Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:24:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081022.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_SRR3081022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081022.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:24:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,120,044
Mapped reads	1,502,140 / 70.85%
Unmapped reads	617,904 / 29.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,036 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	41,494 / 1.96%
Duplication rate	2.21%
Clipped reads	953,755 / 44.99%

2.2. ACGT Content

Number/percentage of A's	25,969,559 / 28.39%
Number/percentage of C's	18,714,039 / 20.46%
Number/percentage of T's	25,805,510 / 28.21%
Number/percentage of G's	20,974,103 / 22.93%
Number/percentage of N's	1,044 / 0%
GC Percentage	43.39%

2.3. Coverage

Mean	0.0296

Standard Deviation	0.2343

2.4. Mapping Quality

Mean Mapping Quality	43.63

2.5. Mismatches and indels

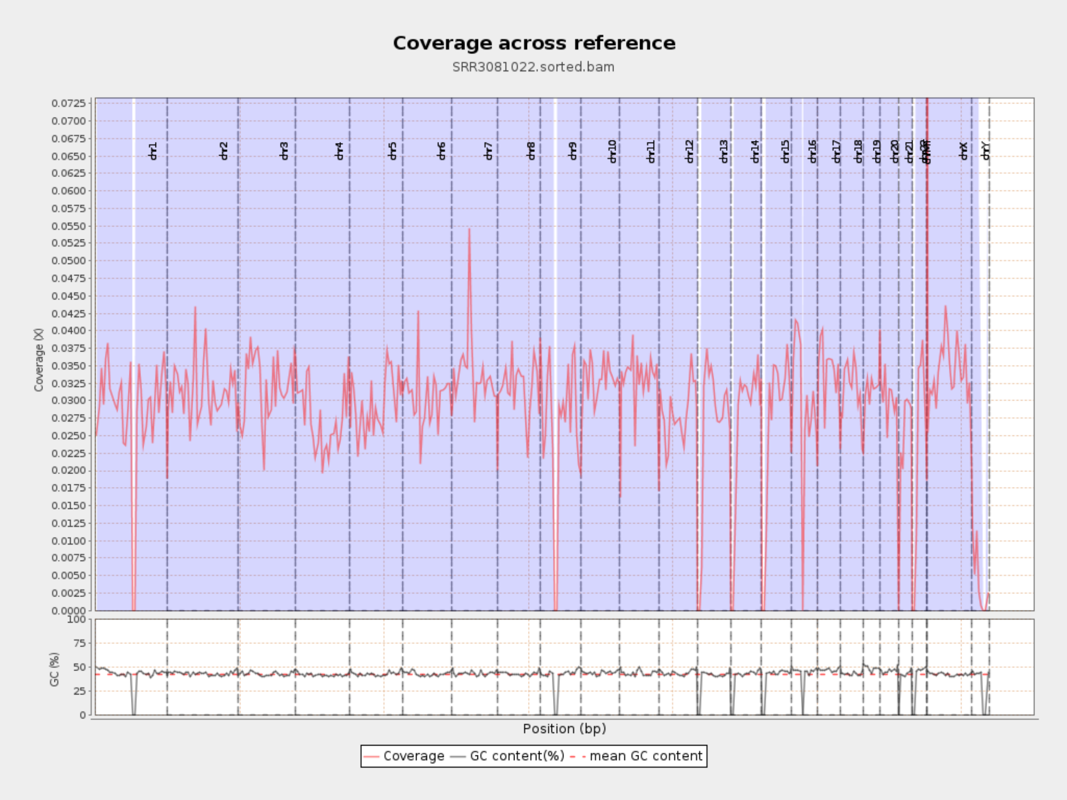
General error rate	0.77%
Mismatches	697,264
Insertions	6,309
Mapped reads with at least one insertion	0.42%
Deletions	18,696
Mapped reads with at least one deletion	1.23%
Homopolymer indels	44.55%

2.6. Chromosome stats

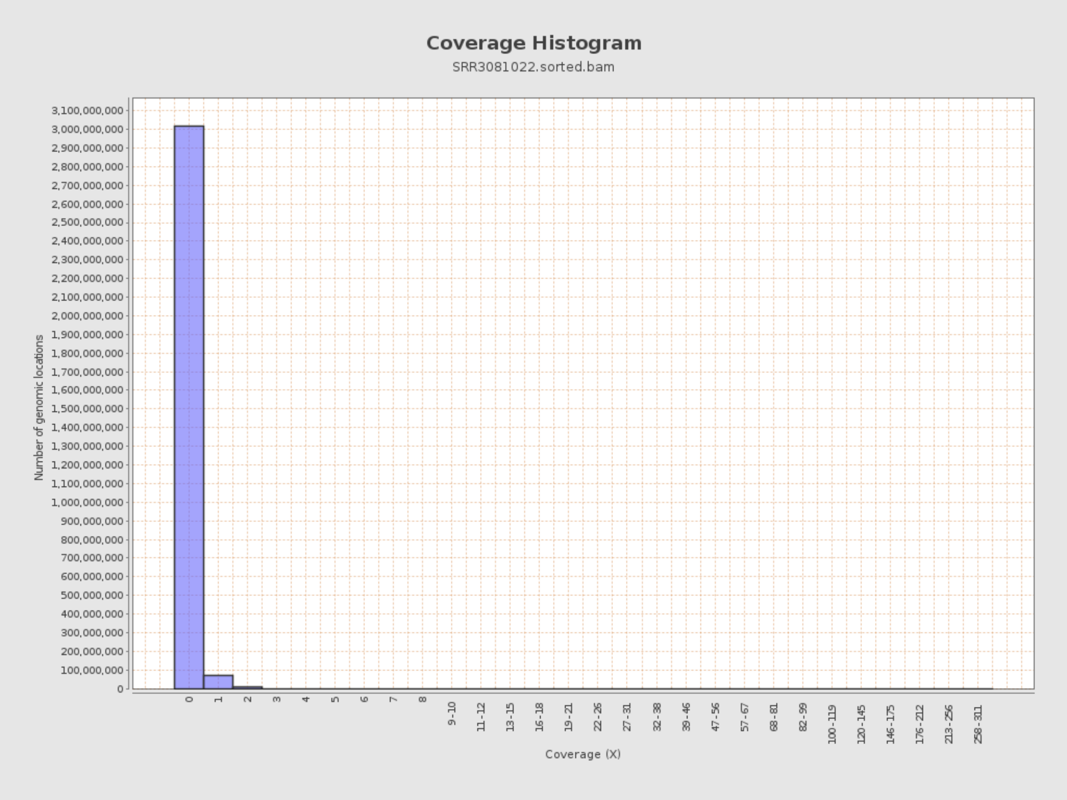
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7103742	0.0285	0.2697
chr2	243199373	7643008	0.0314	0.2637
chr3	198022430	6304163	0.0318	0.1975
chr4	191154276	5253627	0.0275	0.1933
chr5	180915260	5361909	0.0296	0.1916
chr6	171115067	5222856	0.0305	0.2336
chr7	159138663	5438444	0.0342	0.3781

chr8	146364022	4646005	0.0317	0.235
chr9	141213431	3705417	0.0262	0.2164
chr10	135534747	4503283	0.0332	0.2279
chr11	135006516	4492143	0.0333	0.2389
chr12	133851895	3773747	0.0282	0.1875
chr13	115169878	2981346	0.0259	0.1777
chr14	107349540	2832267	0.0264	0.1882
chr15	102531392	2716972	0.0265	0.1963
chr16	90354753	2609368	0.0289	0.2004
chr17	81195210	2786605	0.0343	0.2181
chr18	78077248	2493489	0.0319	0.3779
chr19	59128983	1871139	0.0316	0.2409
chr20	63025520	1870979	0.0297	0.1987
chr21	48129895	1166116	0.0242	0.1828
chr22	51304566	1163118	0.0227	0.1673
chrMT	16571	26891	1.6228	1.7298
chrX	155270560	5294814	0.0341	0.2208
chrY	59373566	235790	0.004	0.0878

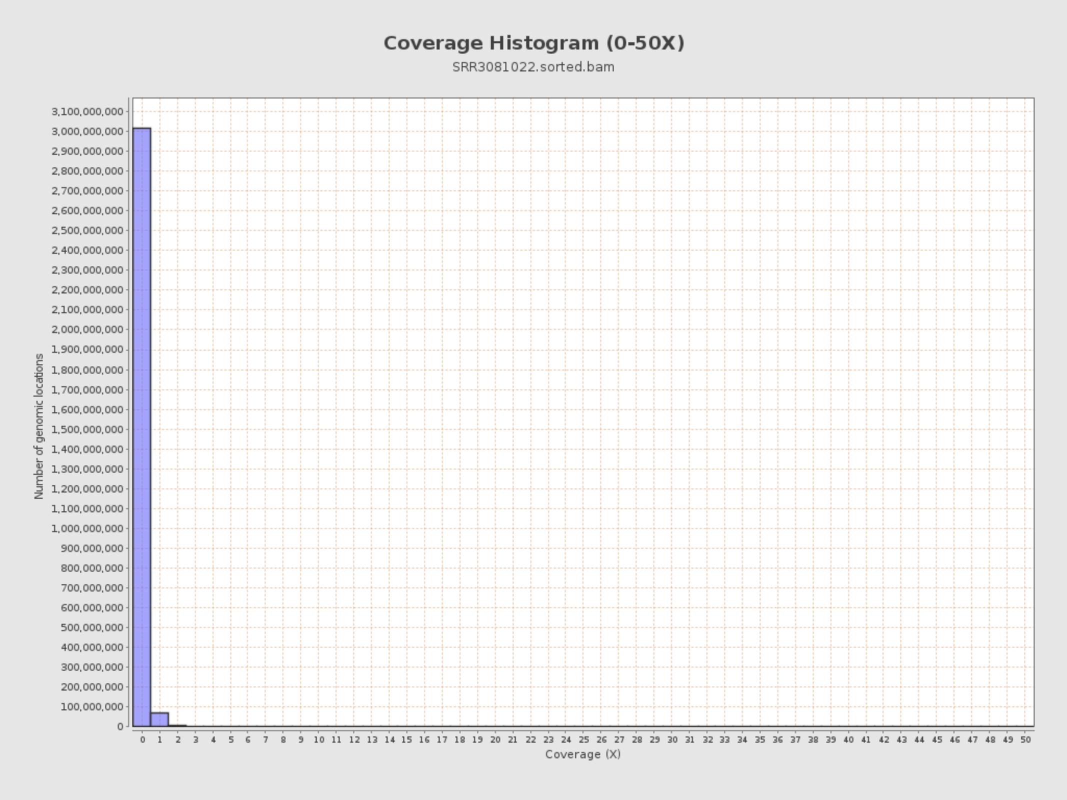
3. Results : Coverage across reference



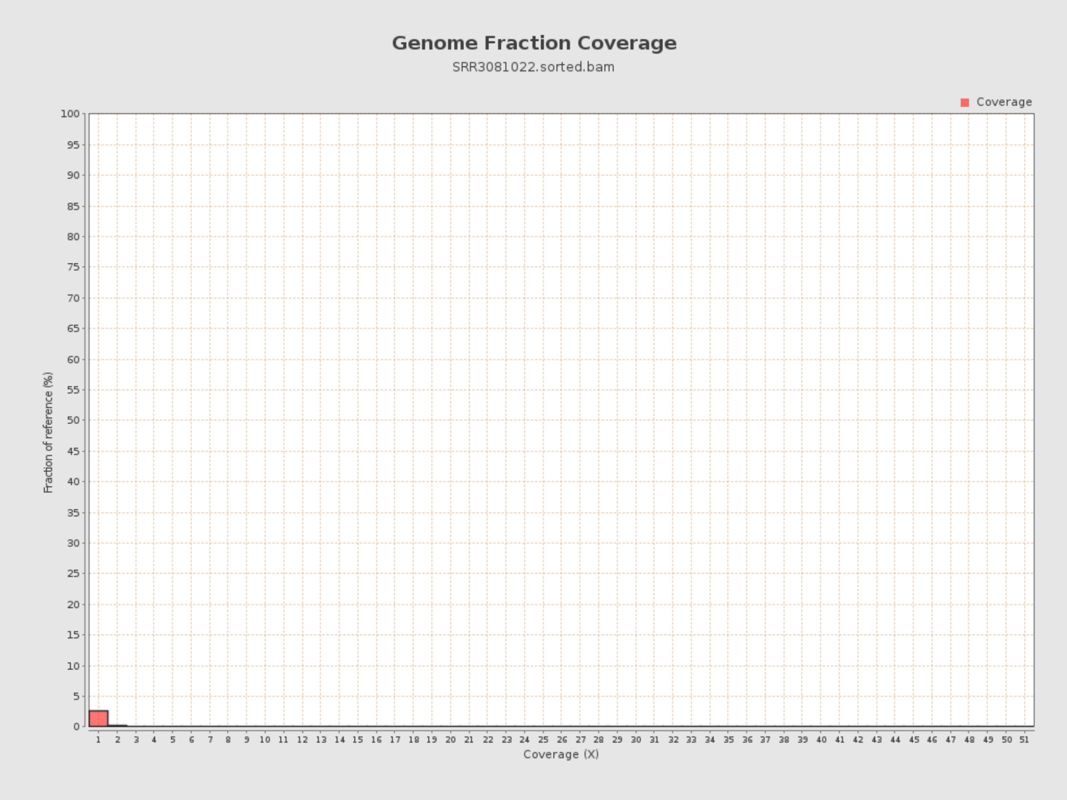
4. Results : Coverage Histogram



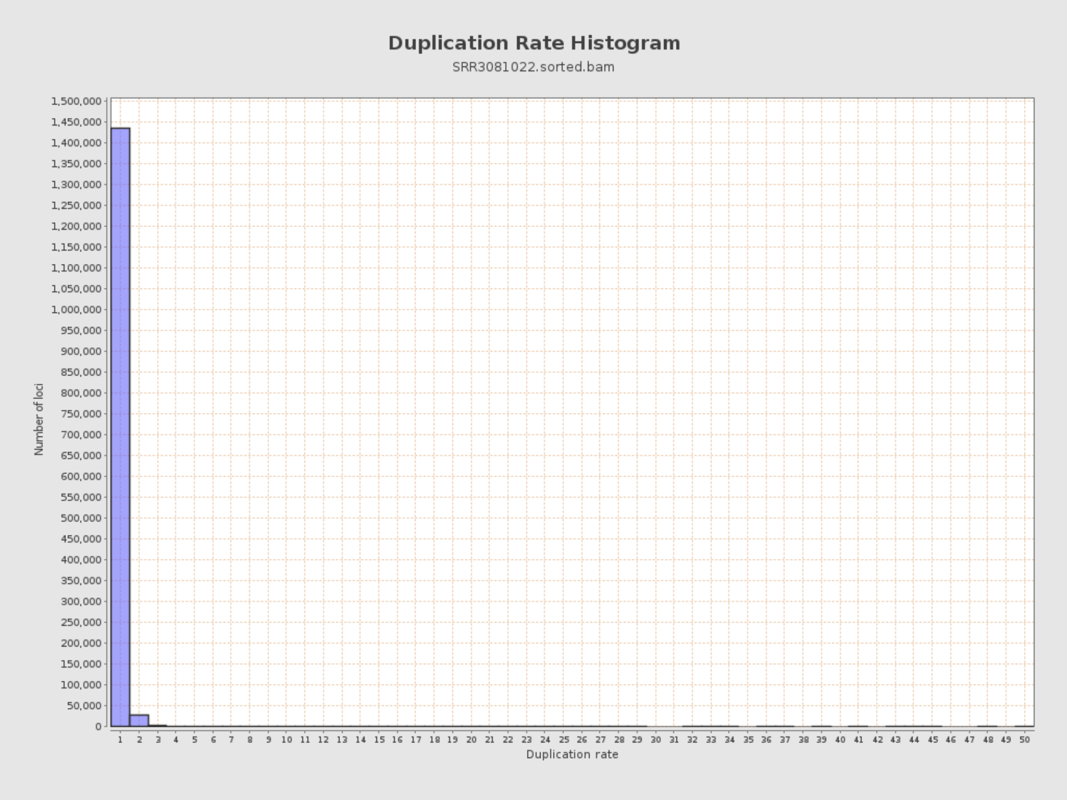
5. Results : Coverage Histogram (0-50X)



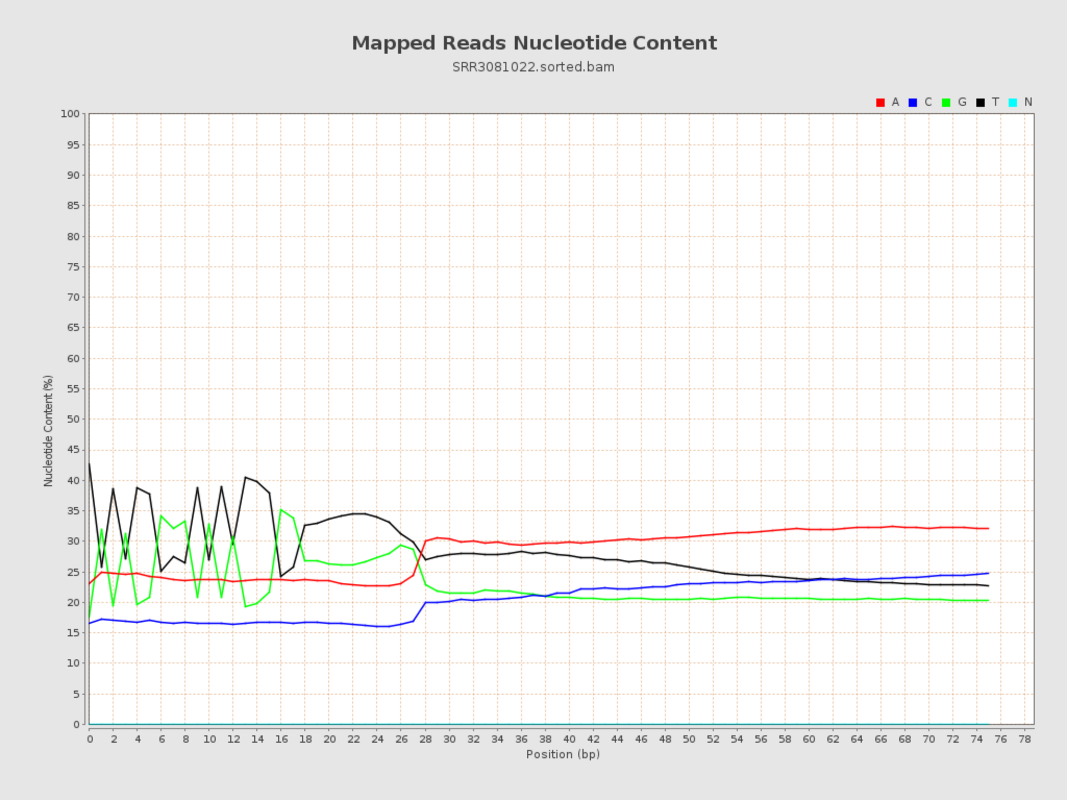
6. Results : Genome Fraction Coverage



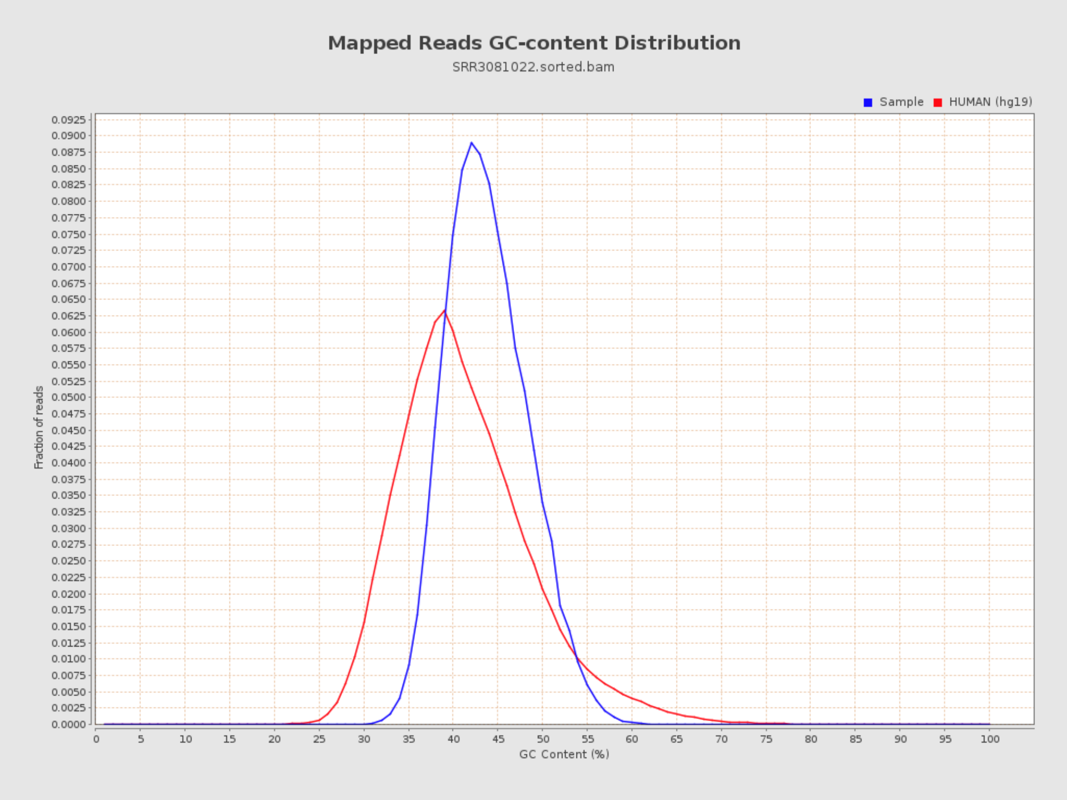
7. Results : Duplication Rate Histogram



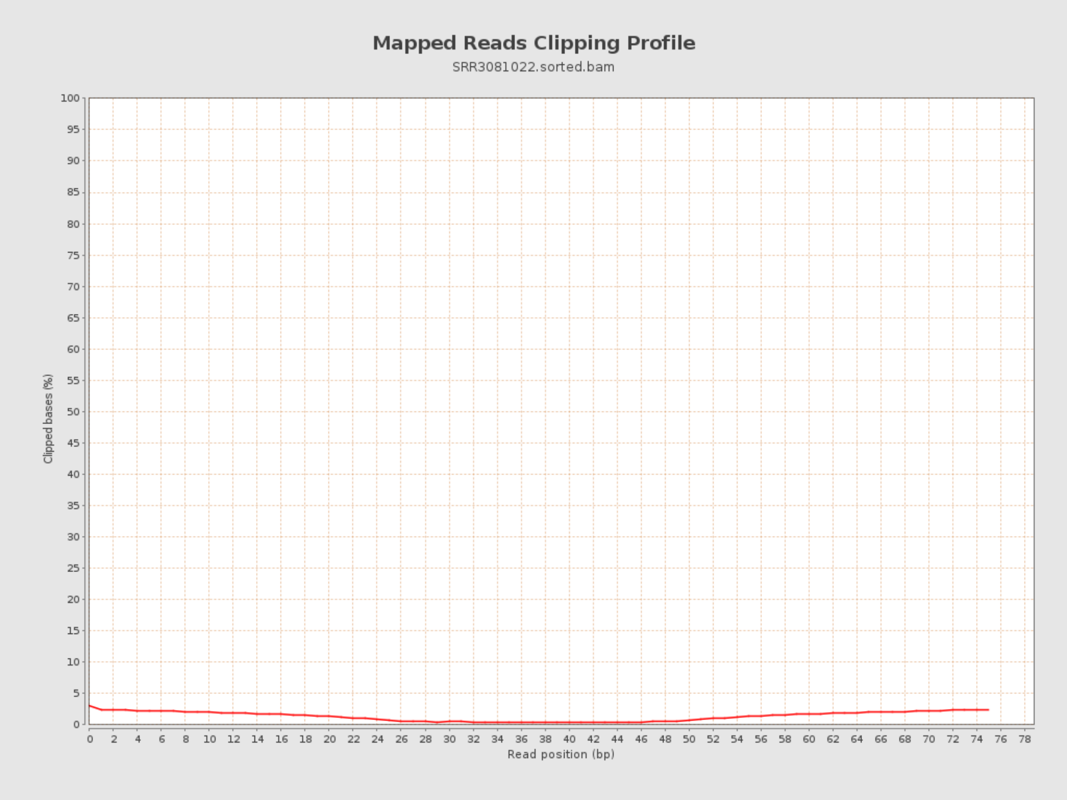
8. Results : Mapped Reads Nucleotide Content



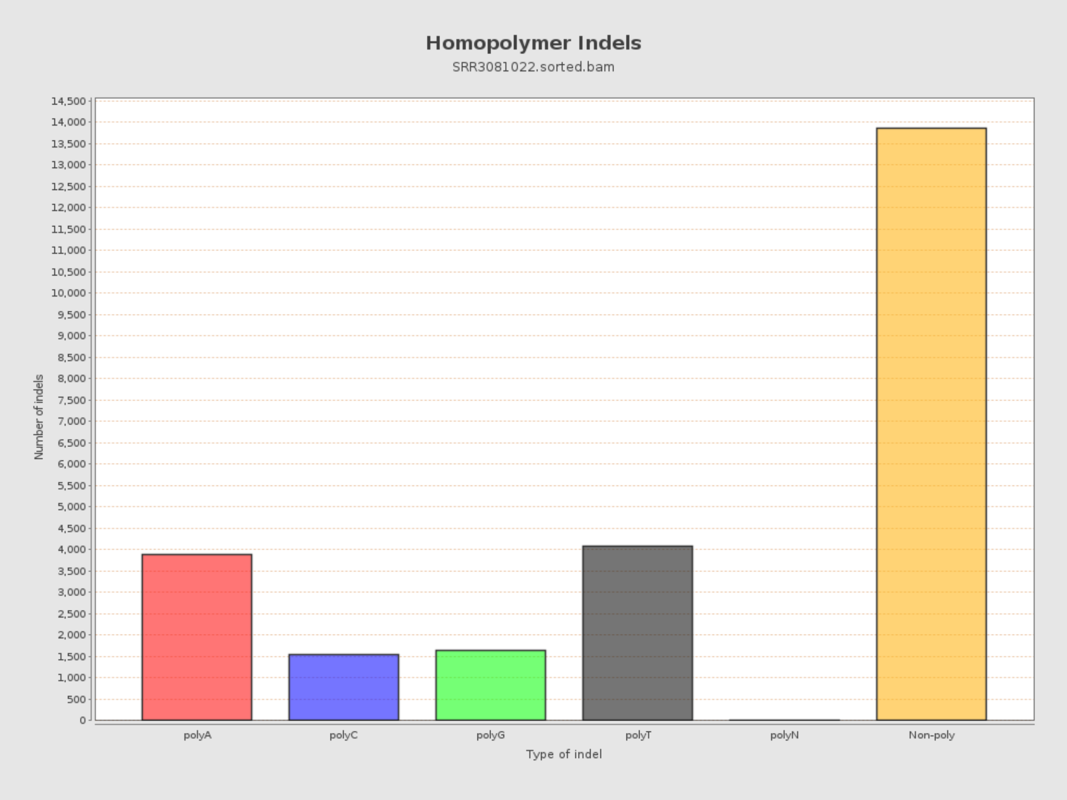
9. Results : Mapped Reads GC-content Distribution



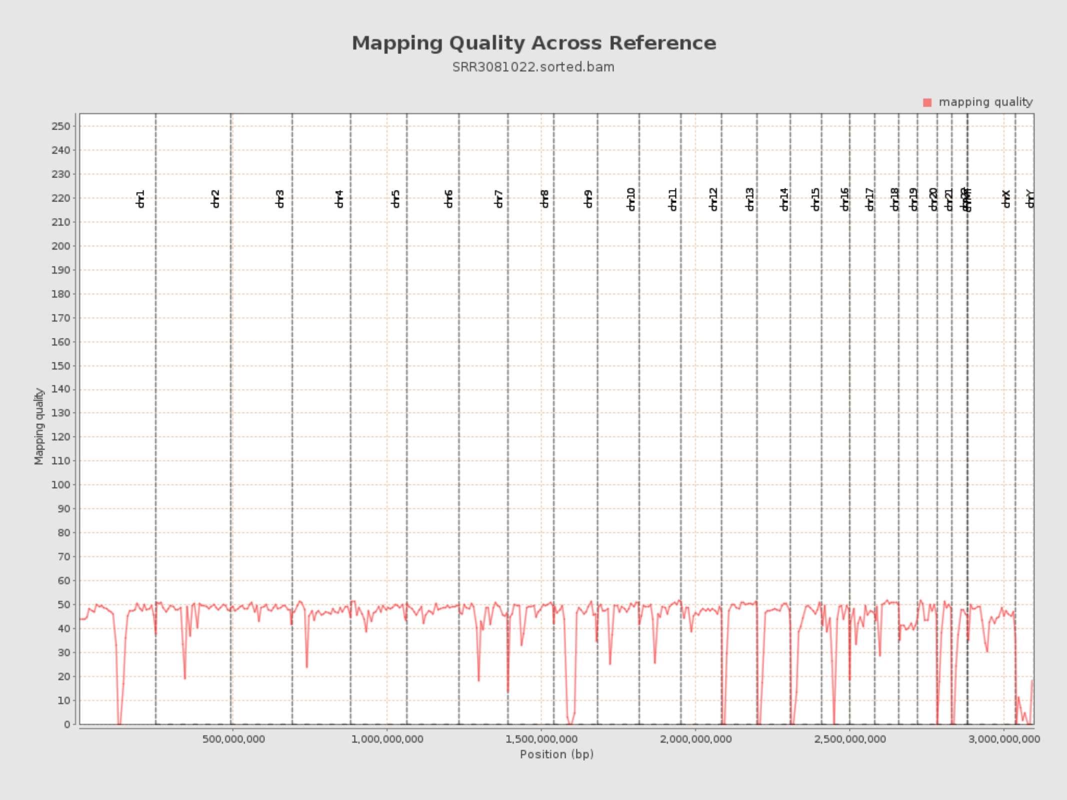
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram