Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:17:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081692.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_SRR3081692 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081692.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:17:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081692.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,596,581
Mapped reads	1,344,088 / 84.19%
Unmapped reads	252,493 / 15.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,707 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	64,965 / 4.07%
Duplication rate	4.06%
Clipped reads	587,816 / 36.82%

2.2. ACGT Content

Number/percentage of A's	25,151,309 / 27.96%
Number/percentage of C's	15,849,275 / 17.62%
Number/percentage of T's	29,419,734 / 32.71%
Number/percentage of G's	19,472,248 / 21.65%
Number/percentage of N's	61,462 / 0.07%
GC Percentage	39.27%

2.3. Coverage

Mean	0.0291

Standard Deviation	0.2656

2.4. Mapping Quality

Mean Mapping Quality	47.36

2.5. Mismatches and indels

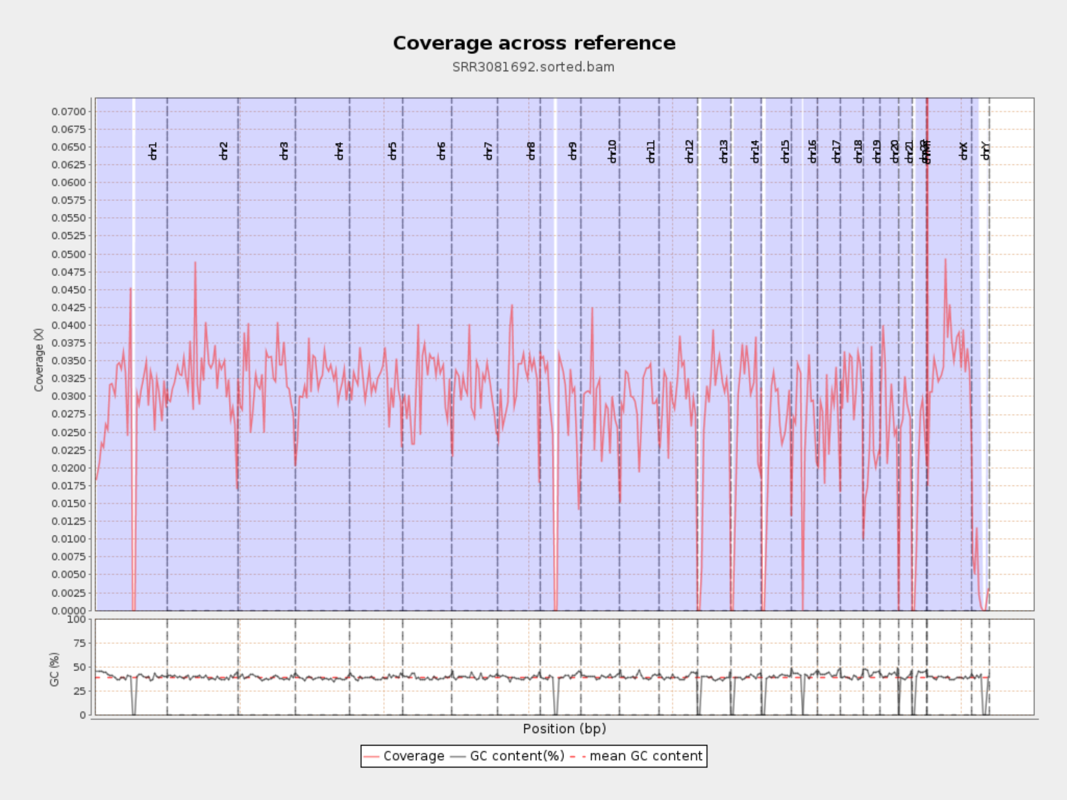
General error rate	0.9%
Mismatches	794,322
Insertions	7,620
Mapped reads with at least one insertion	0.56%
Deletions	20,459
Mapped reads with at least one deletion	1.51%
Homopolymer indels	49.47%

2.6. Chromosome stats

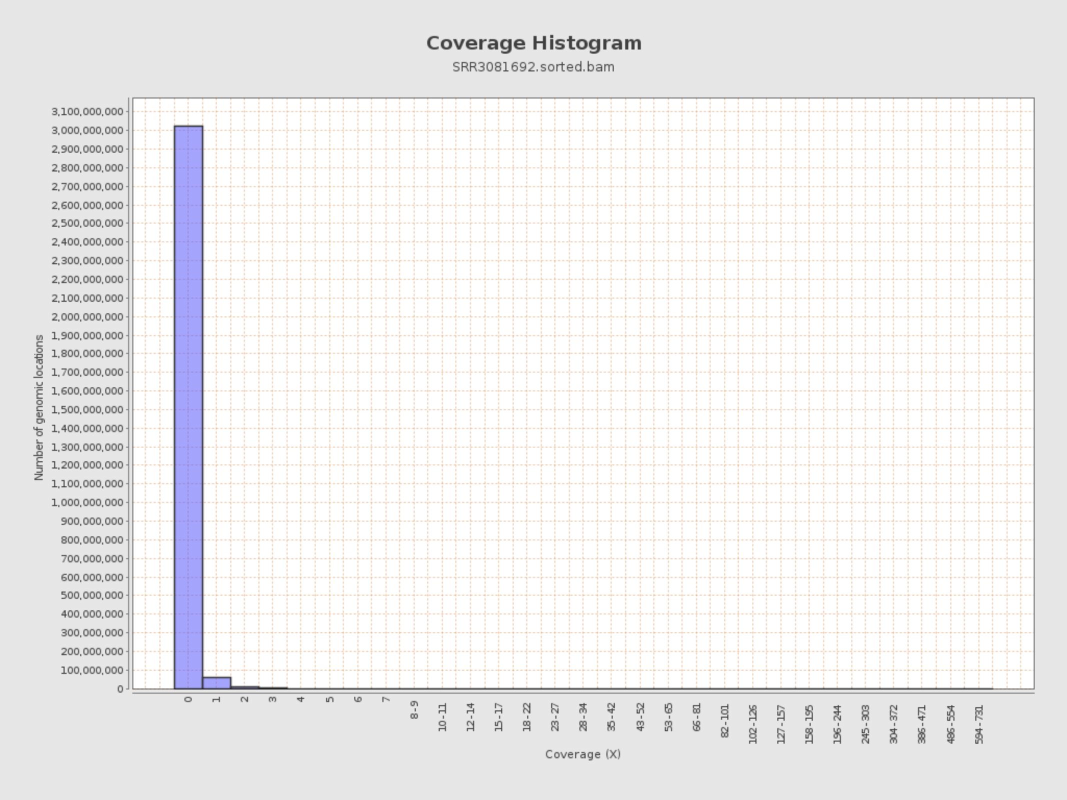
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7023596	0.0282	0.3702
chr2	243199373	7960772	0.0327	0.2935
chr3	198022430	6433884	0.0325	0.2102
chr4	191154276	6087154	0.0318	0.2159
chr5	180915260	5782609	0.032	0.2103
chr6	171115067	5393648	0.0315	0.2286
chr7	159138663	4942999	0.0311	0.3005

chr8	146364022	4674786	0.0319	0.4785
chr9	141213431	3828671	0.0271	0.2579
chr10	135534747	3792145	0.028	0.2457
chr11	135006516	3999170	0.0296	0.2353
chr12	133851895	4000087	0.0299	0.2047
chr13	115169878	3055252	0.0265	0.1911
chr14	107349540	2812416	0.0262	0.1965
chr15	102531392	2356951	0.023	0.1779
chr16	90354753	2302844	0.0255	0.1951
chr17	81195210	2151561	0.0265	0.2028
chr18	78077248	2531323	0.0324	0.3973
chr19	59128983	1292260	0.0219	0.2831
chr20	63025520	1792473	0.0284	0.2023
chr21	48129895	1180514	0.0245	0.1922
chr22	51304566	885571	0.0173	0.1526
chrMT	16571	10000	0.6035	0.8881
chrX	155270560	5479839	0.0353	0.2337
chrY	59373566	216106	0.0036	0.0964

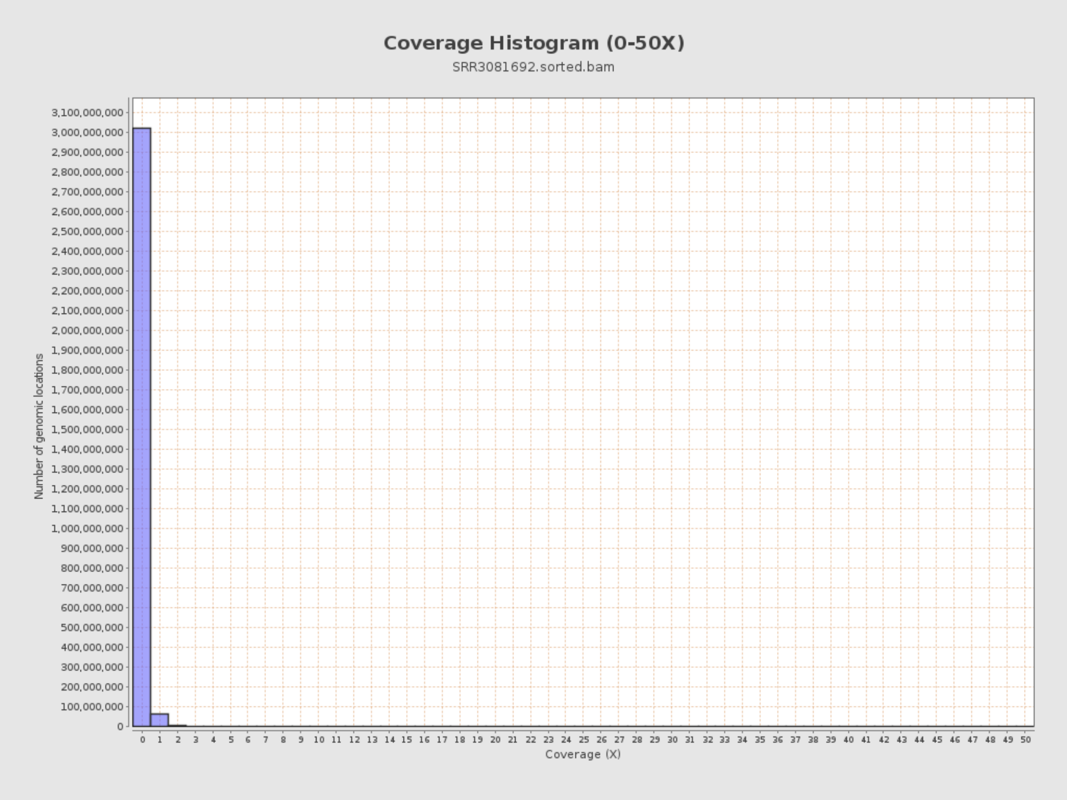
3. Results : Coverage across reference



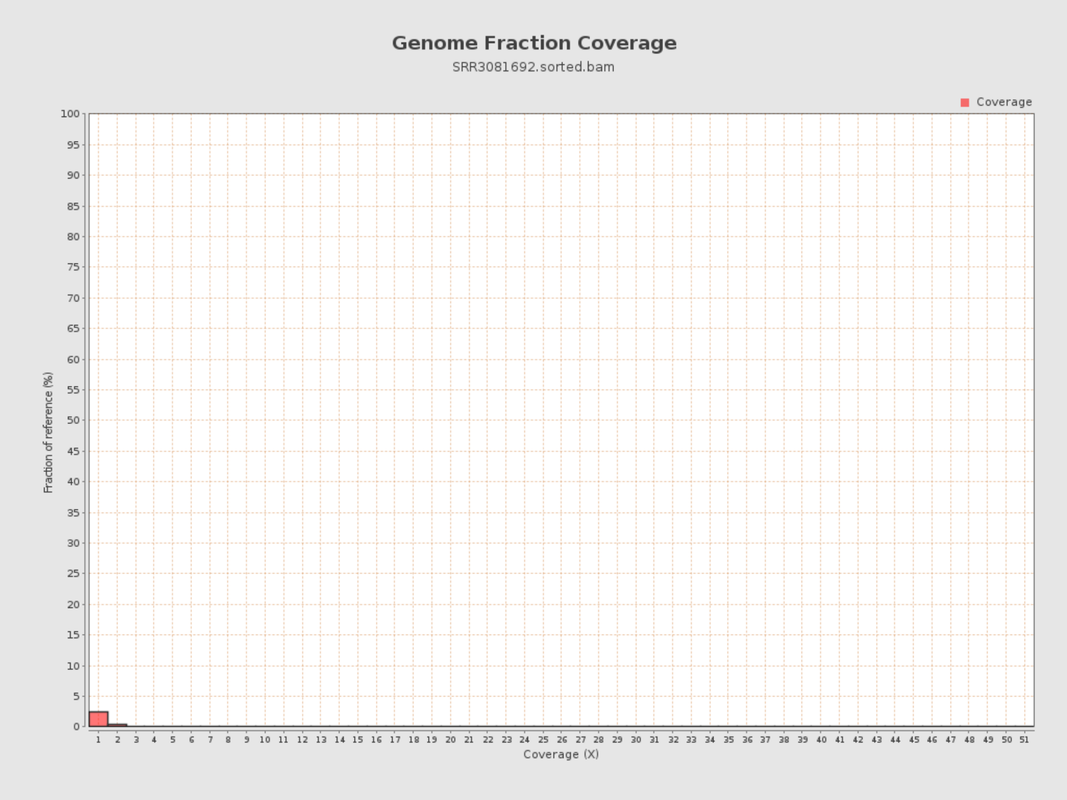
4. Results : Coverage Histogram



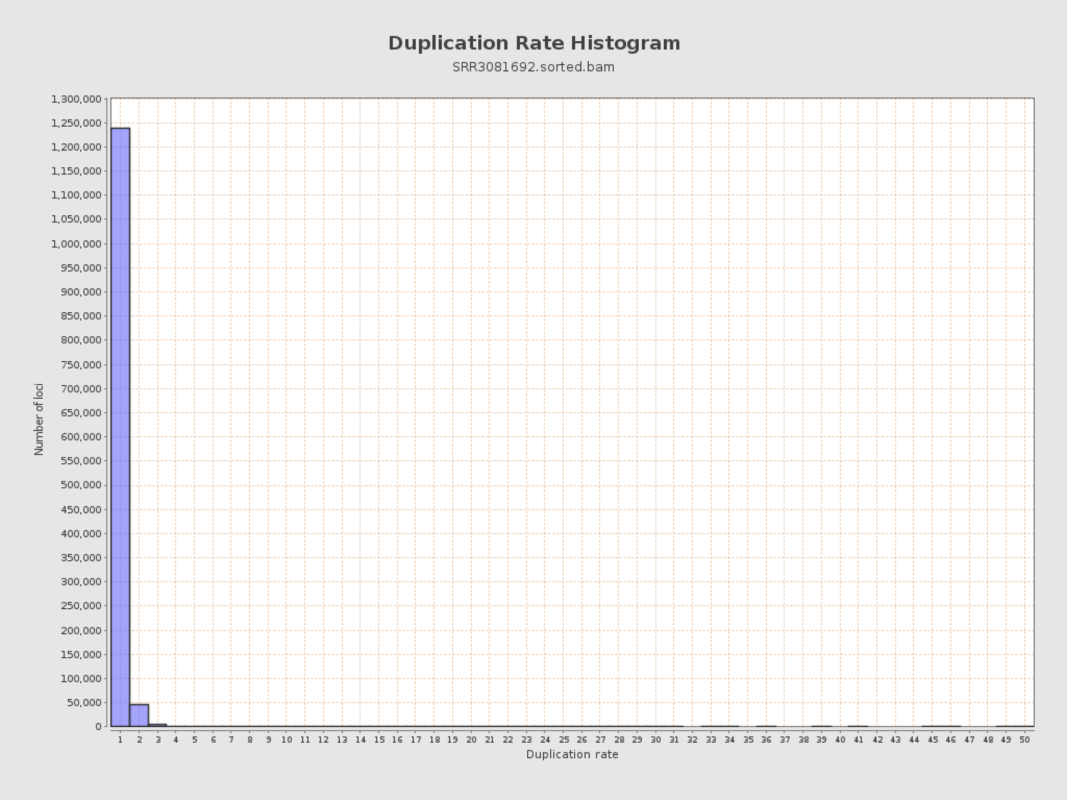
5. Results : Coverage Histogram (0-50X)



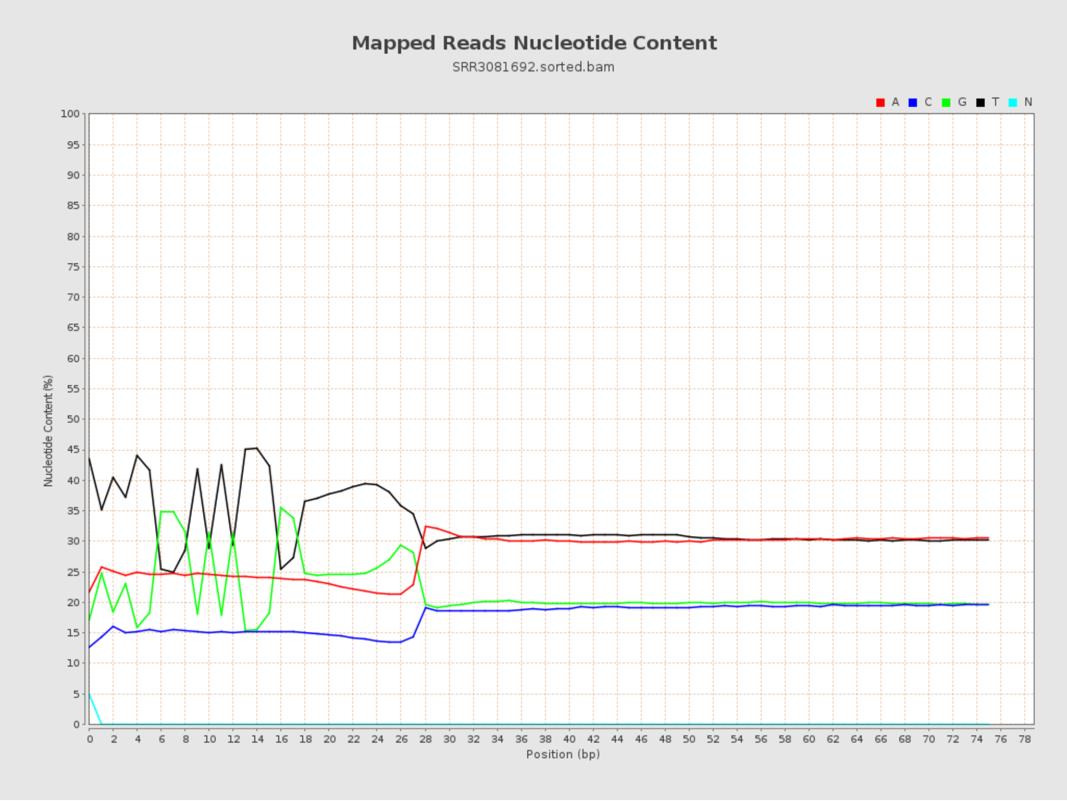
6. Results : Genome Fraction Coverage



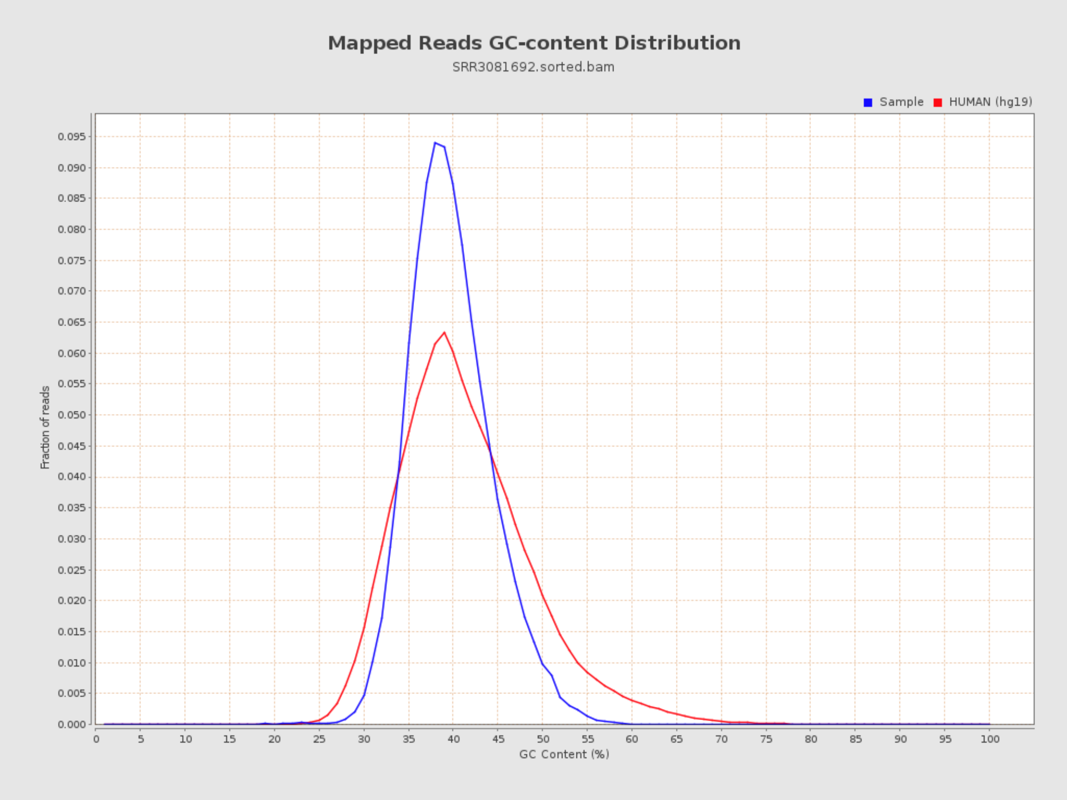
7. Results : Duplication Rate Histogram



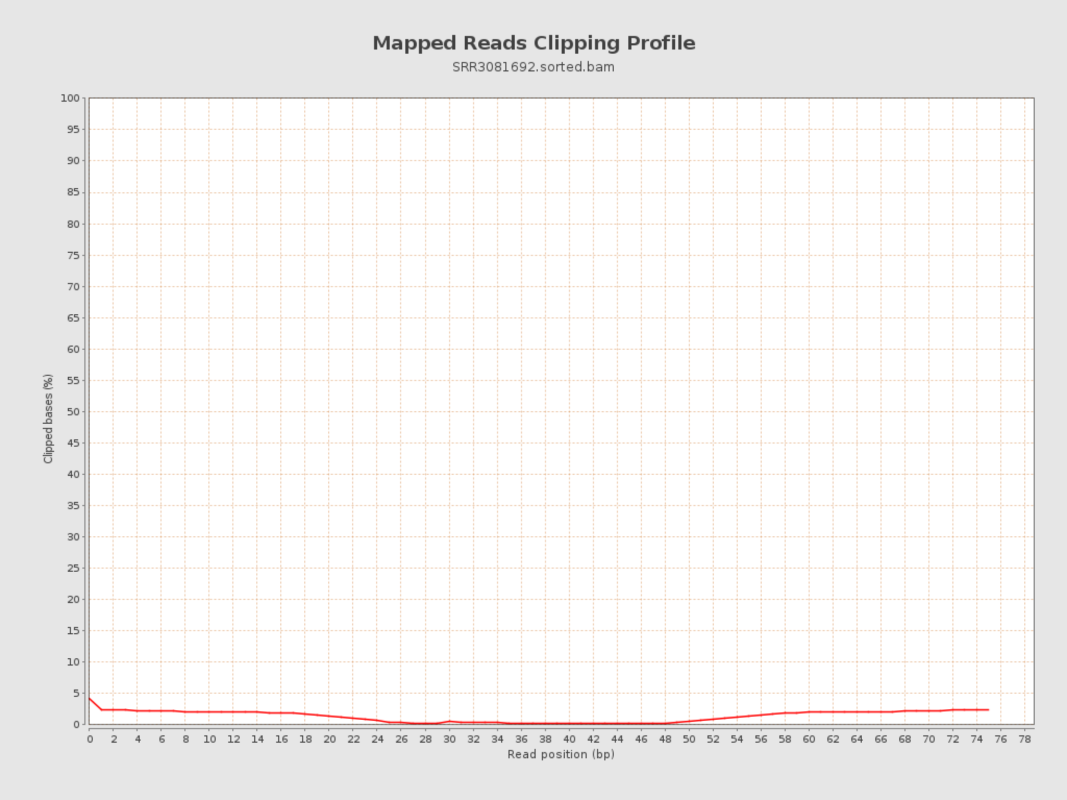
8. Results : Mapped Reads Nucleotide Content



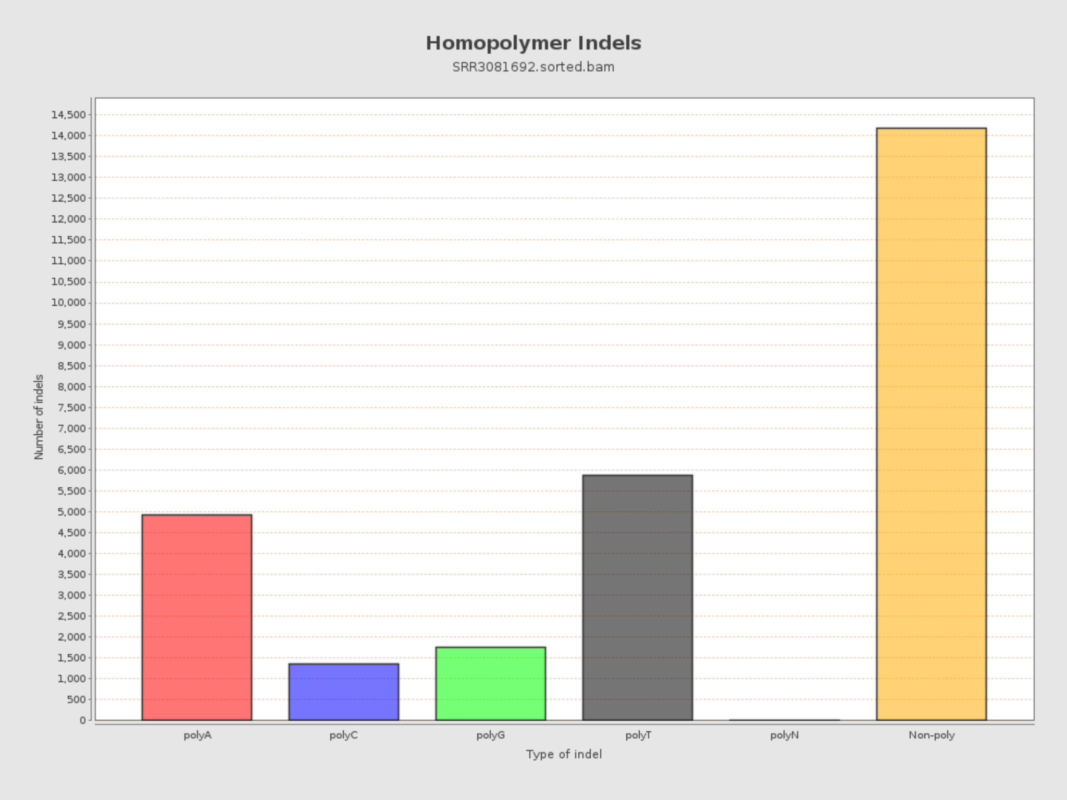
9. Results : Mapped Reads GC-content Distribution



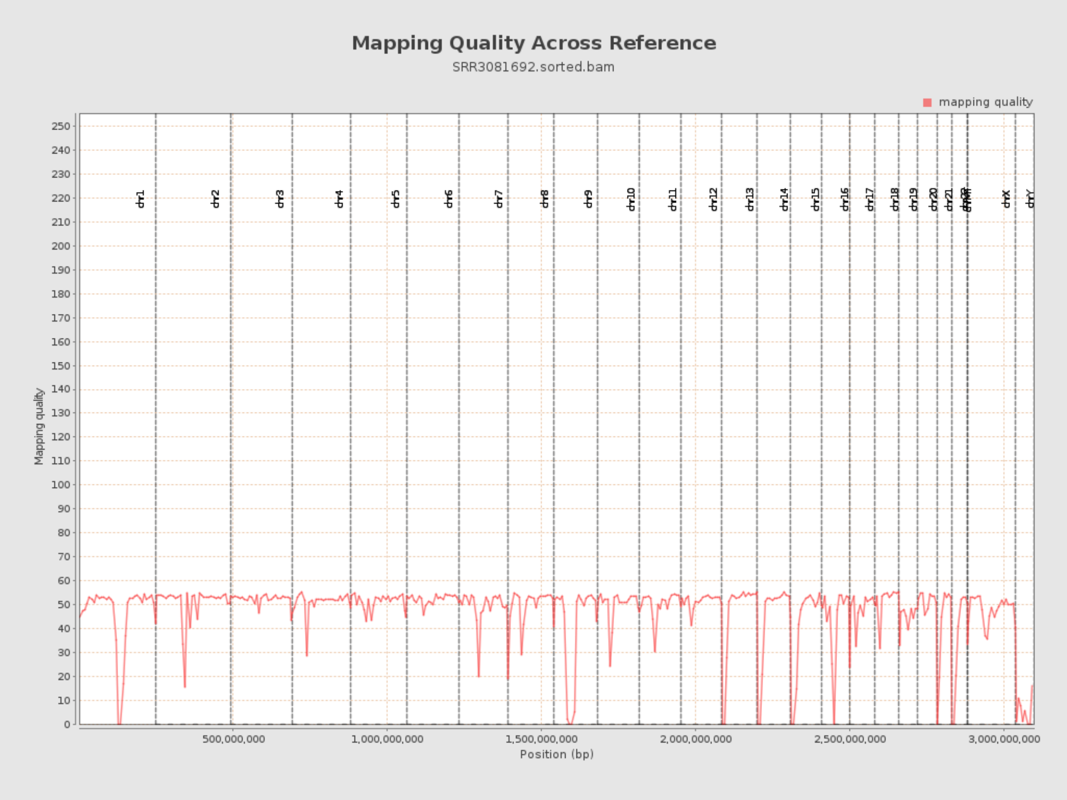
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram