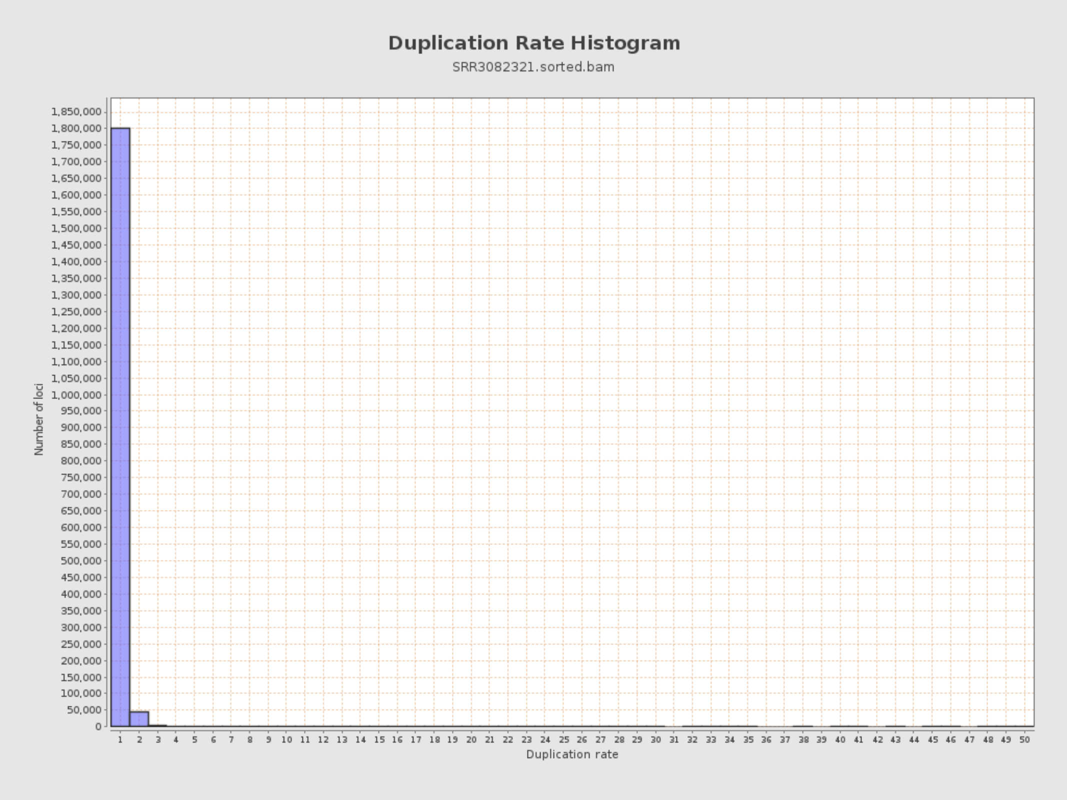
5. Results : Coverage Histogram (0-50X)



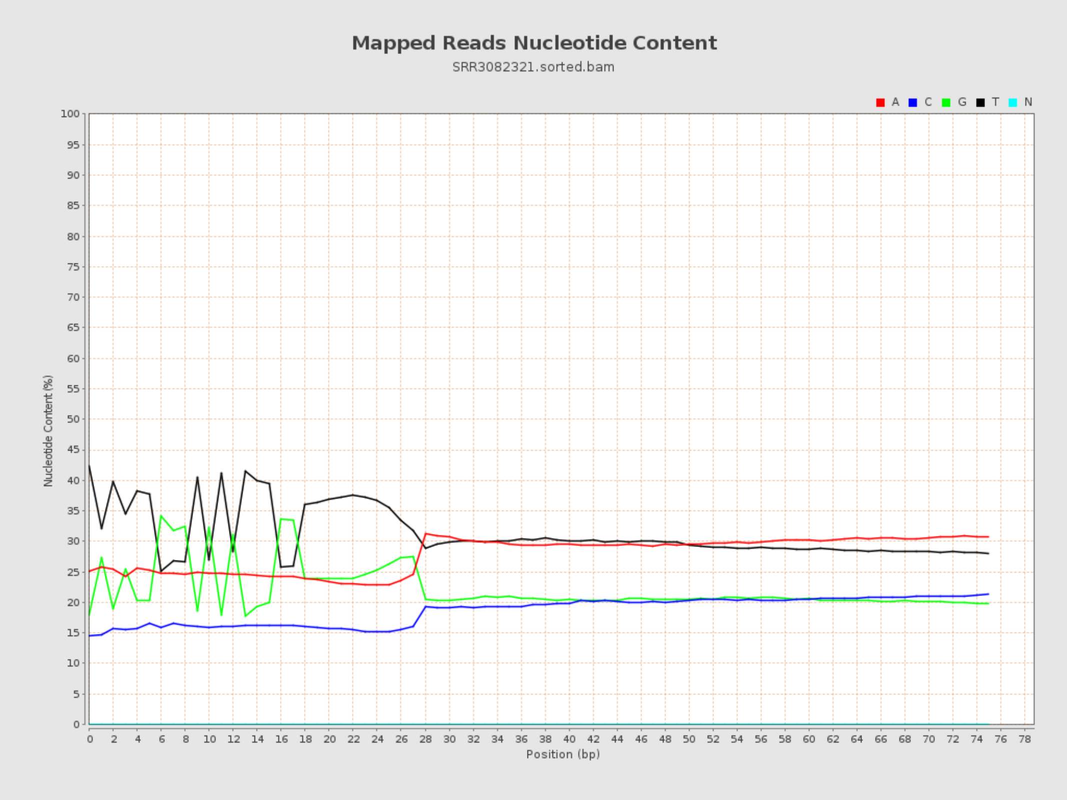
6. Results : Genome Fraction Coverage



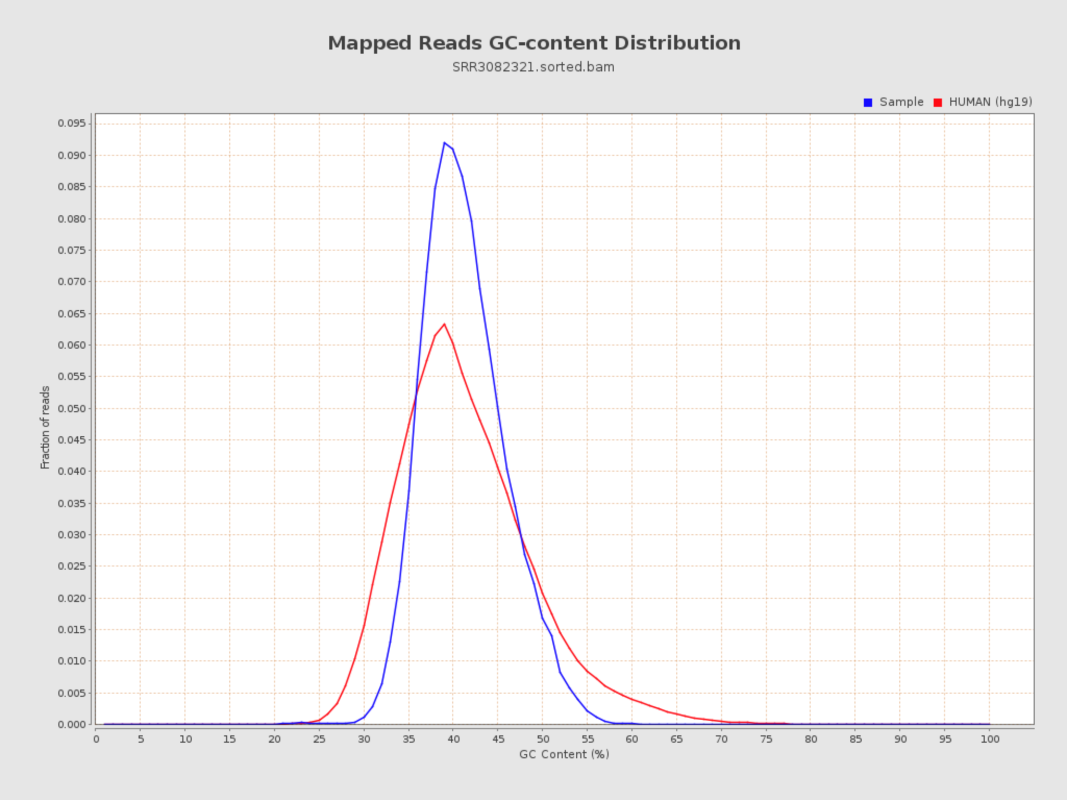
7. Results : Duplication Rate Histogram



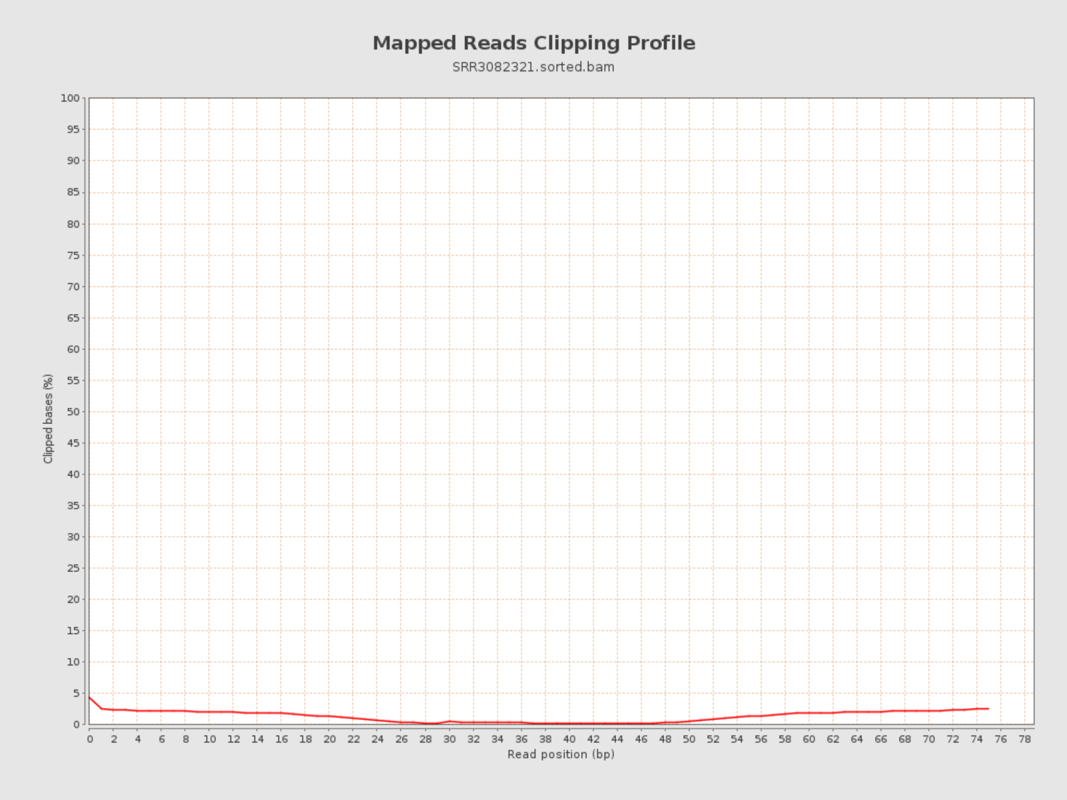
8. Results : Mapped Reads Nucleotide Content



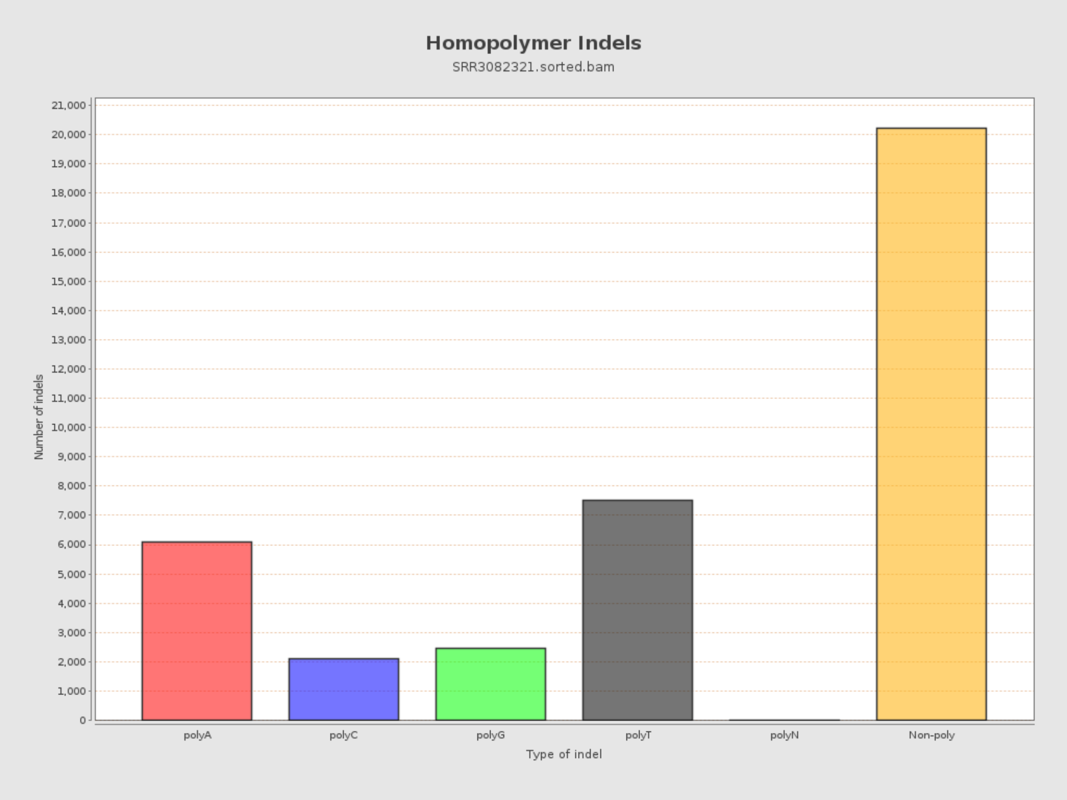
9. Results : Mapped Reads GC-content Distribution



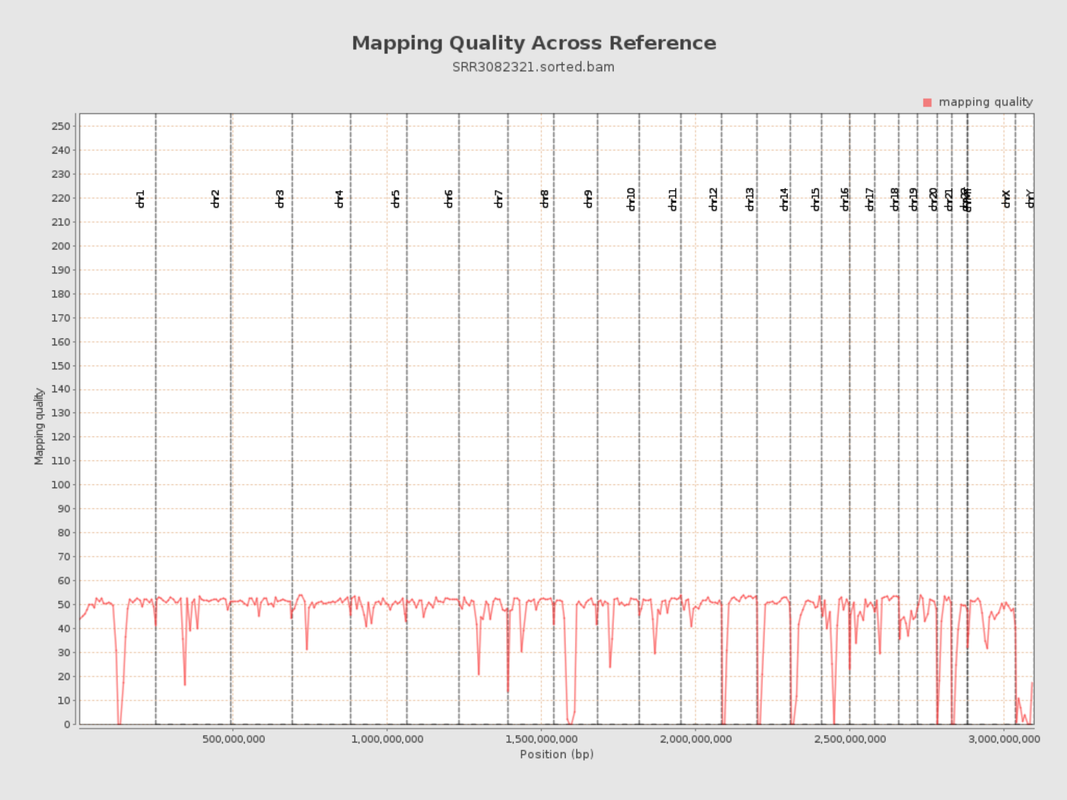
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram