Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:32:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708651.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_SRR1708651 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708651.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:32:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708651.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,249,187
Mapped reads	3,103,149 / 95.51%
Unmapped reads	146,038 / 4.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	77 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	13,141 / 0.4%
Duplication rate	0.42%
Clipped reads	41,130 / 1.27%

2.2. ACGT Content

Number/percentage of A's	47,681,960 / 30.81%
Number/percentage of C's	29,542,562 / 19.09%
Number/percentage of T's	47,719,544 / 30.83%
Number/percentage of G's	29,816,618 / 19.27%
Number/percentage of N's	4,968 / 0%
GC Percentage	38.35%

2.3. Coverage

Mean	0.05

Standard Deviation	0.2301

2.4. Mapping Quality

Mean Mapping Quality	46.38

2.5. Mismatches and indels

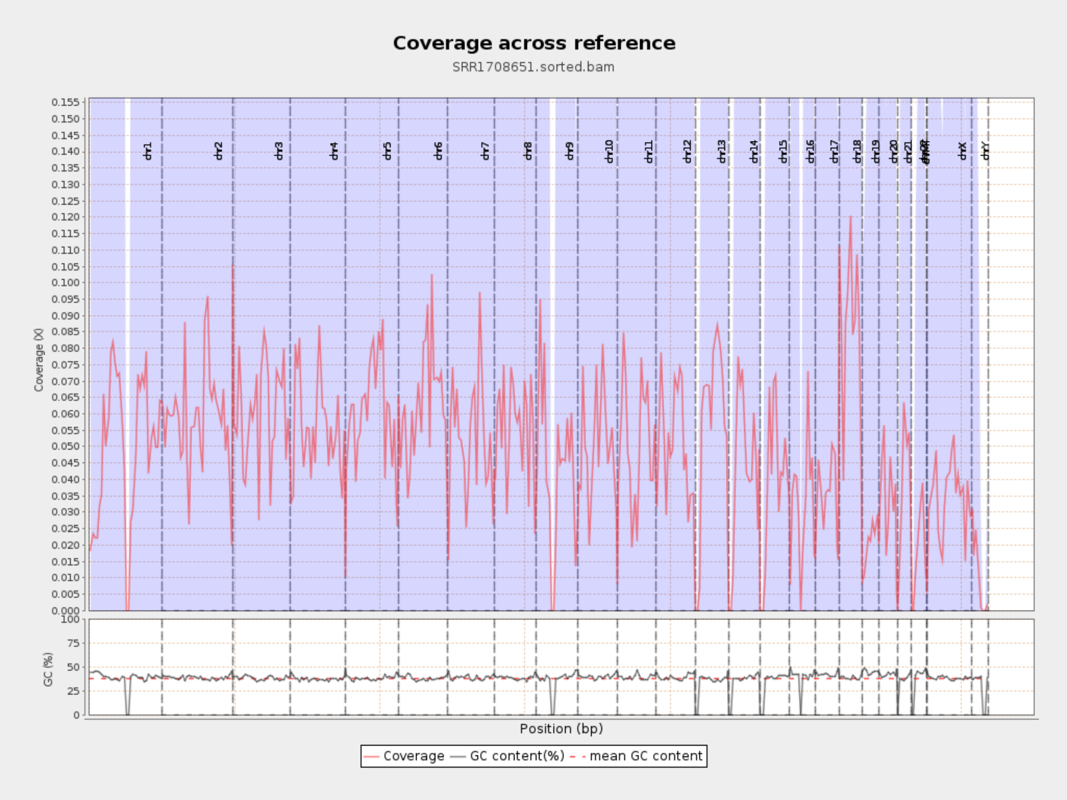
General error rate	0.17%
Mismatches	252,810
Insertions	10,376
Mapped reads with at least one insertion	0.33%
Deletions	8,932
Mapped reads with at least one deletion	0.29%
Homopolymer indels	48.31%

2.6. Chromosome stats

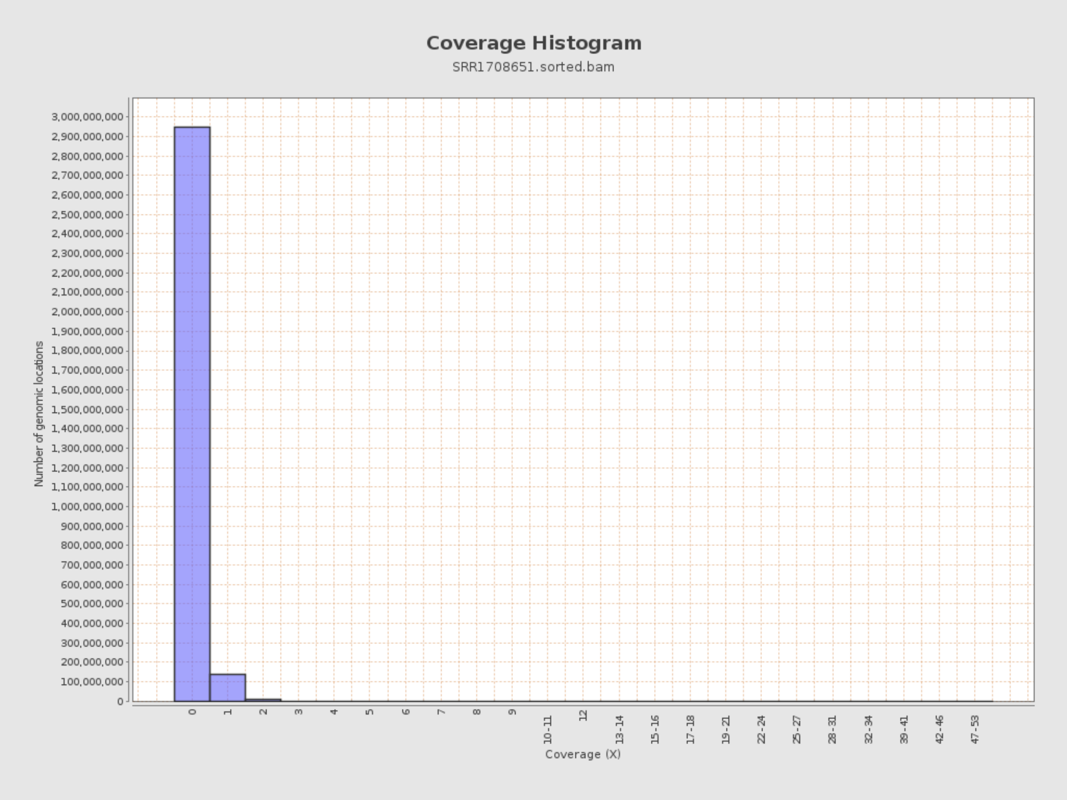
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12393170	0.0497	0.2304
chr2	243199373	14258582	0.0586	0.2482
chr3	198022430	12086837	0.061	0.2531
chr4	191154276	10707388	0.056	0.2427
chr5	180915260	11059221	0.0611	0.2536
chr6	171115067	10855712	0.0634	0.2583
chr7	159138663	8461926	0.0532	0.2367

chr8	146364022	8172143	0.0558	0.2422
chr9	141213431	6274847	0.0444	0.2171
chr10	135534747	6950405	0.0513	0.2322
chr11	135006516	6875538	0.0509	0.2327
chr12	133851895	6761930	0.0505	0.2311
chr13	115169878	6533784	0.0567	0.2449
chr14	107349540	4655685	0.0434	0.2142
chr15	102531392	4039458	0.0394	0.2051
chr16	90354753	2973393	0.0329	0.1861
chr17	81195210	2832629	0.0349	0.1922
chr18	78077248	6826104	0.0874	0.3047
chr19	59128983	1243903	0.021	0.1478
chr20	63025520	2233967	0.0354	0.1928
chr21	48129895	1788402	0.0372	0.1986
chr22	51304566	963773	0.0188	0.1405
chrMT	16571	149	0.009	0.0944
chrX	155270560	5247839	0.0338	0.1879
chrY	59373566	584350	0.0098	0.1022

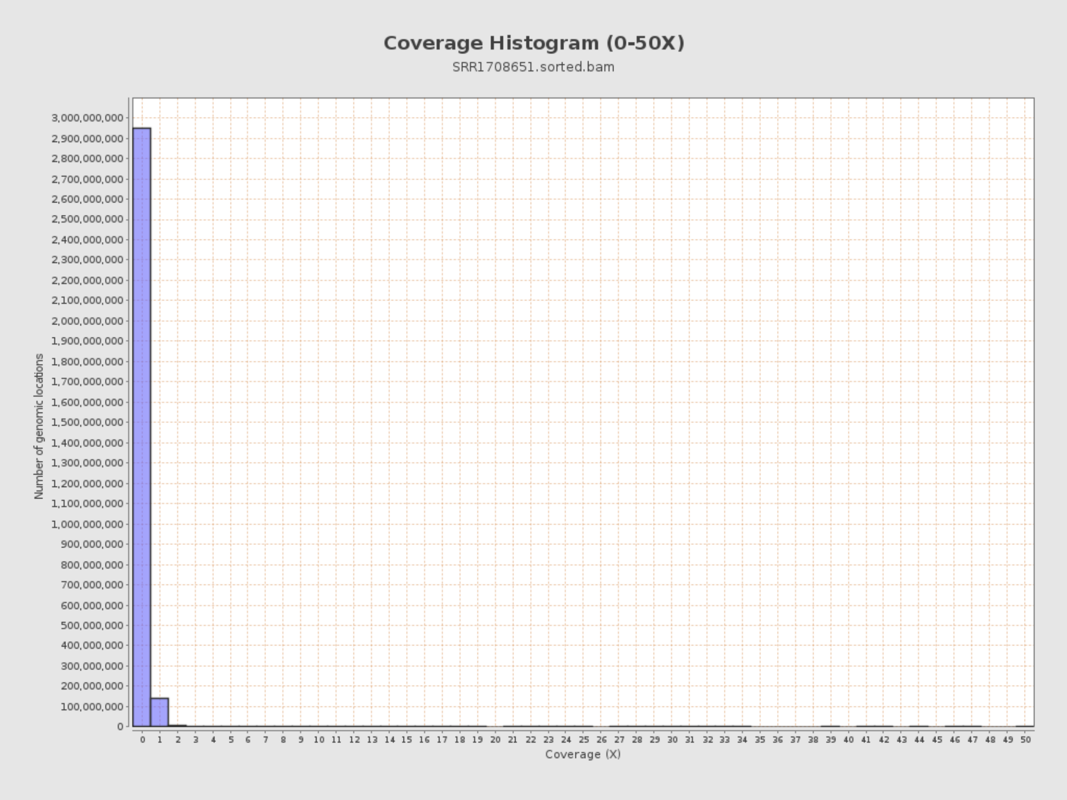
3. Results : Coverage across reference



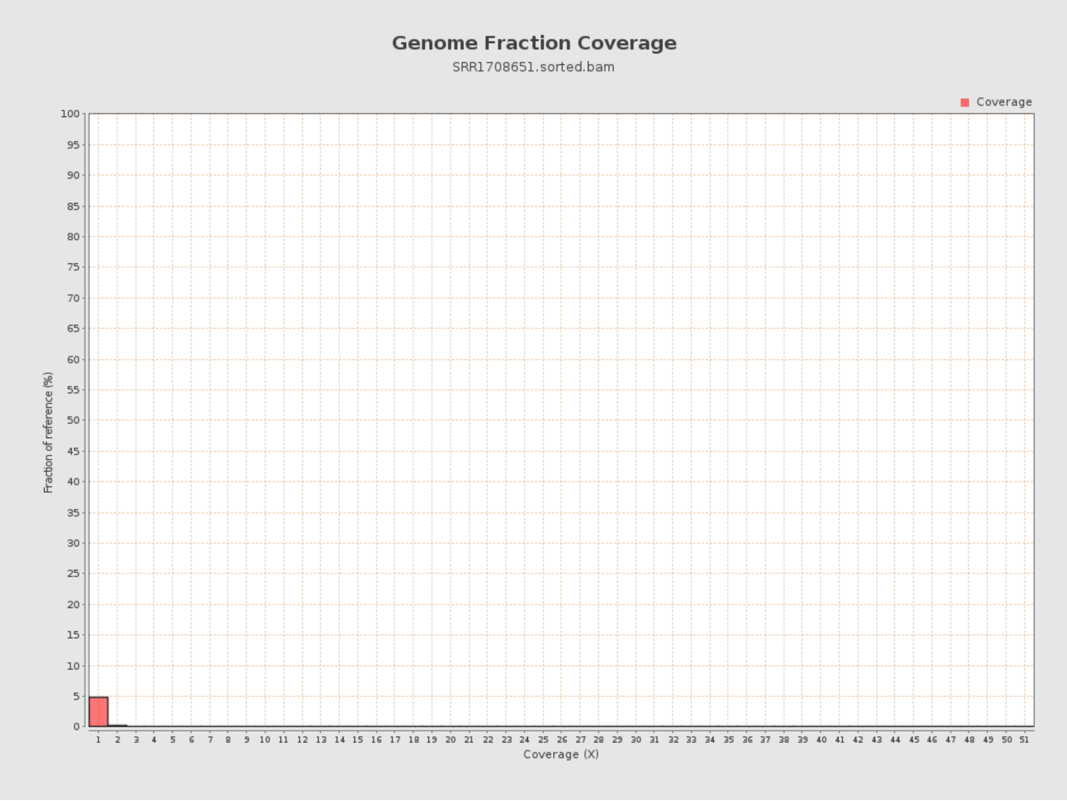
4. Results : Coverage Histogram



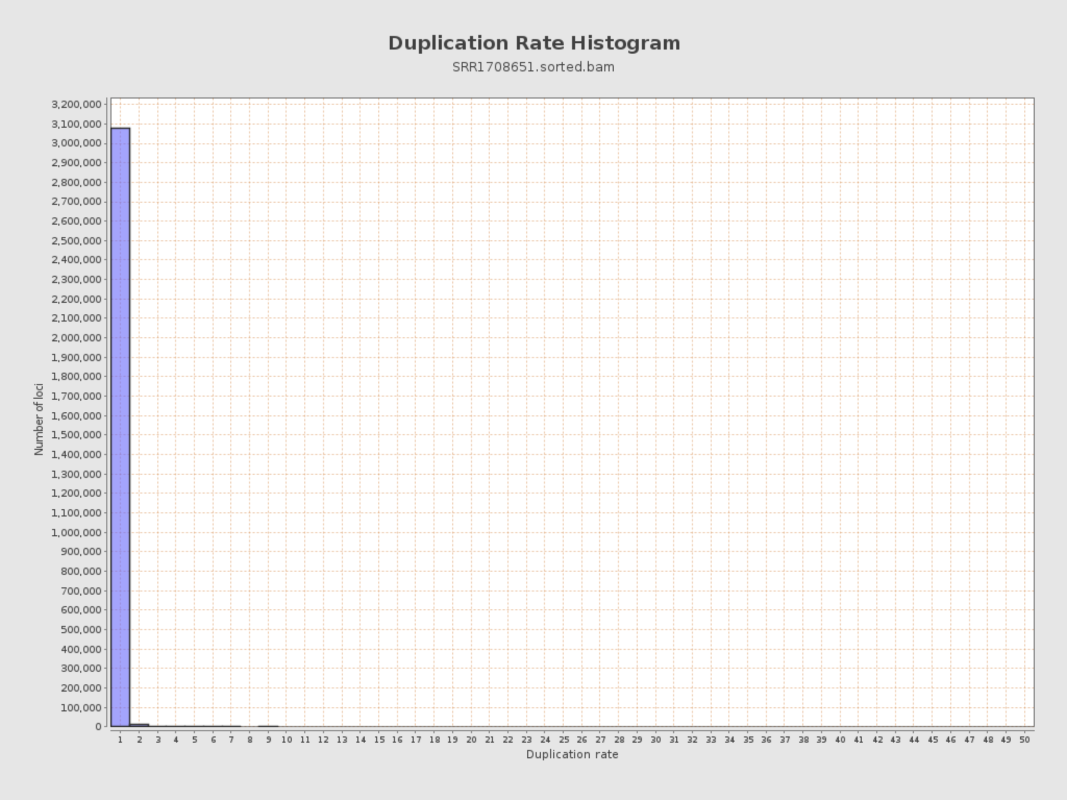
5. Results : Coverage Histogram (0-50X)



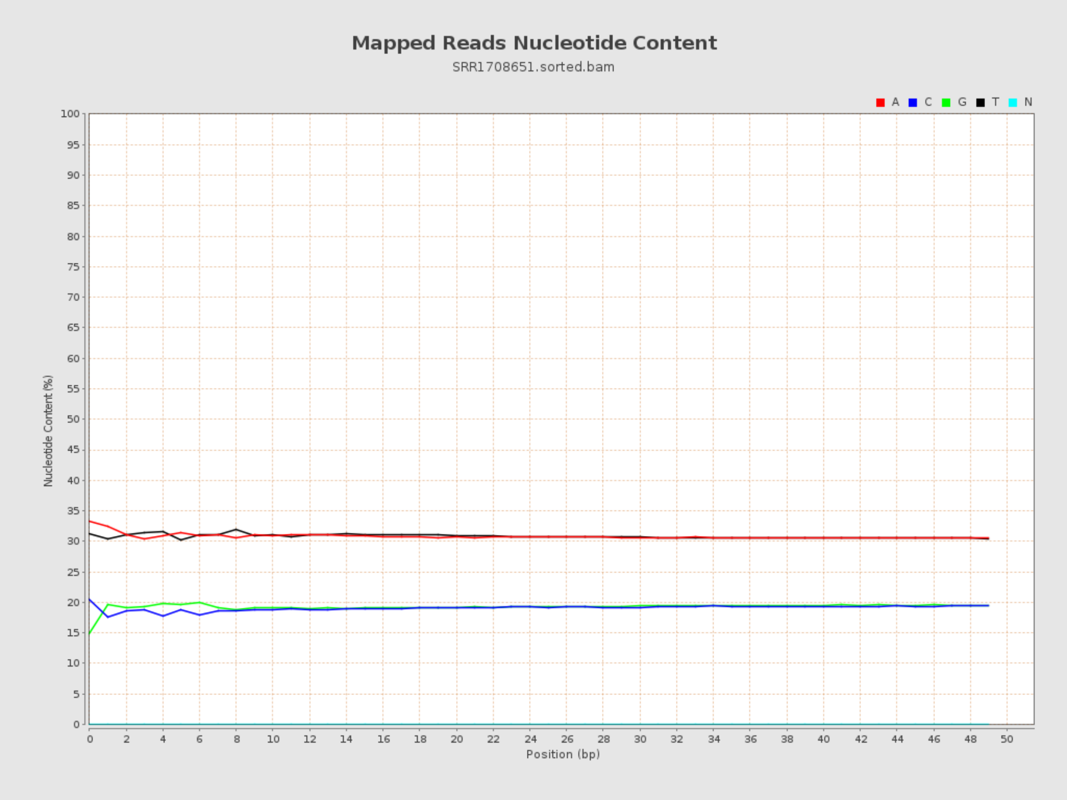
6. Results : Genome Fraction Coverage



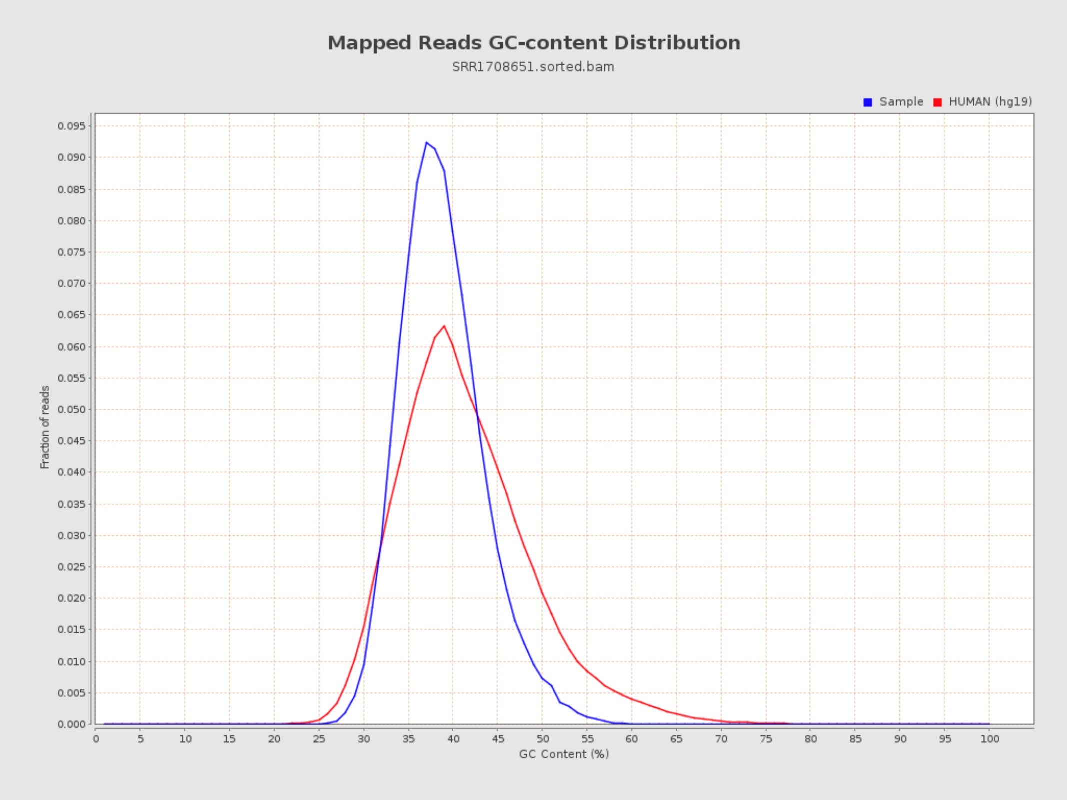
7. Results : Duplication Rate Histogram



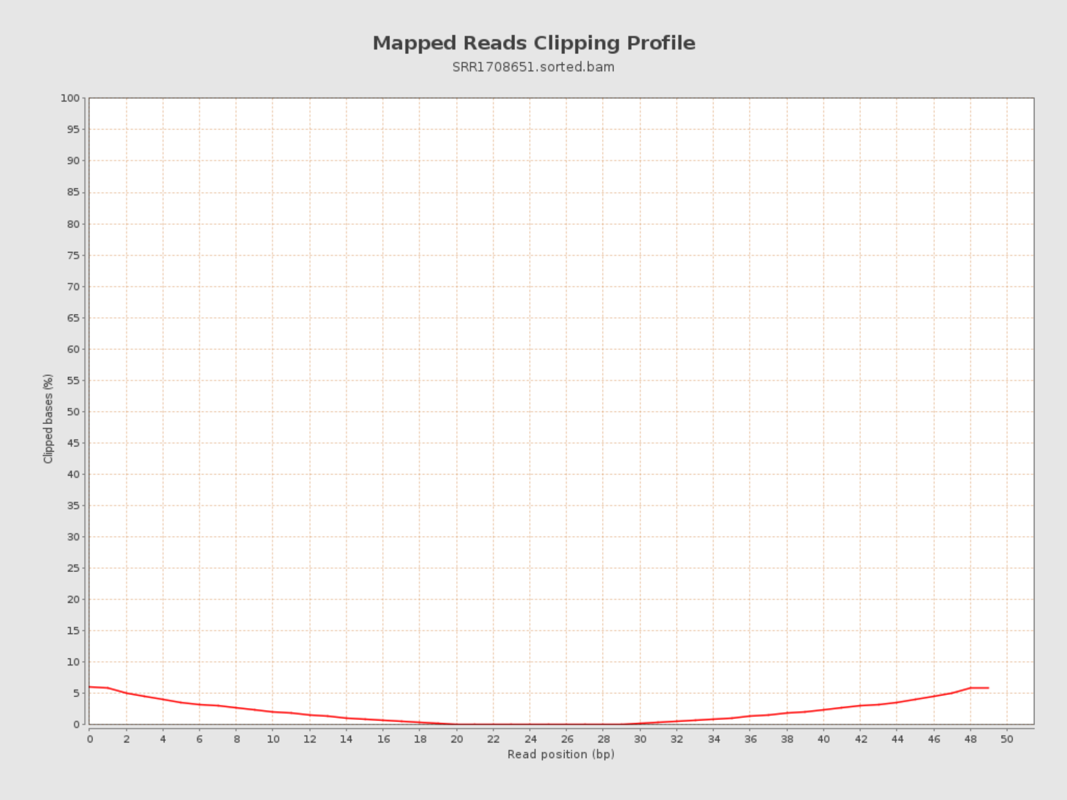
8. Results : Mapped Reads Nucleotide Content



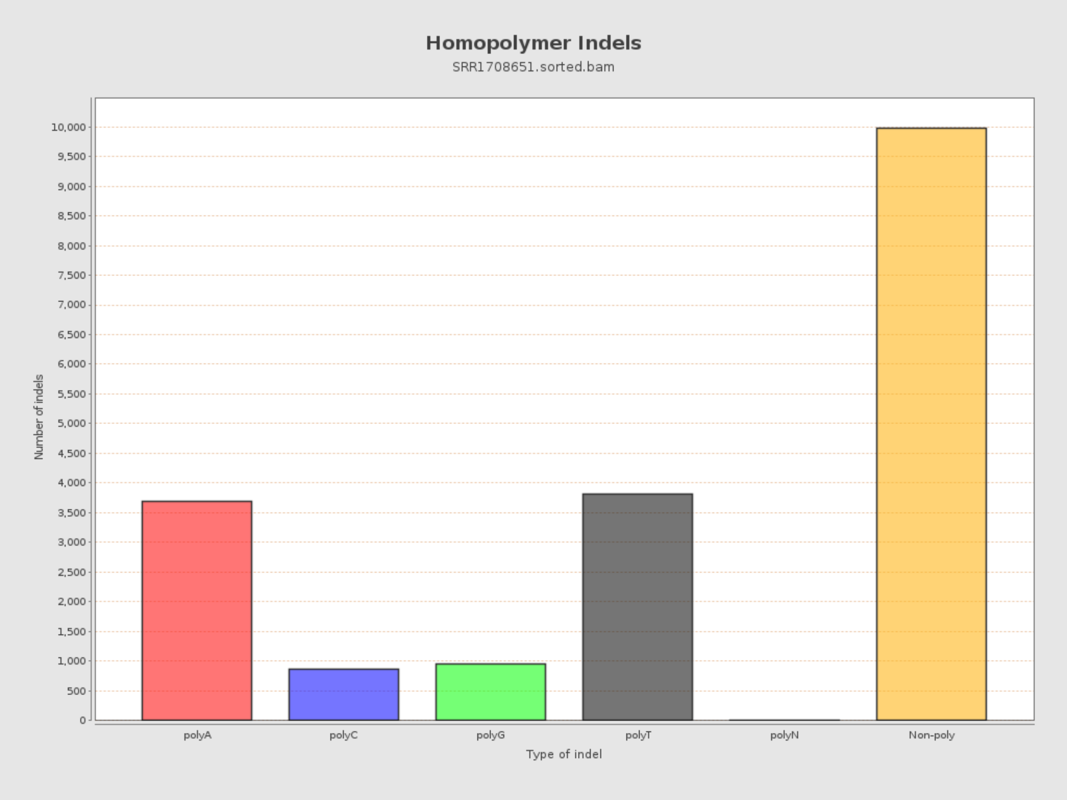
9. Results : Mapped Reads GC-content Distribution



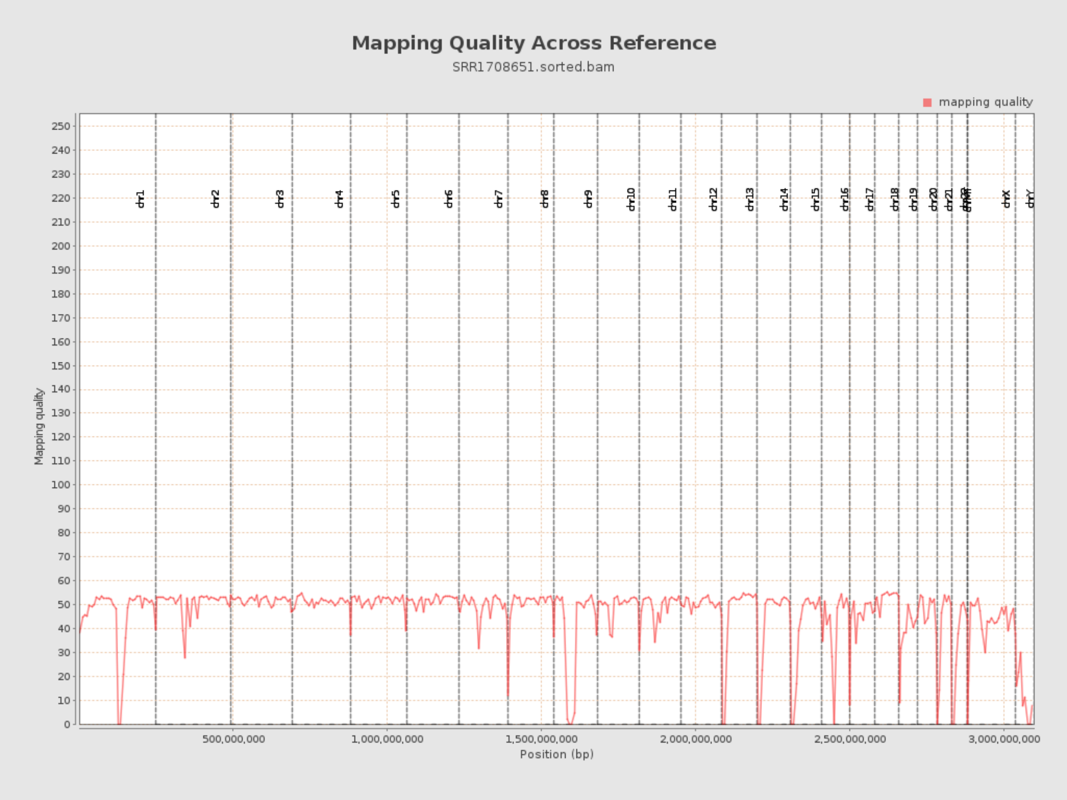
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram