Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:09:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081052.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_SRR3081052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081052.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:09:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081052.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,531,739
Mapped reads	1,196,927 / 78.14%
Unmapped reads	334,812 / 21.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,992 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	29,011 / 1.89%
Duplication rate	1.94%
Clipped reads	598,368 / 39.06%

2.2. ACGT Content

Number/percentage of A's	22,164,327 / 28.7%
Number/percentage of C's	14,697,333 / 19.03%
Number/percentage of T's	23,343,913 / 30.23%
Number/percentage of G's	17,014,919 / 22.03%
Number/percentage of N's	1,036 / 0%
GC Percentage	41.07%

2.3. Coverage

Mean	0.025

Standard Deviation	0.2204

2.4. Mapping Quality

Mean Mapping Quality	46.72

2.5. Mismatches and indels

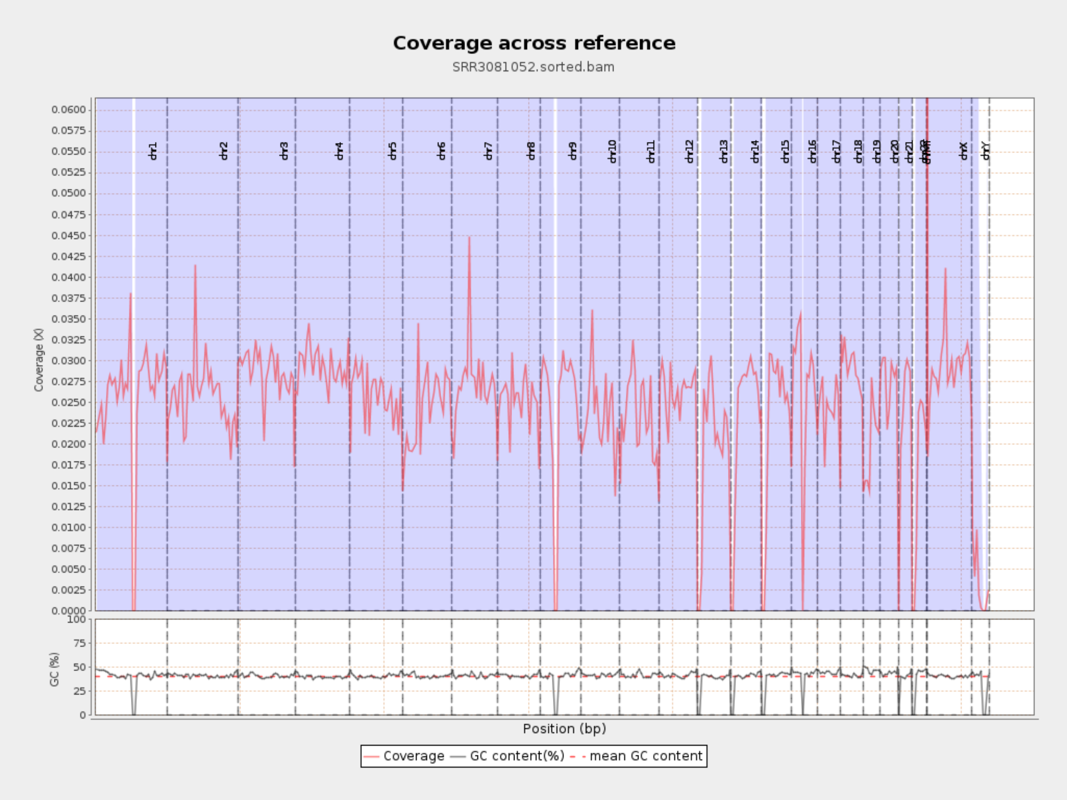
General error rate	0.76%
Mismatches	576,675
Insertions	5,025
Mapped reads with at least one insertion	0.42%
Deletions	16,265
Mapped reads with at least one deletion	1.34%
Homopolymer indels	47.71%

2.6. Chromosome stats

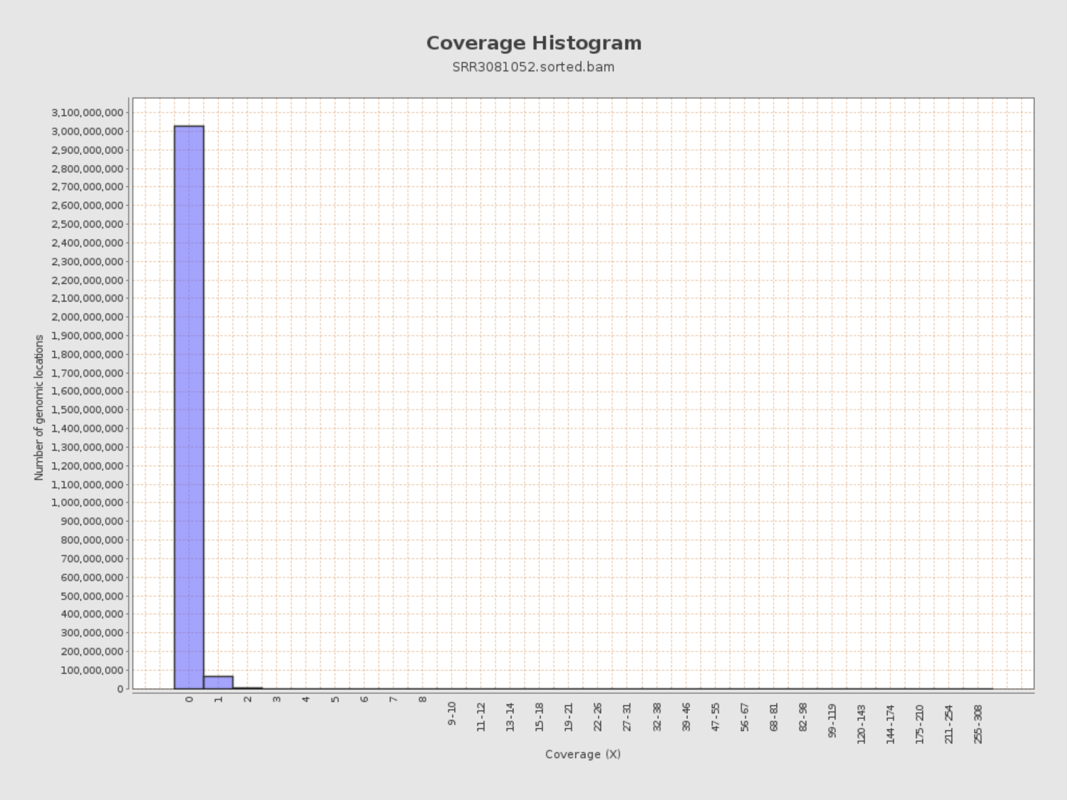
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6375636	0.0256	0.3134
chr2	243199373	6272194	0.0258	0.23
chr3	198022430	5665828	0.0286	0.1824
chr4	191154276	5591718	0.0293	0.1907
chr5	180915260	4709662	0.026	0.1742
chr6	171115067	4141213	0.0242	0.2022
chr7	159138663	4336715	0.0273	0.3215

chr8	146364022	3690019	0.0252	0.2313
chr9	141213431	3417178	0.0242	0.2101
chr10	135534747	3190842	0.0235	0.2052
chr11	135006516	3173389	0.0235	0.2155
chr12	133851895	3517776	0.0263	0.1758
chr13	115169878	2222572	0.0193	0.1491
chr14	107349540	2471761	0.023	0.1704
chr15	102531392	2298412	0.0224	0.1662
chr16	90354753	2328868	0.0258	0.1836
chr17	81195210	1954816	0.0241	0.1887
chr18	78077248	2287929	0.0293	0.3809
chr19	59128983	1189202	0.0201	0.2428
chr20	63025520	1712891	0.0272	0.1809
chr21	48129895	1115251	0.0232	0.173
chr22	51304566	835482	0.0163	0.1367
chrMT	16571	12992	0.784	1.0422
chrX	155270560	4546422	0.0293	0.2006
chrY	59373566	190946	0.0032	0.0809

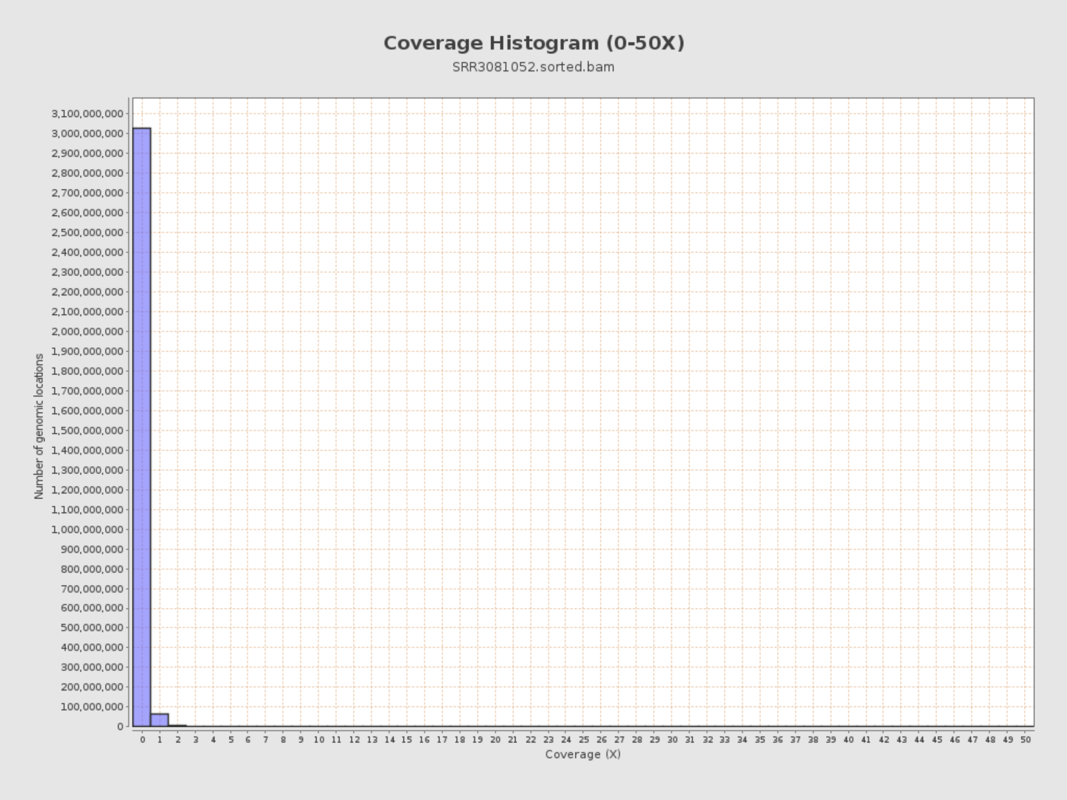
3. Results : Coverage across reference



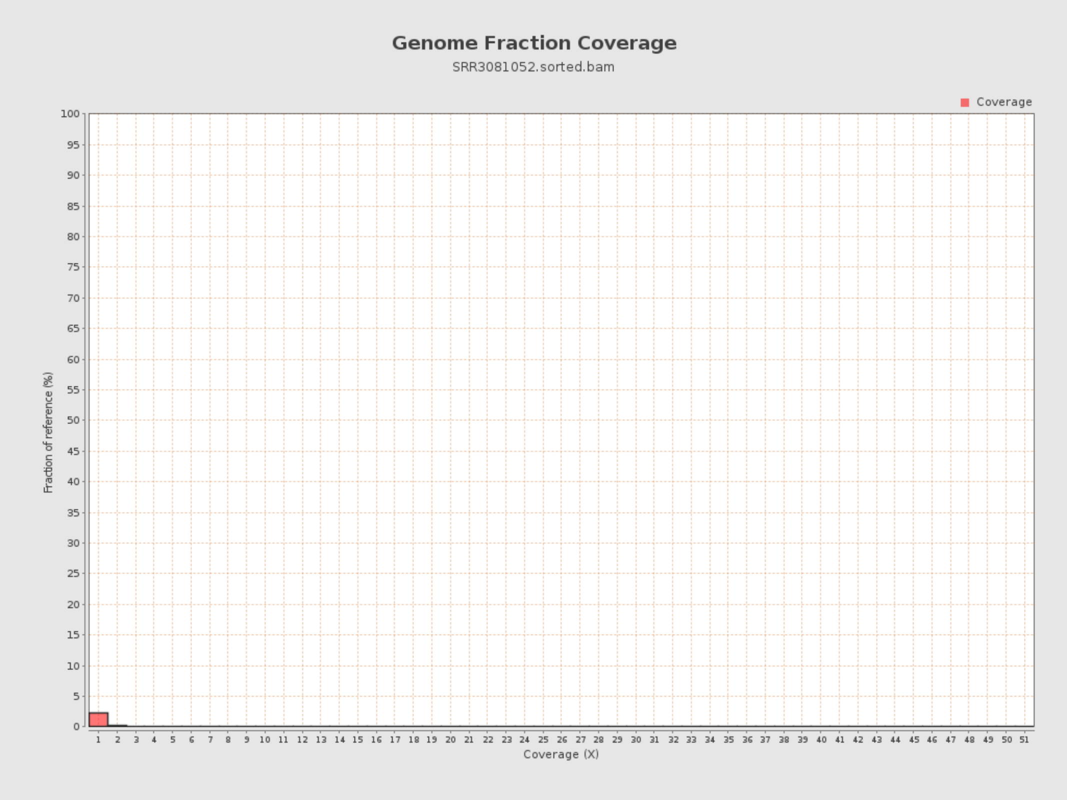
4. Results : Coverage Histogram



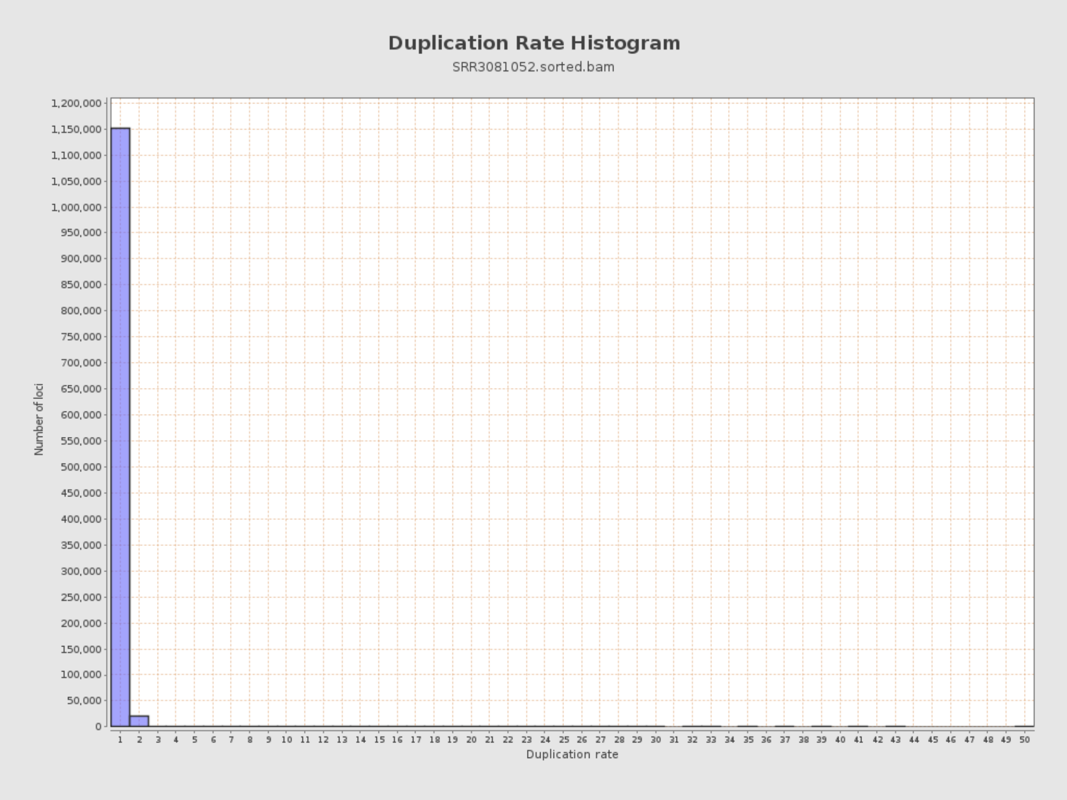
5. Results : Coverage Histogram (0-50X)



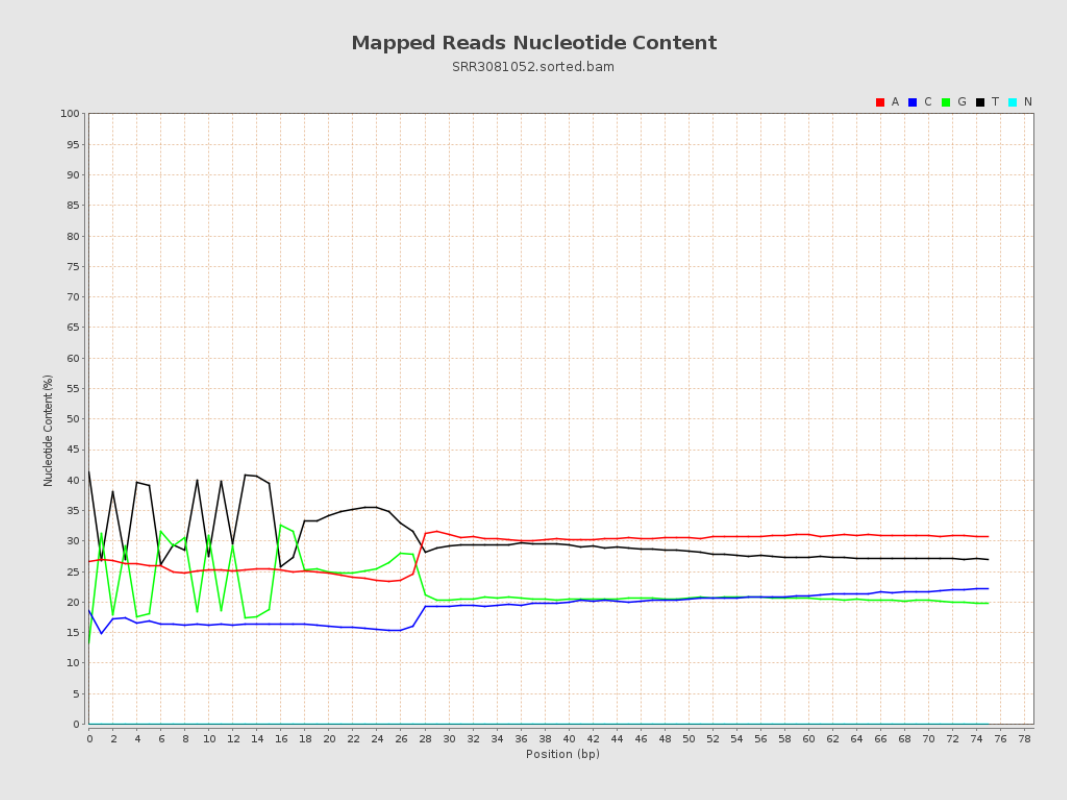
6. Results : Genome Fraction Coverage



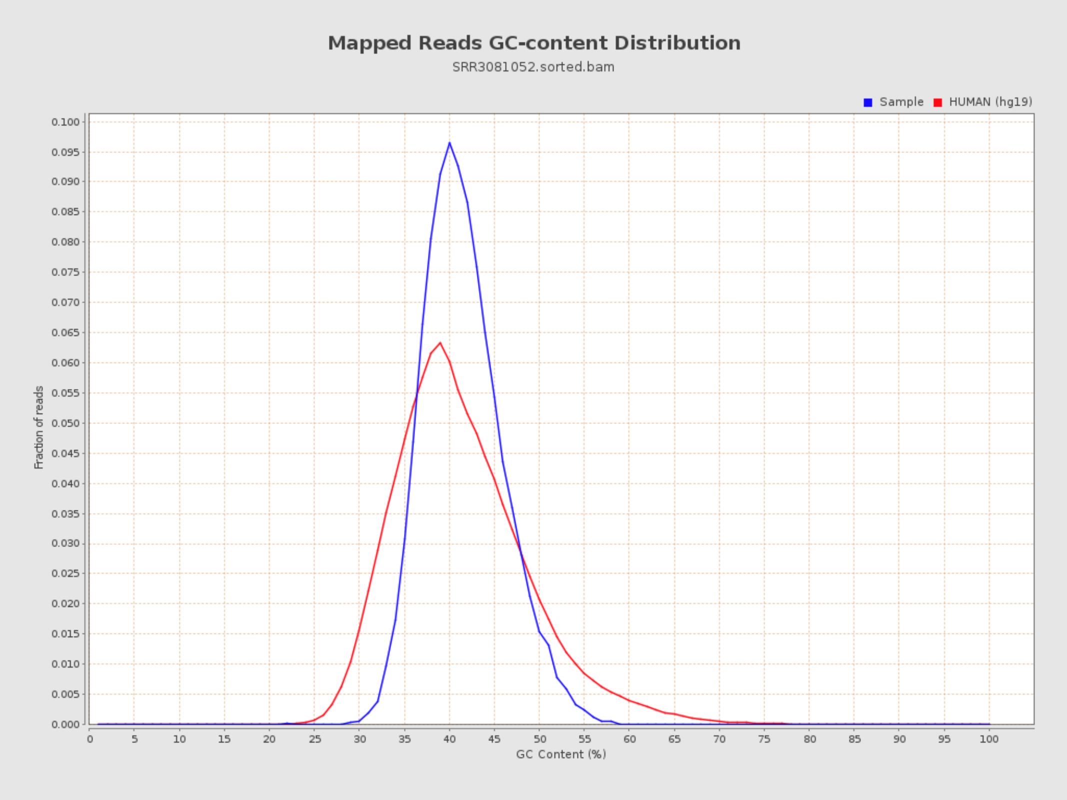
7. Results : Duplication Rate Histogram



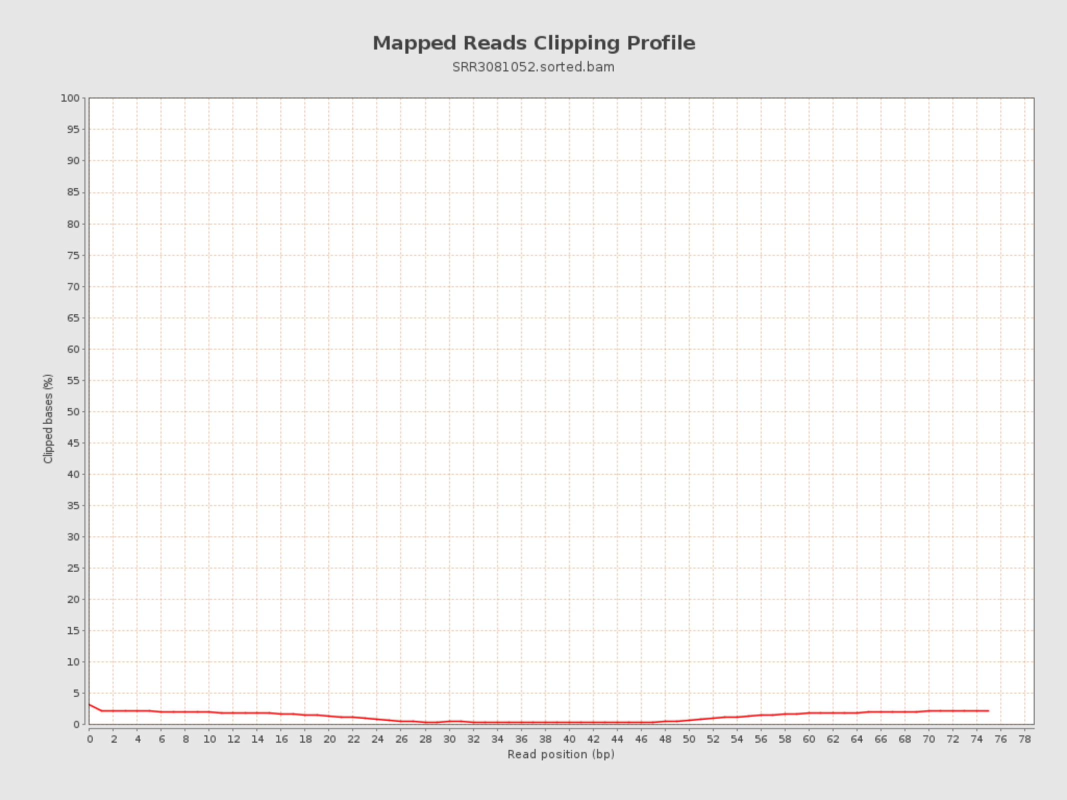
8. Results : Mapped Reads Nucleotide Content



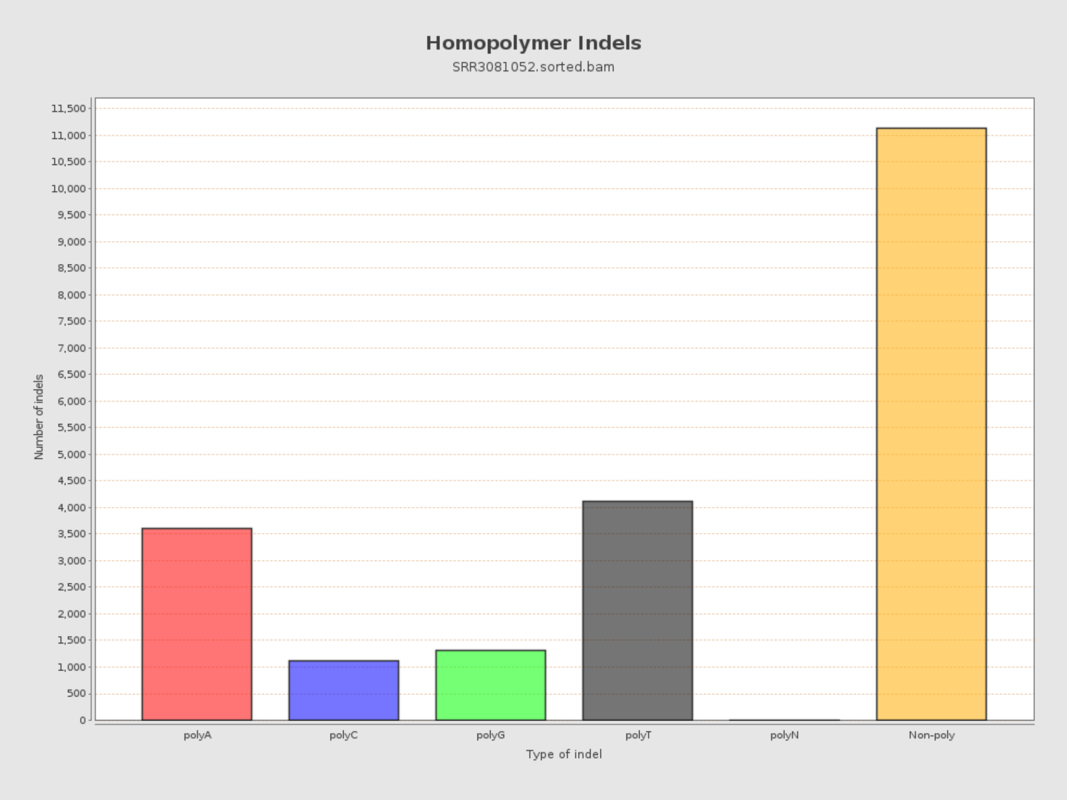
9. Results : Mapped Reads GC-content Distribution



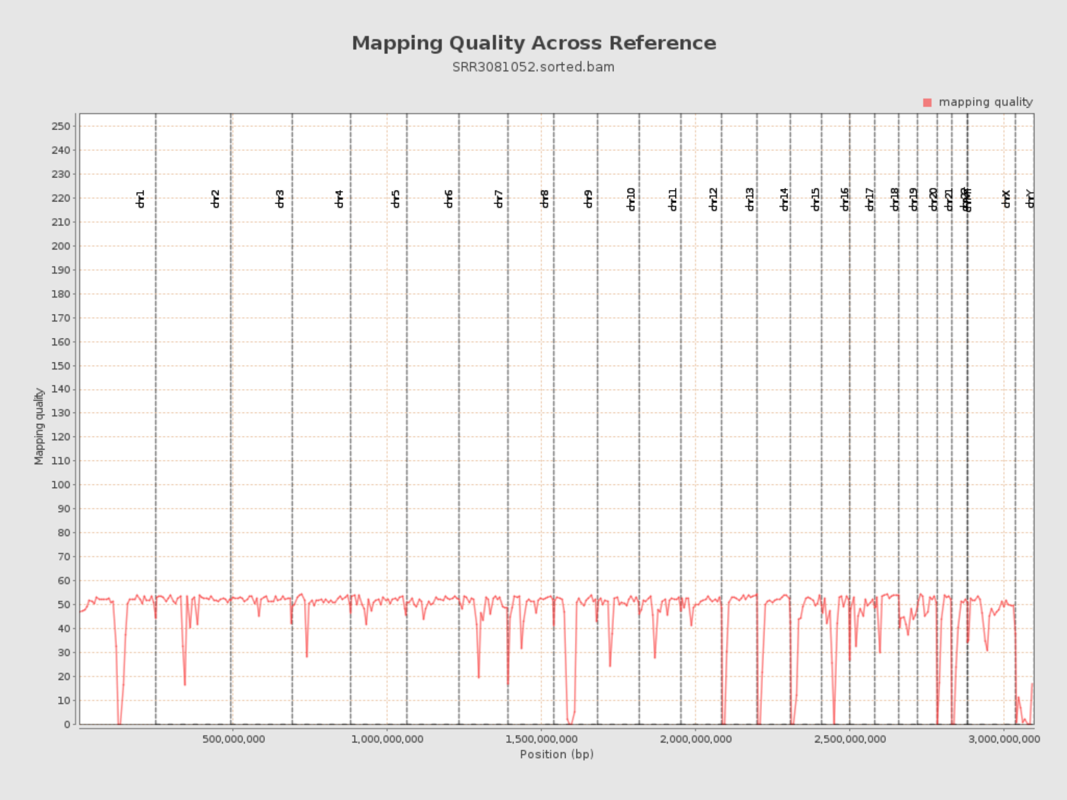
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram