Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:16:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549070.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_SRR1549070 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549070.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:16:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,195,714
Mapped reads	8,862,742 / 86.93%
Unmapped reads	1,332,972 / 13.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	316,260 / 3.1%
Duplication rate	2.51%
Clipped reads	406,782 / 3.99%

2.2. ACGT Content

Number/percentage of A's	103,937,447 / 29.52%
Number/percentage of C's	71,996,109 / 20.45%
Number/percentage of T's	104,328,796 / 29.63%
Number/percentage of G's	71,827,224 / 20.4%
Number/percentage of N's	6,635 / 0%
GC Percentage	40.85%

2.3. Coverage

Mean	0.1137
Standard Deviation	0.9269

2.4. Mapping Quality

Mean Mapping Quality	43.96

2.5. Mismatches and indels

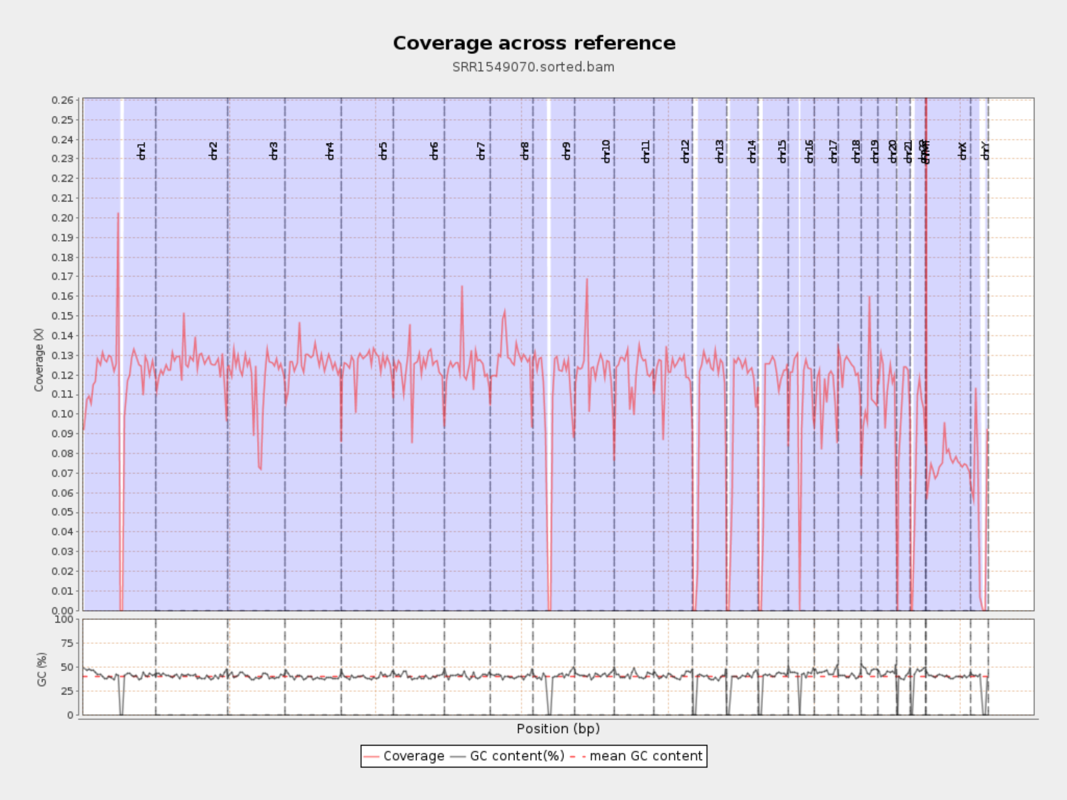
General error rate	0.31%
Mismatches	1,079,872
Insertions	8,778
Mapped reads with at least one insertion	0.1%
Deletions	28,959
Mapped reads with at least one deletion	0.33%
Homopolymer indels	43.96%

2.6. Chromosome stats

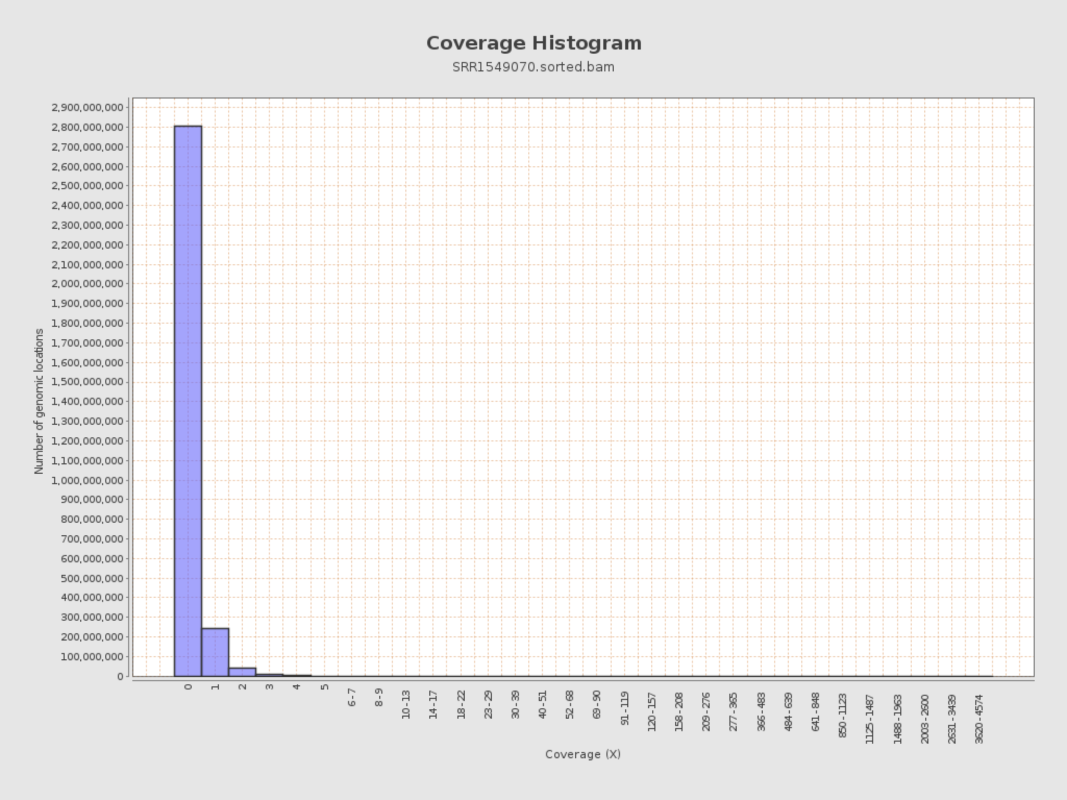
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28872844	0.1158	2.035
chr2	243199373	30566610	0.1257	0.5837
chr3	198022430	23516122	0.1188	0.4
chr4	191154276	24125347	0.1262	0.4439
chr5	180915260	22708896	0.1255	0.4179
chr6	171115067	21194990	0.1239	0.4933
chr7	159138663	19783953	0.1243	0.8162
chr8	146364022	18751971	0.1281	2.2783

chr9	141213431	14973723	0.106	0.5533
chr10	135534747	16797561	0.1239	0.672
chr11	135006516	16418024	0.1216	0.5667
chr12	133851895	16278399	0.1216	0.425
chr13	115169878	11946864	0.1037	0.367
chr14	107349540	10983616	0.1023	0.4183
chr15	102531392	10197222	0.0995	0.3604
chr16	90354753	9647924	0.1068	0.4313
chr17	81195210	8966716	0.1104	0.4243
chr18	78077248	9655106	0.1237	1.0673
chr19	59128983	6402766	0.1083	1.4946
chr20	63025520	7261267	0.1152	0.4037
chr21	48129895	4665381	0.0969	0.4231
chr22	51304566	3857170	0.0752	0.3466
chrMT	16571	15480	0.9342	1.4117
chrX	155270560	11551228	0.0744	0.3975
chrY	59373566	2994317	0.0504	0.4793

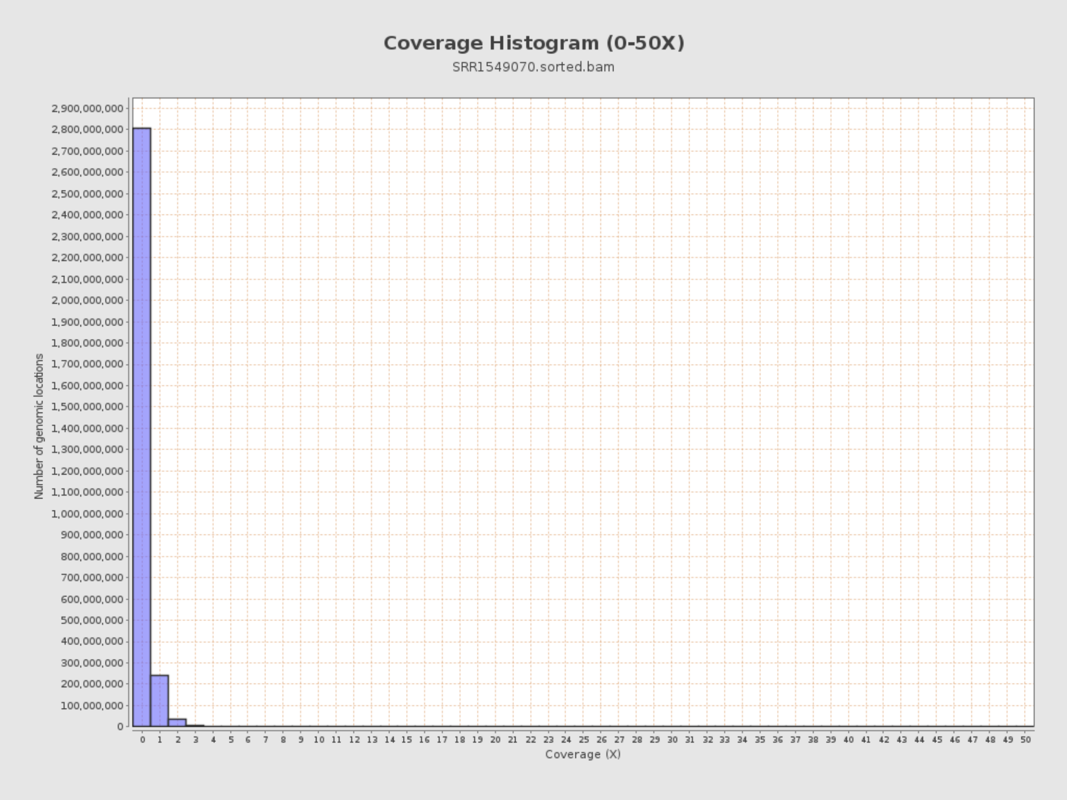
3. Results : Coverage across reference



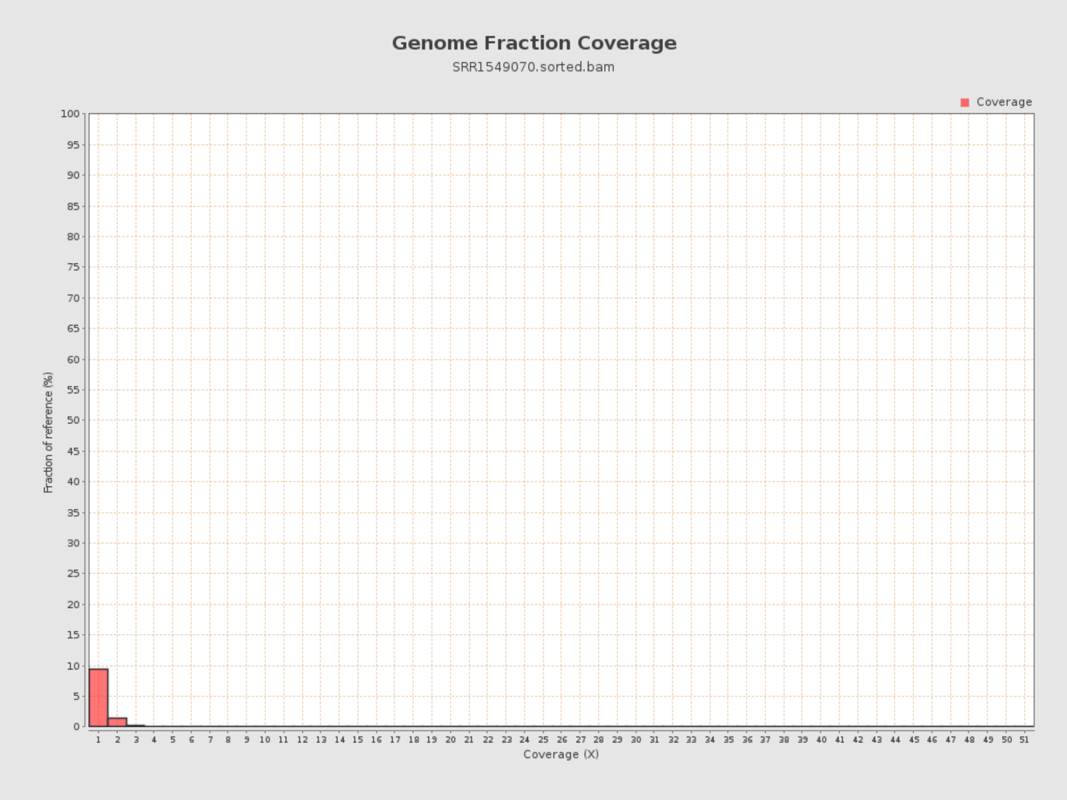
4. Results : Coverage Histogram



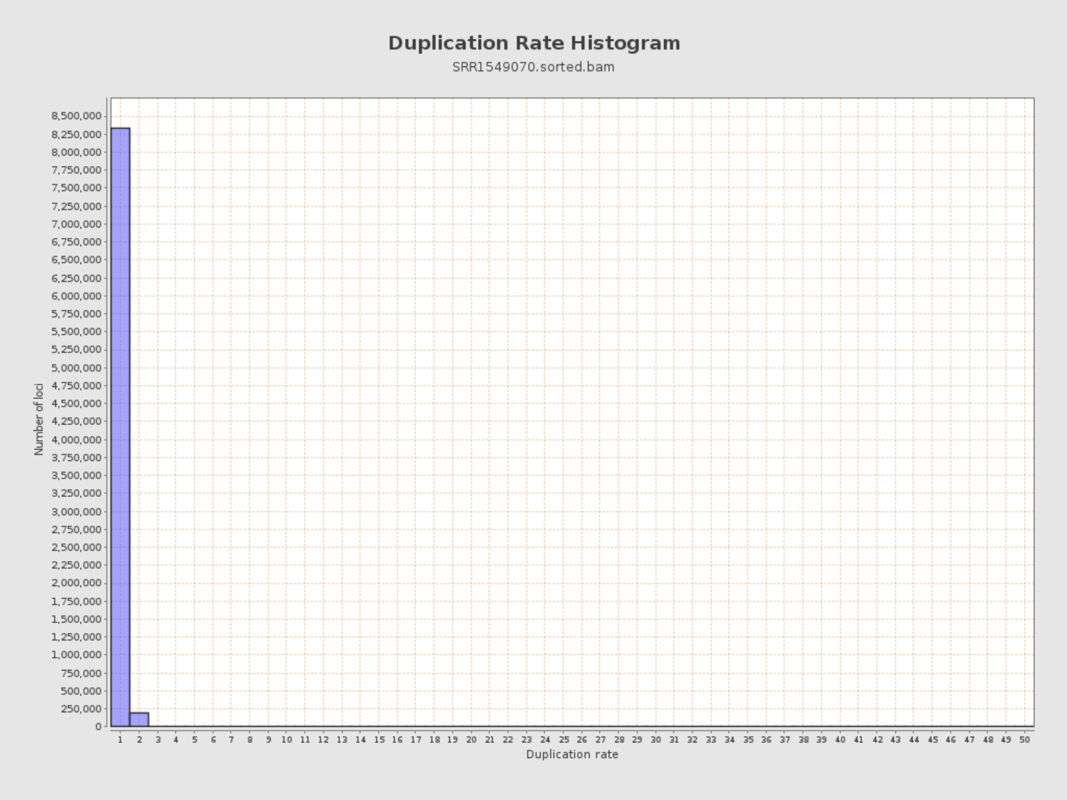
5. Results : Coverage Histogram (0-50X)



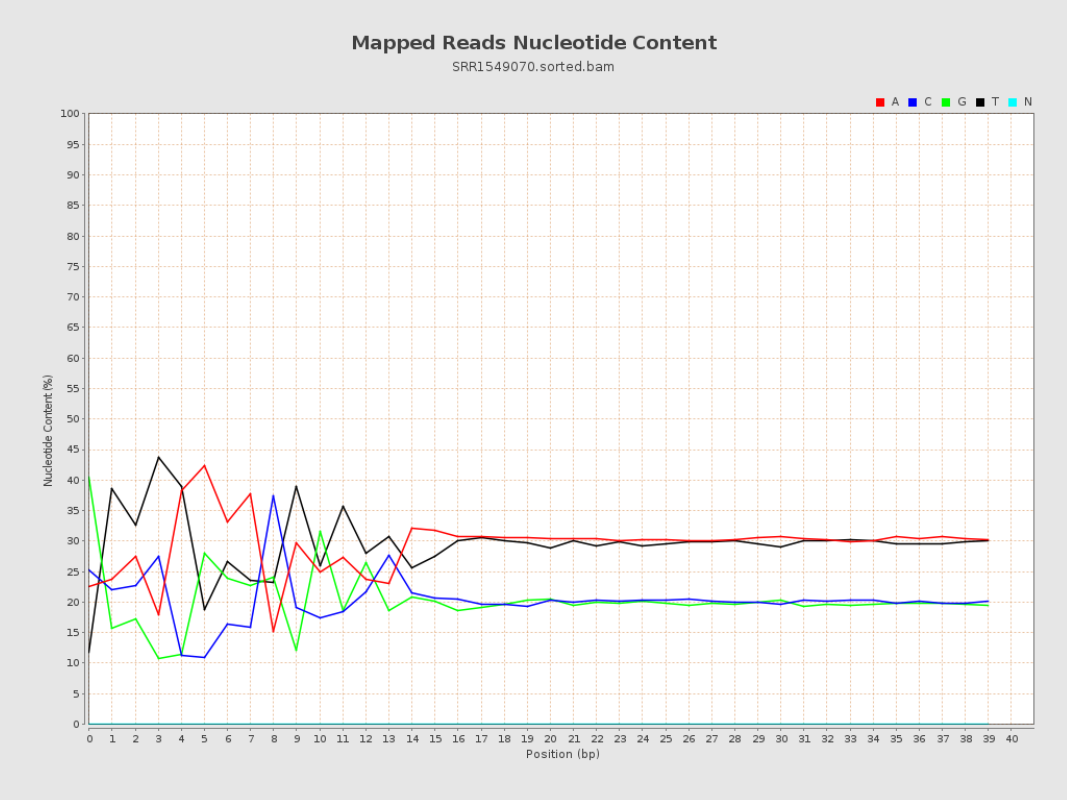
6. Results : Genome Fraction Coverage



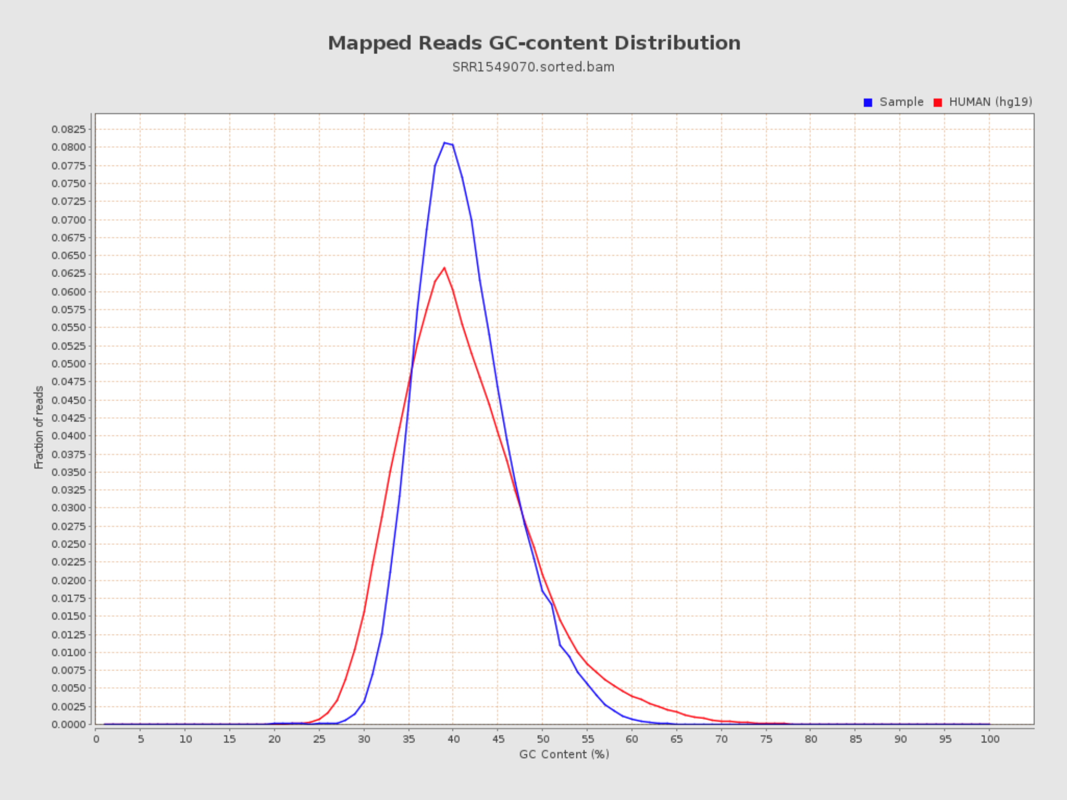
7. Results : Duplication Rate Histogram



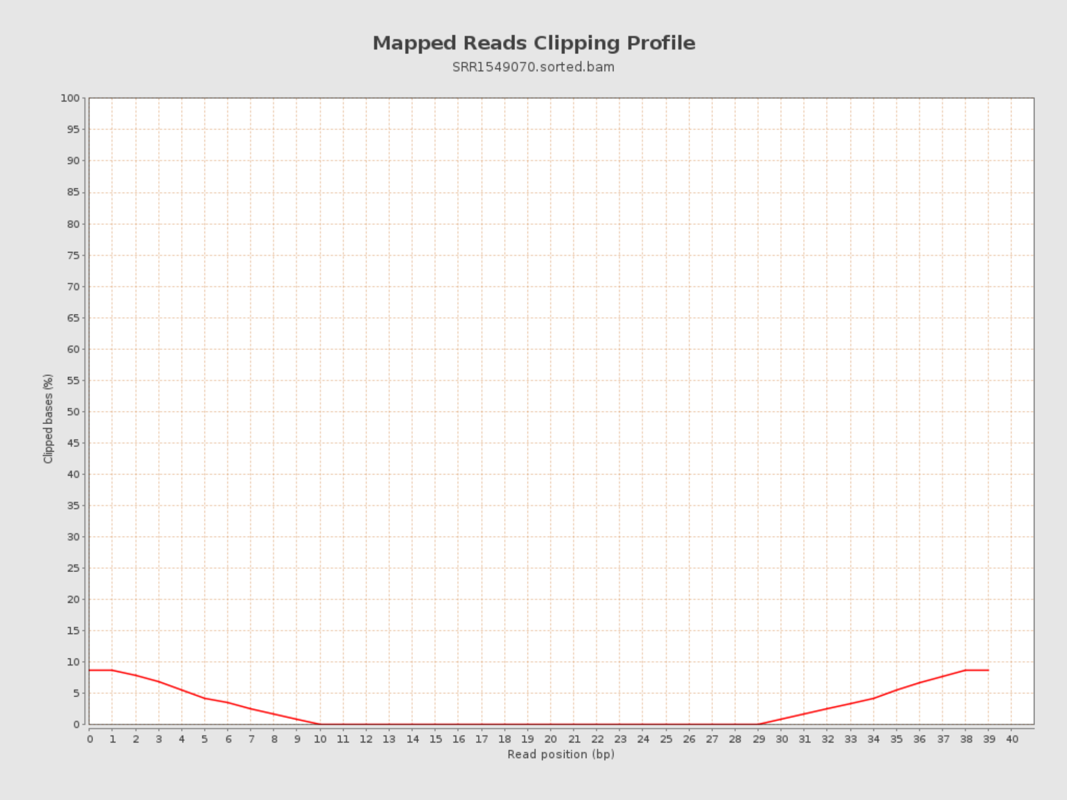
8. Results : Mapped Reads Nucleotide Content



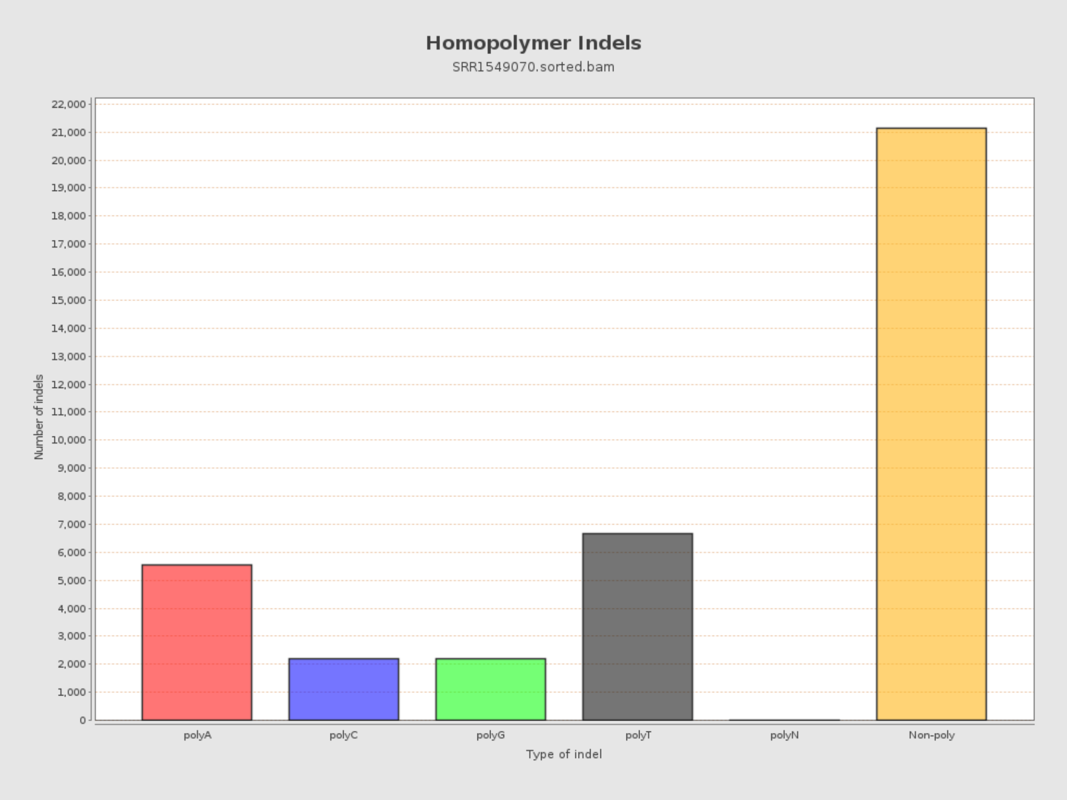
9. Results : Mapped Reads GC-content Distribution



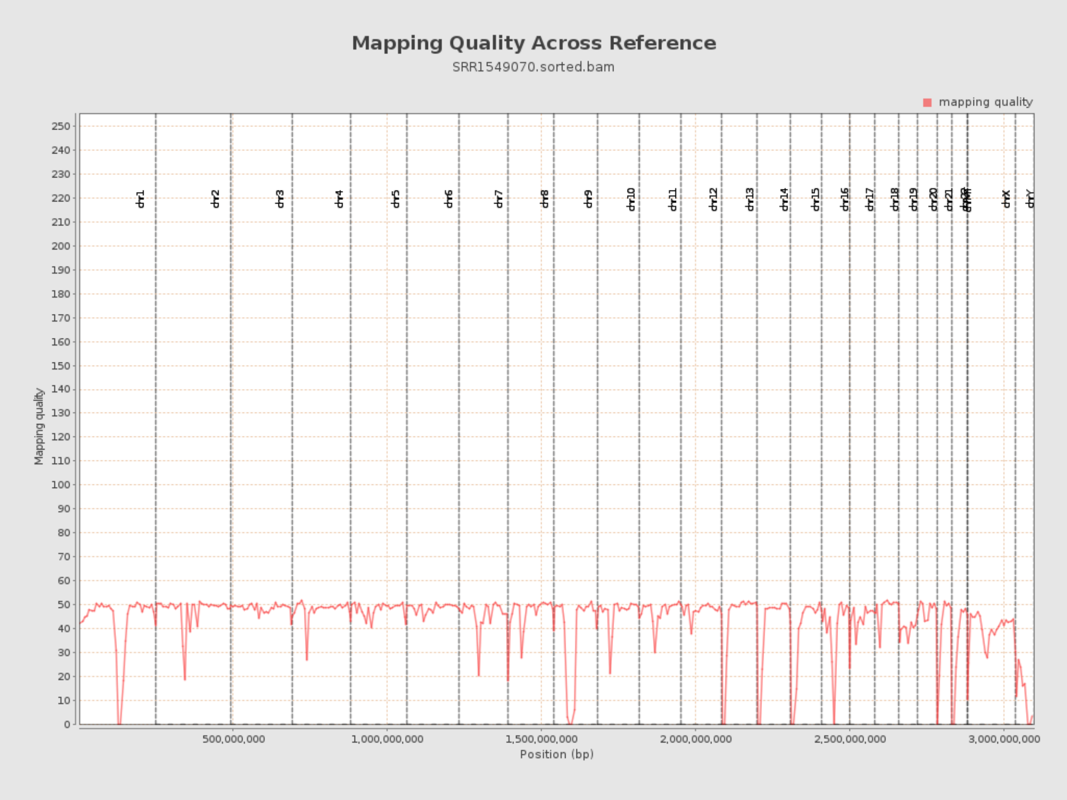
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram