Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:39:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081036.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_SRR3081036 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081036.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:39:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081036.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,847,777
Mapped reads	1,444,887 / 78.2%
Unmapped reads	402,890 / 21.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,125 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	34,237 / 1.85%
Duplication rate	1.8%
Clipped reads	723,339 / 39.15%

2.2. ACGT Content

Number/percentage of A's	27,688,395 / 29.55%
Number/percentage of C's	17,718,568 / 18.91%
Number/percentage of T's	27,974,348 / 29.86%
Number/percentage of G's	20,306,326 / 21.67%
Number/percentage of N's	1,231 / 0%
GC Percentage	40.59%

2.3. Coverage

Mean	0.0303

Standard Deviation	0.2597

2.4. Mapping Quality

Mean Mapping Quality	46.7

2.5. Mismatches and indels

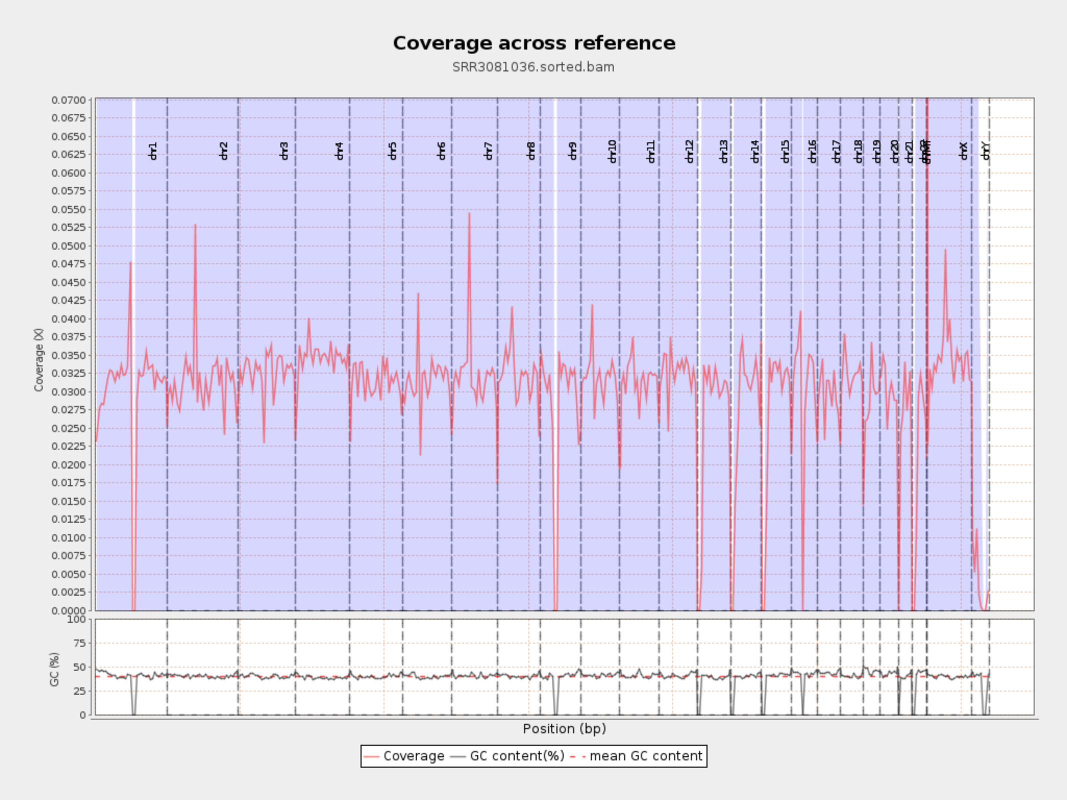
General error rate	0.8%
Mismatches	737,666
Insertions	6,174
Mapped reads with at least one insertion	0.42%
Deletions	19,810
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.82%

2.6. Chromosome stats

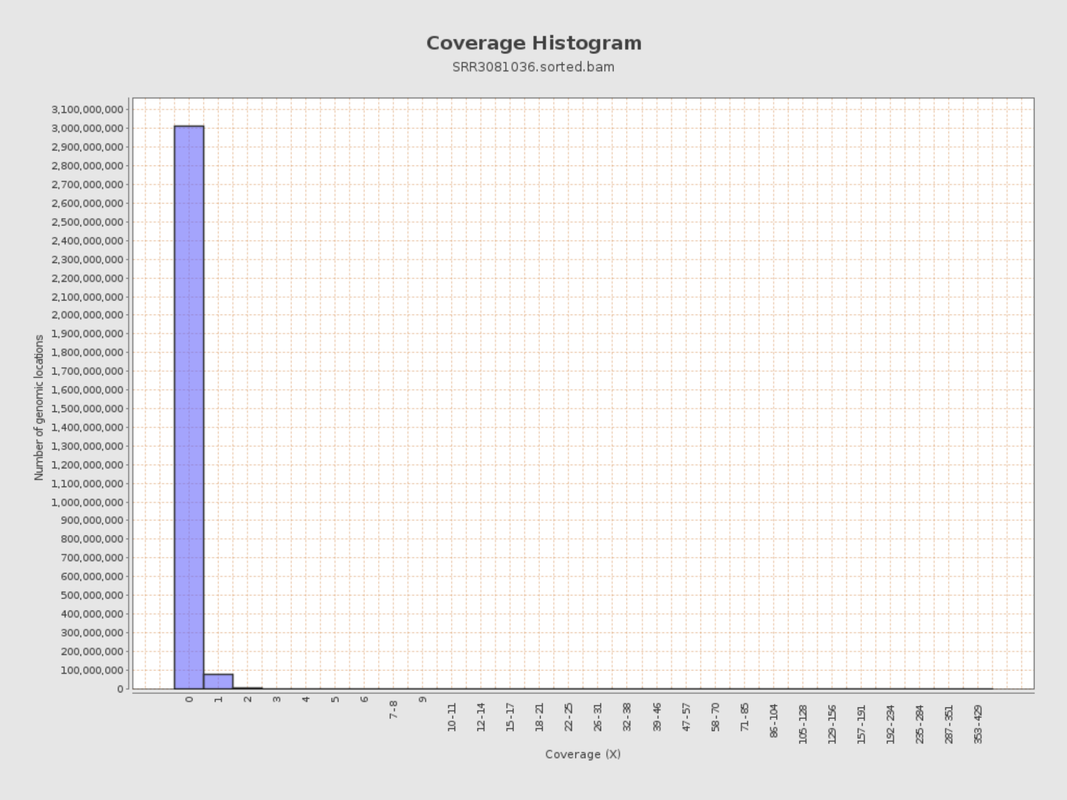
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7485725	0.03	0.4152
chr2	243199373	7693807	0.0316	0.2729
chr3	198022430	6478996	0.0327	0.1946
chr4	191154276	6586512	0.0345	0.2065
chr5	180915260	5704313	0.0315	0.1917
chr6	171115067	5392682	0.0315	0.23
chr7	159138663	5179145	0.0325	0.3719

chr8	146364022	4726659	0.0323	0.31
chr9	141213431	3937791	0.0279	0.2361
chr10	135534747	4284305	0.0316	0.2334
chr11	135006516	4264570	0.0316	0.2431
chr12	133851895	4364665	0.0326	0.1965
chr13	115169878	2992121	0.026	0.1731
chr14	107349540	2832452	0.0264	0.1836
chr15	102531392	2720705	0.0265	0.179
chr16	90354753	2677543	0.0296	0.2059
chr17	81195210	2393530	0.0295	0.2072
chr18	78077248	2535474	0.0325	0.4498
chr19	59128983	1708349	0.0289	0.293
chr20	63025520	1876602	0.0298	0.1901
chr21	48129895	1242242	0.0258	0.1852
chr22	51304566	1033407	0.0201	0.1534
chrMT	16571	20230	1.2208	1.3969
chrX	155270560	5370770	0.0346	0.2212
chrY	59373566	220232	0.0037	0.0848

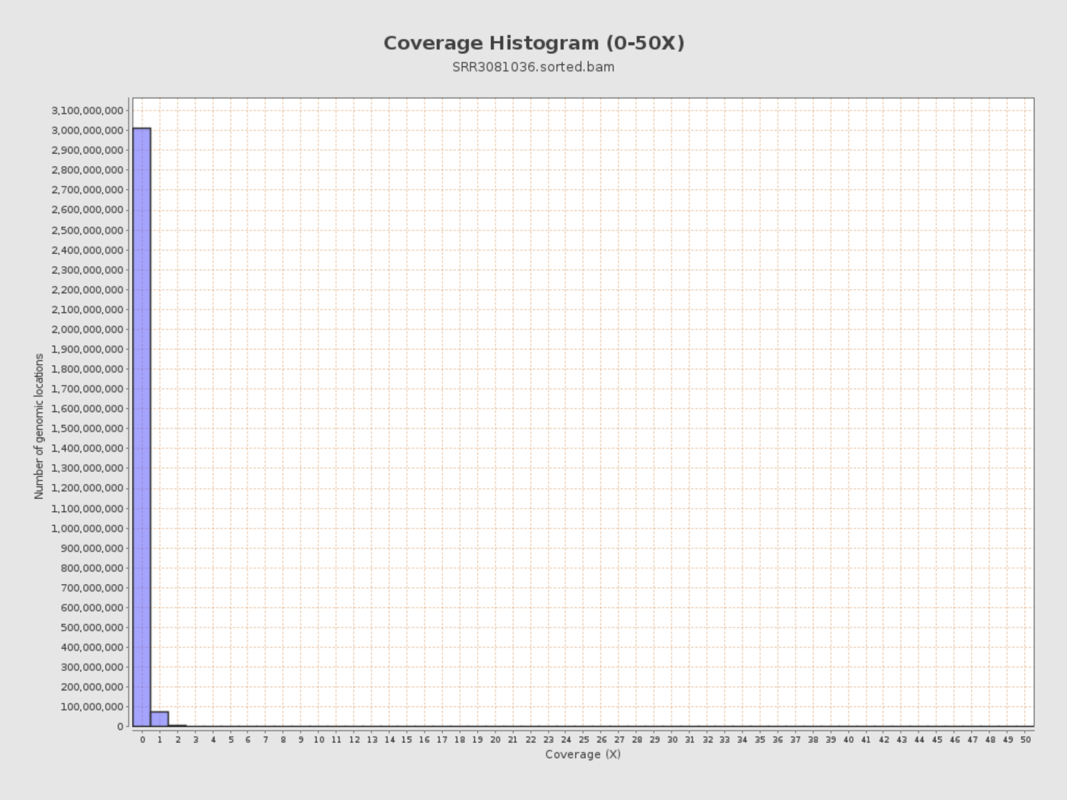
3. Results : Coverage across reference



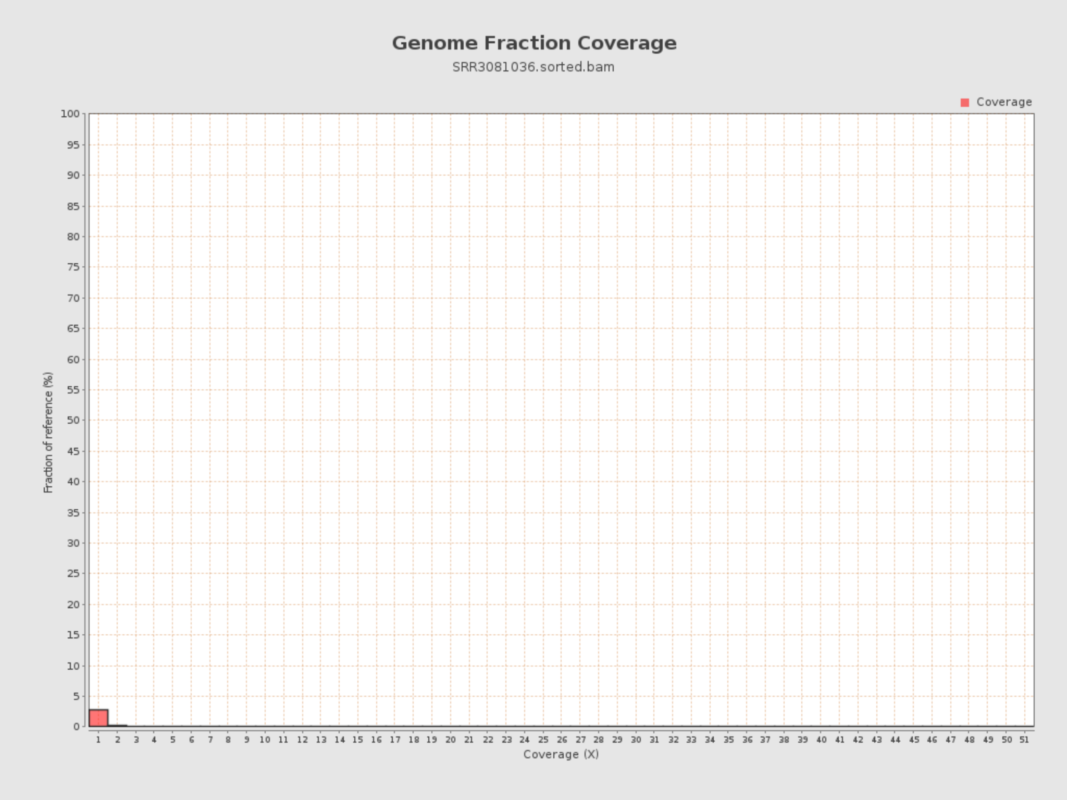
4. Results : Coverage Histogram



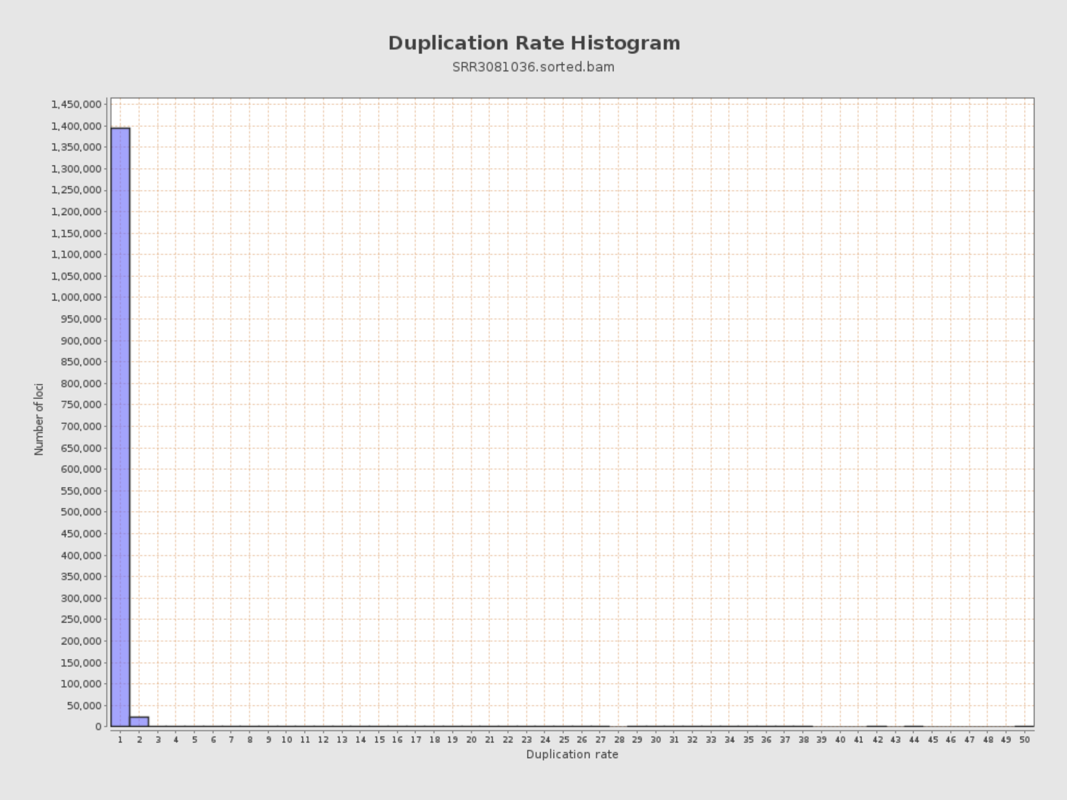
5. Results : Coverage Histogram (0-50X)



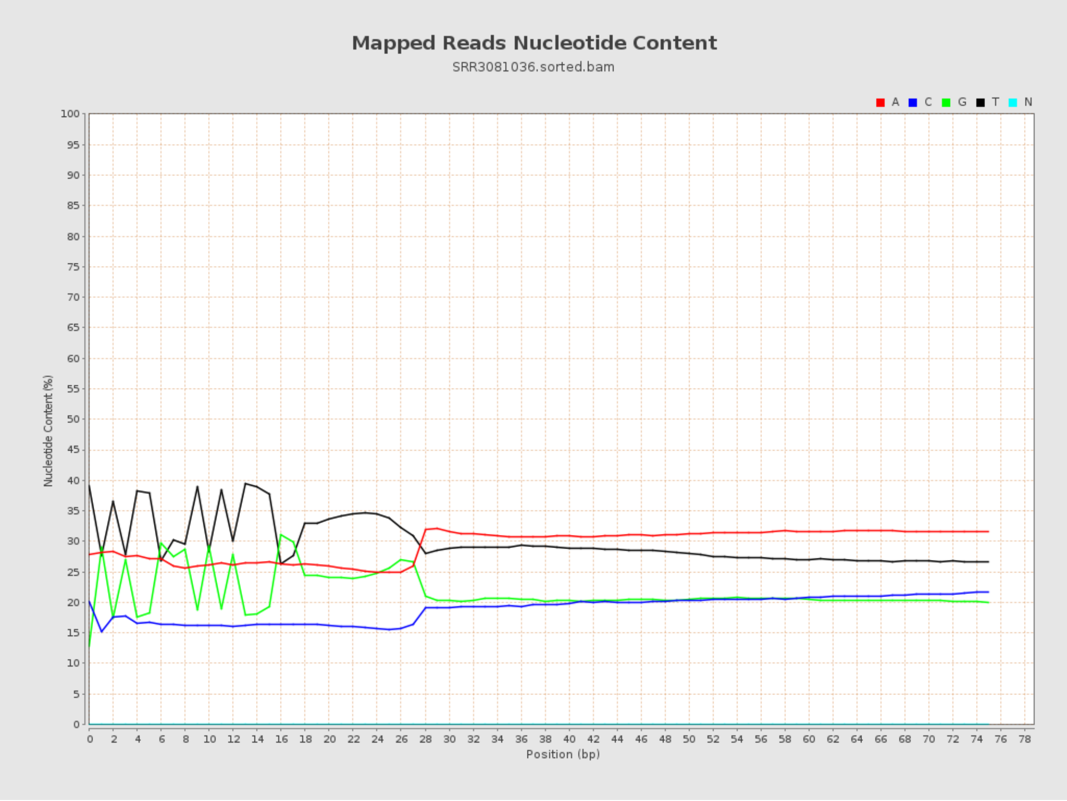
6. Results : Genome Fraction Coverage



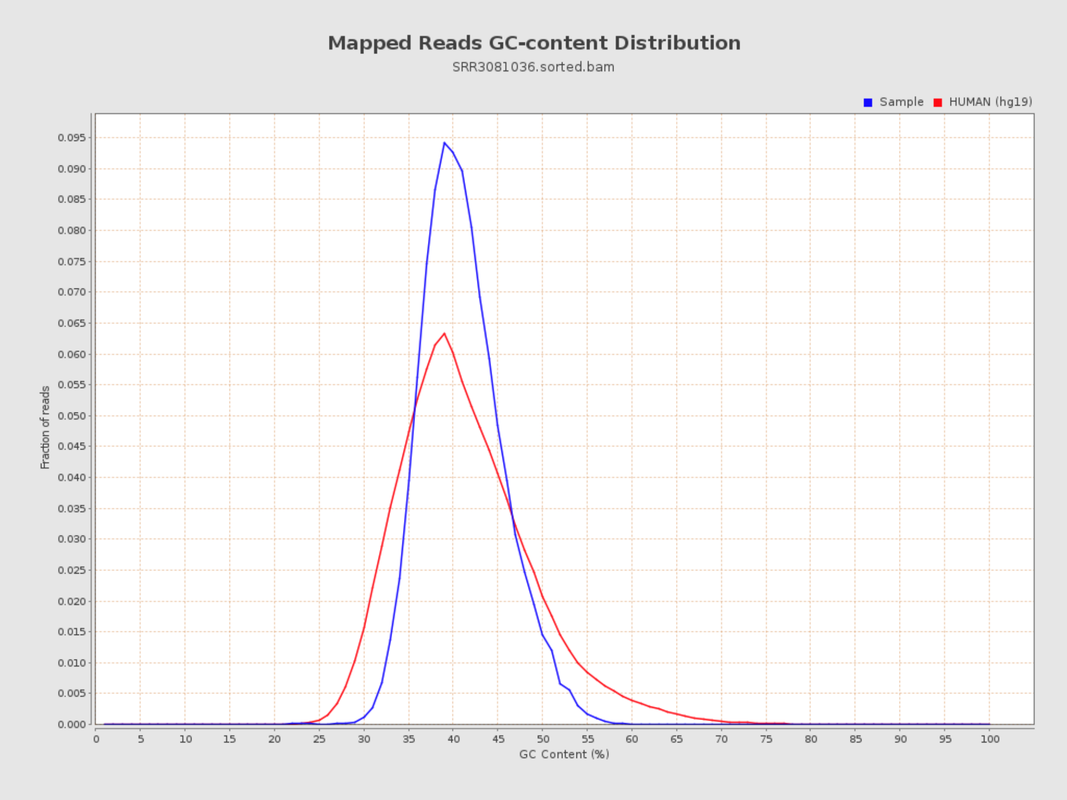
7. Results : Duplication Rate Histogram



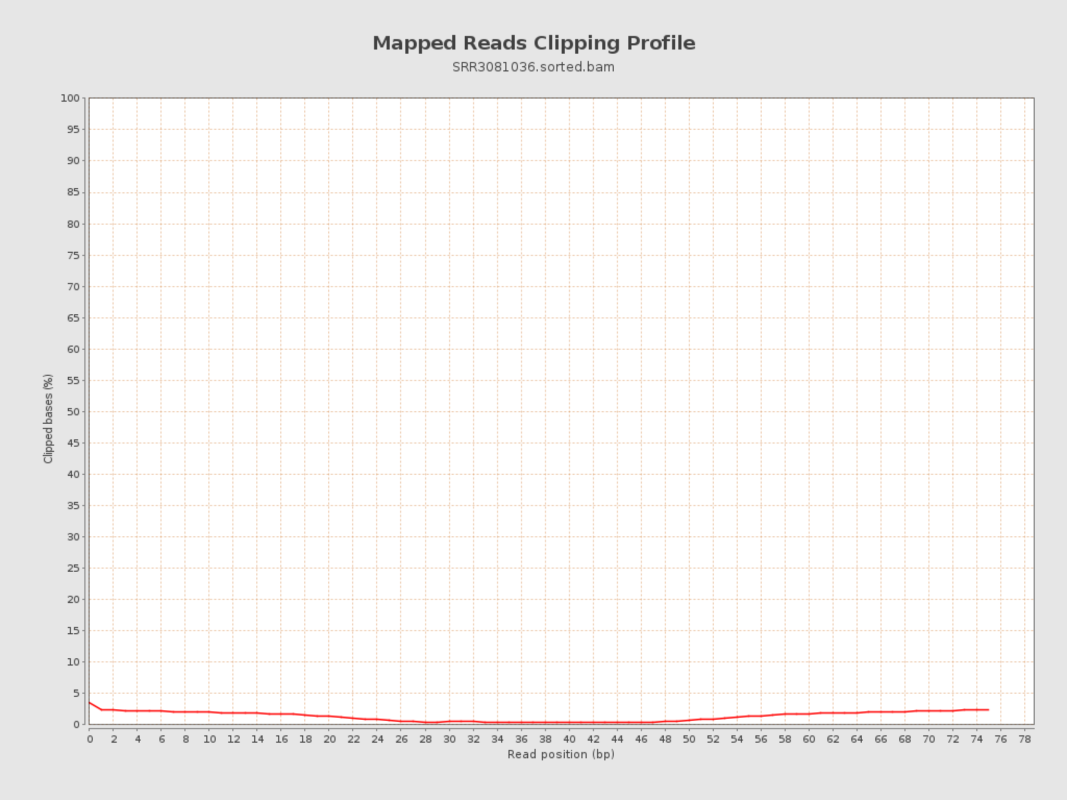
8. Results : Mapped Reads Nucleotide Content



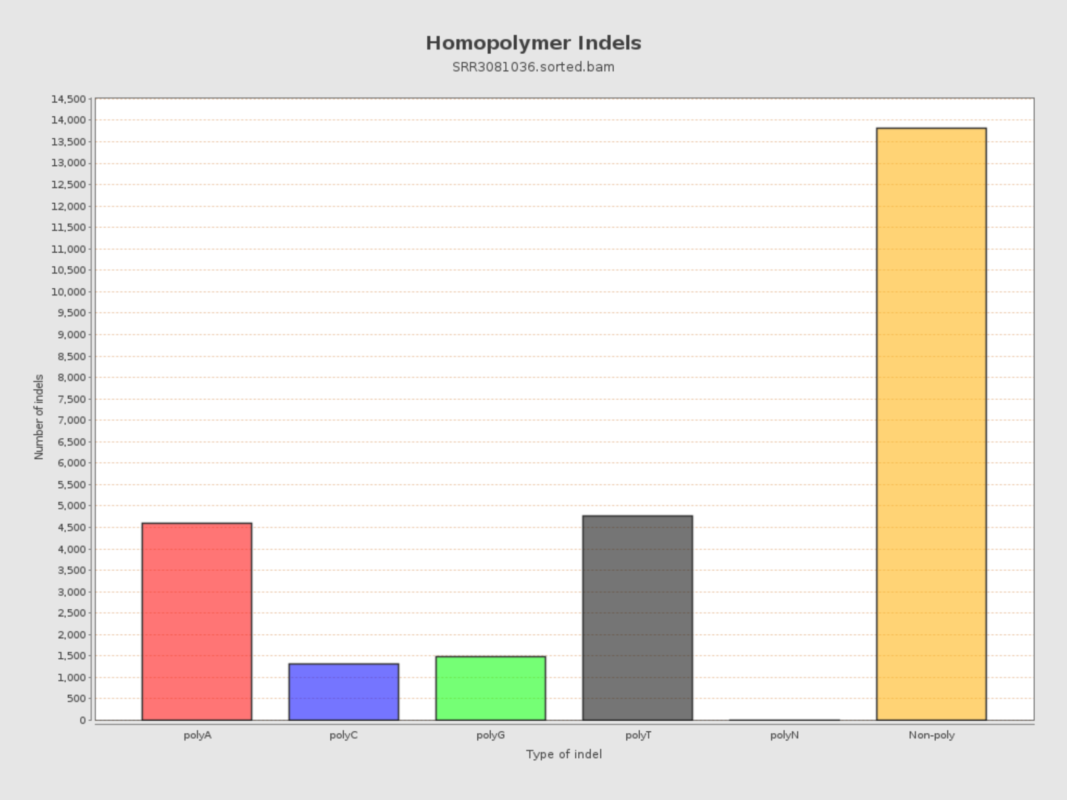
9. Results : Mapped Reads GC-content Distribution



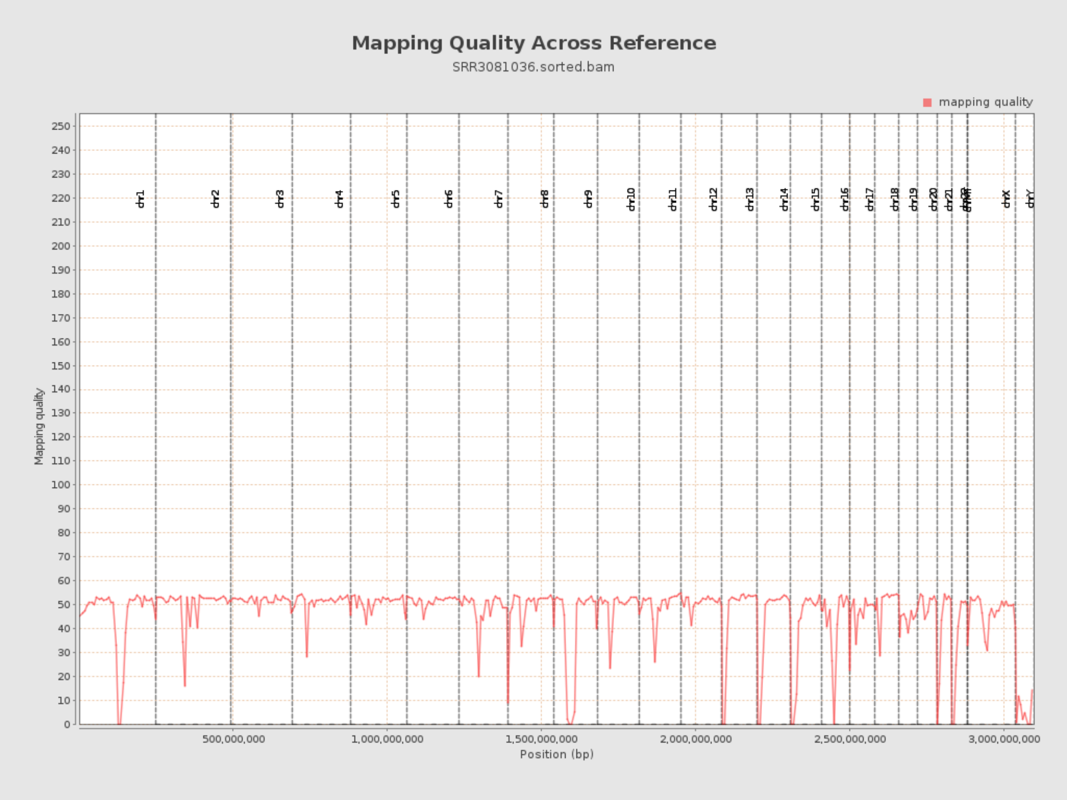
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram