Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:47:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081212.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_SRR3081212 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081212.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:47:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081212.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,229,522
Mapped reads	8,261,670 / 89.51%
Unmapped reads	967,852 / 10.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,774 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	377,187 / 4.09%
Duplication rate	2.5%
Clipped reads	2,809,381 / 30.44%

2.2. ACGT Content

Number/percentage of A's	170,614,547 / 29.73%
Number/percentage of C's	108,603,299 / 18.92%
Number/percentage of T's	176,892,818 / 30.82%
Number/percentage of G's	117,695,469 / 20.51%
Number/percentage of N's	148,265 / 0.03%
GC Percentage	39.43%

2.3. Coverage

Mean	0.1855

Standard Deviation	2.0392

2.4. Mapping Quality

Mean Mapping Quality	47.75

2.5. Mismatches and indels

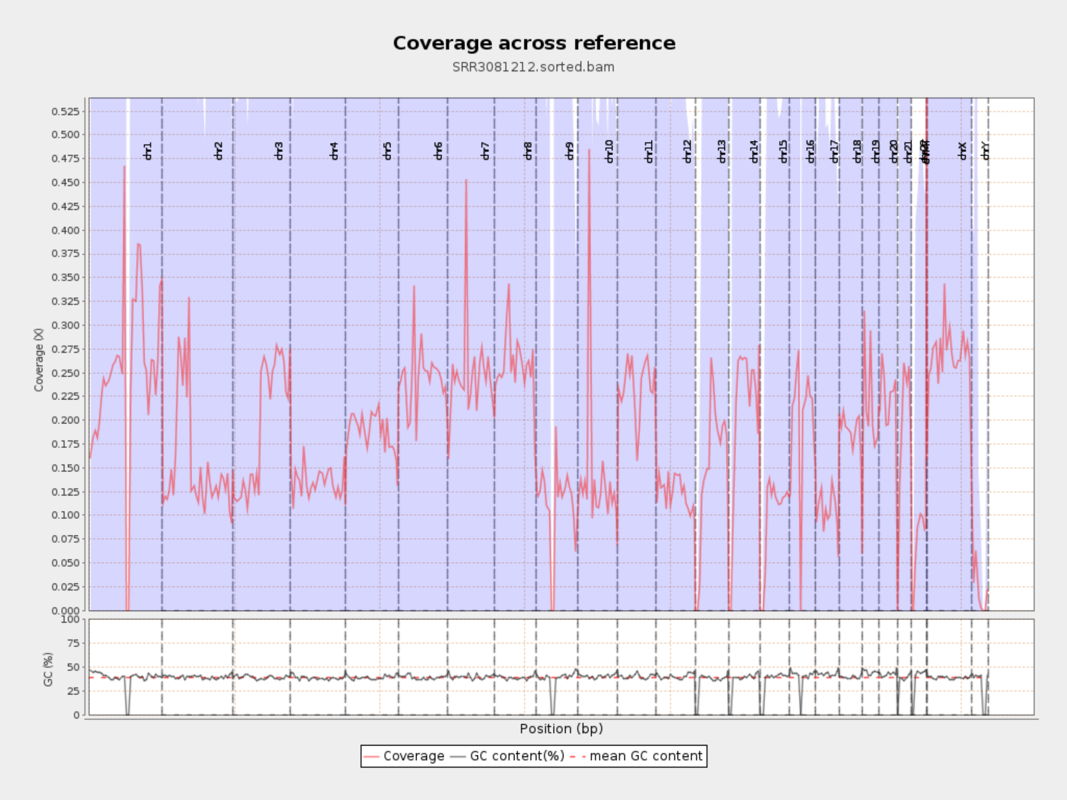
General error rate	1.1%
Mismatches	6,234,374
Insertions	43,434
Mapped reads with at least one insertion	0.52%
Deletions	136,841
Mapped reads with at least one deletion	1.64%
Homopolymer indels	47.74%

2.6. Chromosome stats

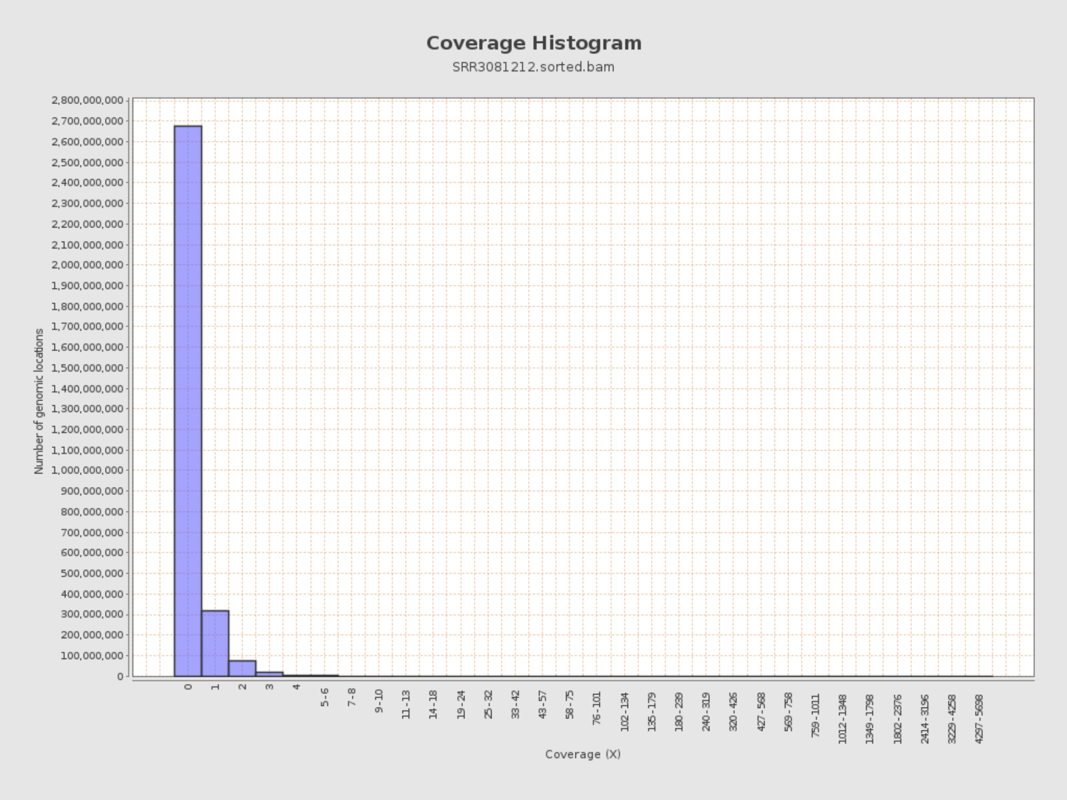
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	62066233	0.249	4.8903
chr2	243199373	37781247	0.1554	1.3449
chr3	198022430	38143803	0.1926	0.8297
chr4	191154276	25950440	0.1358	0.4903
chr5	180915260	34205589	0.1891	0.5697
chr6	171115067	41909967	0.2449	1.147
chr7	159138663	39753872	0.2498	3.145

chr8	146364022	37854212	0.2586	2.7987
chr9	141213431	15708715	0.1112	1.1434
chr10	135534747	19428744	0.1433	3.1164
chr11	135006516	31434040	0.2328	1.725
chr12	133851895	16626487	0.1242	0.4995
chr13	115169878	17571182	0.1526	0.4763
chr14	107349540	21759690	0.2027	0.6592
chr15	102531392	10179767	0.0993	0.3791
chr16	90354753	18184464	0.2013	0.8208
chr17	81195210	8430532	0.1038	0.6963
chr18	78077248	14918116	0.1911	2.2015
chr19	59128983	12715783	0.2151	3.1749
chr20	63025520	14059474	0.2231	0.6218
chr21	48129895	9169402	0.1905	0.6637
chr22	51304566	3448462	0.0672	0.322
chrMT	16571	13333	0.8046	1.0306
chrX	155270560	41434593	0.2669	0.874
chrY	59373566	1422830	0.024	0.3401

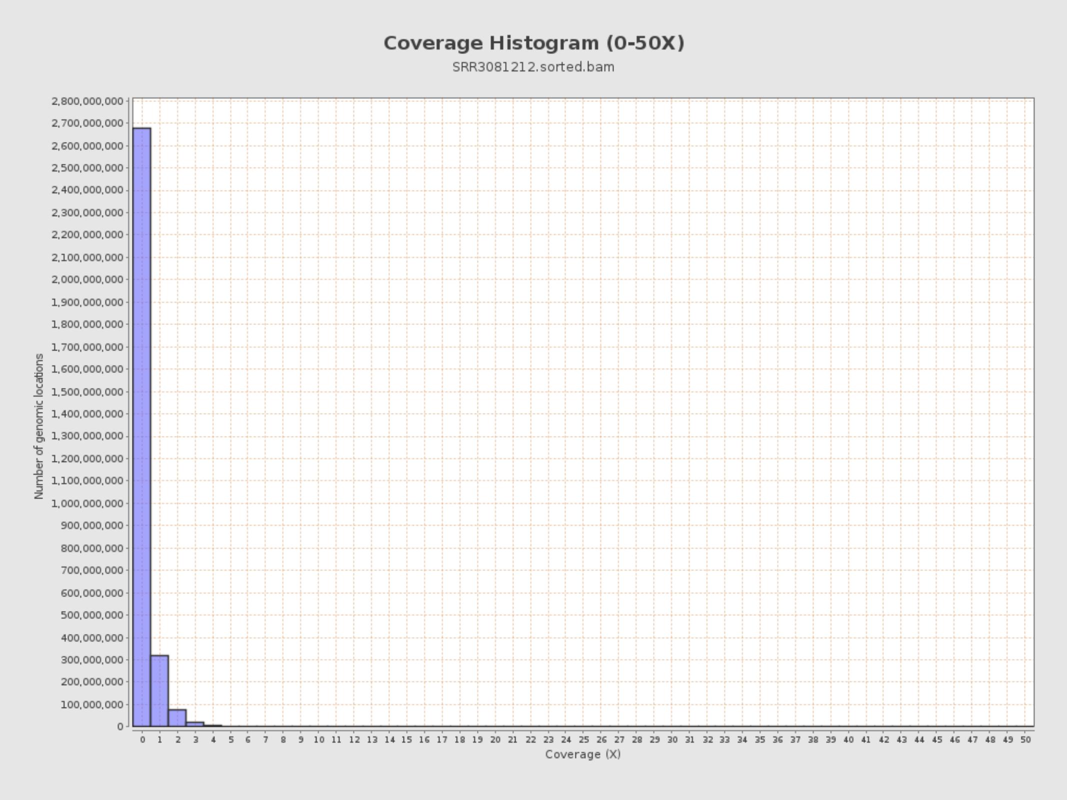
3. Results : Coverage across reference



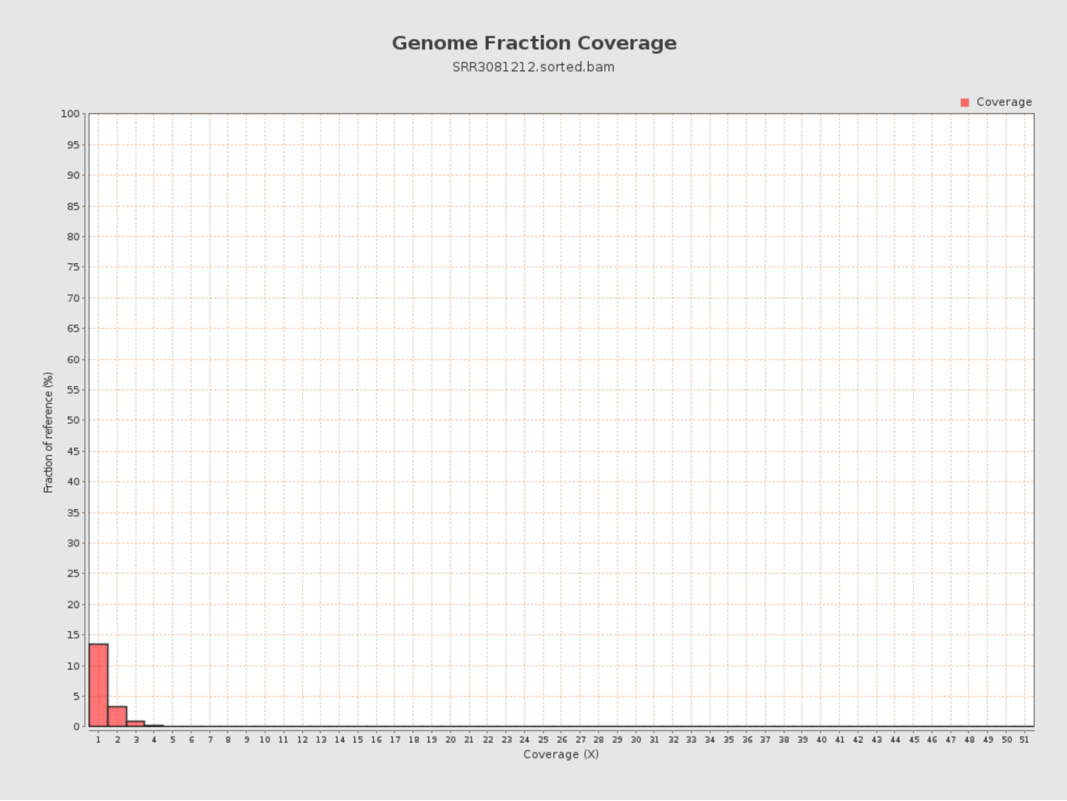
4. Results : Coverage Histogram



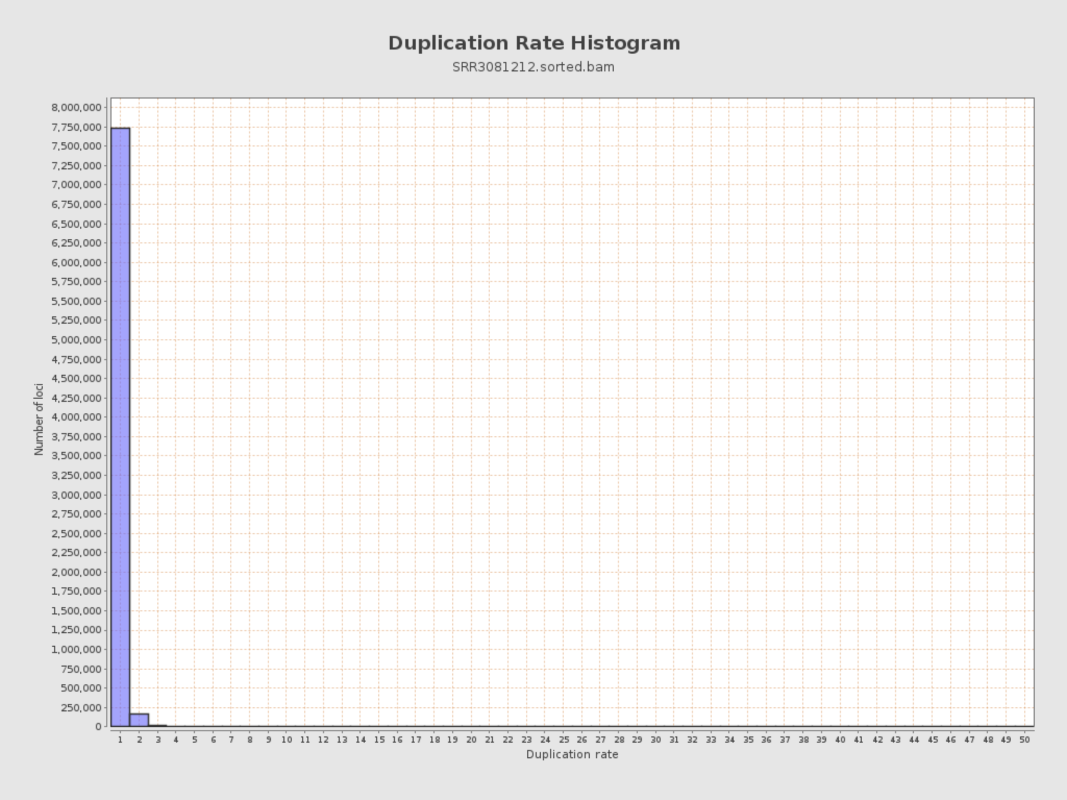
5. Results : Coverage Histogram (0-50X)



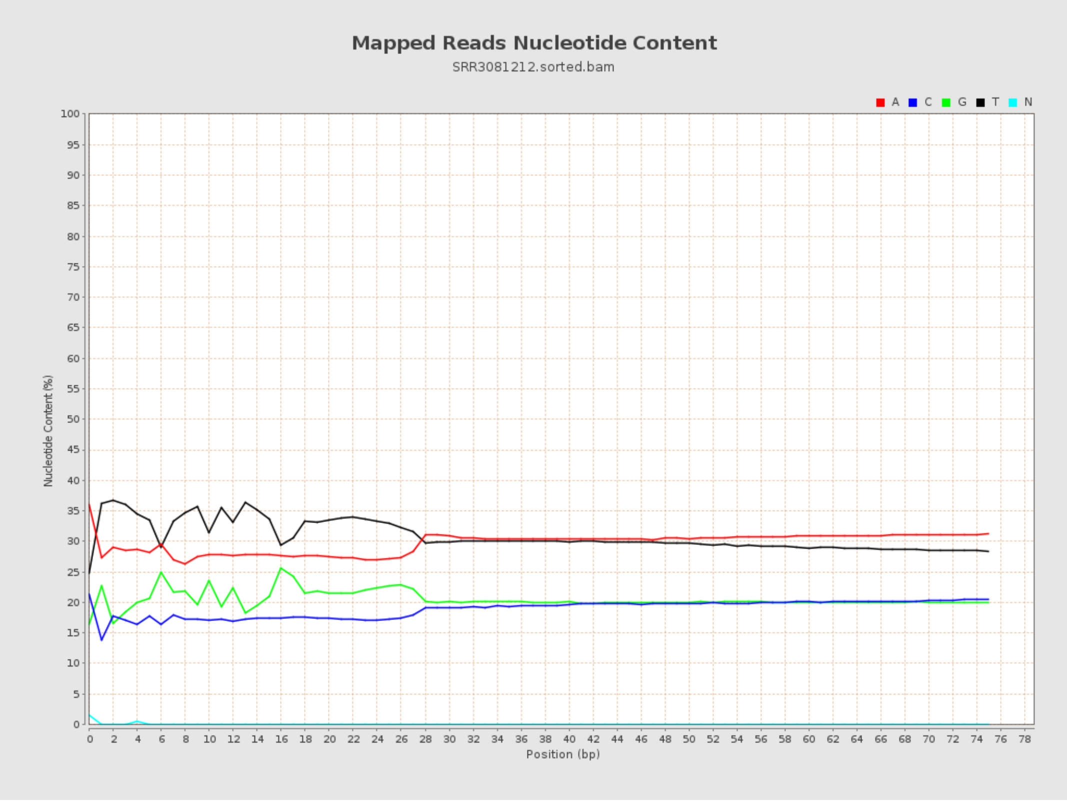
6. Results : Genome Fraction Coverage



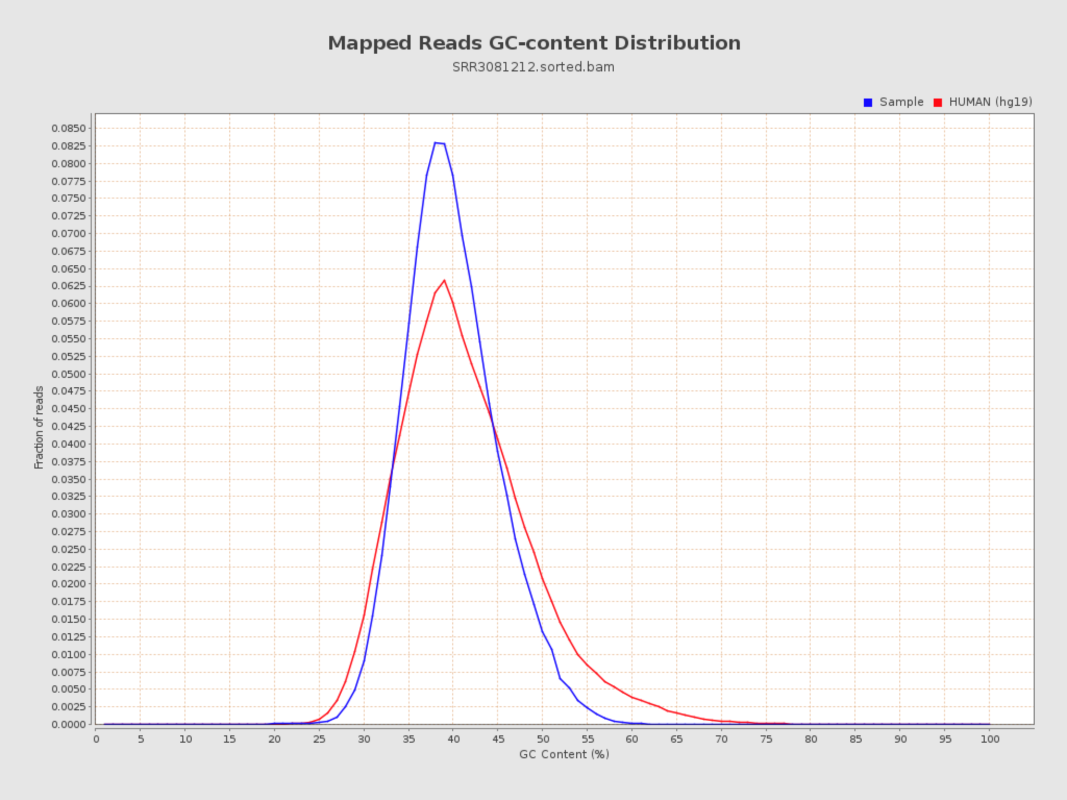
7. Results : Duplication Rate Histogram



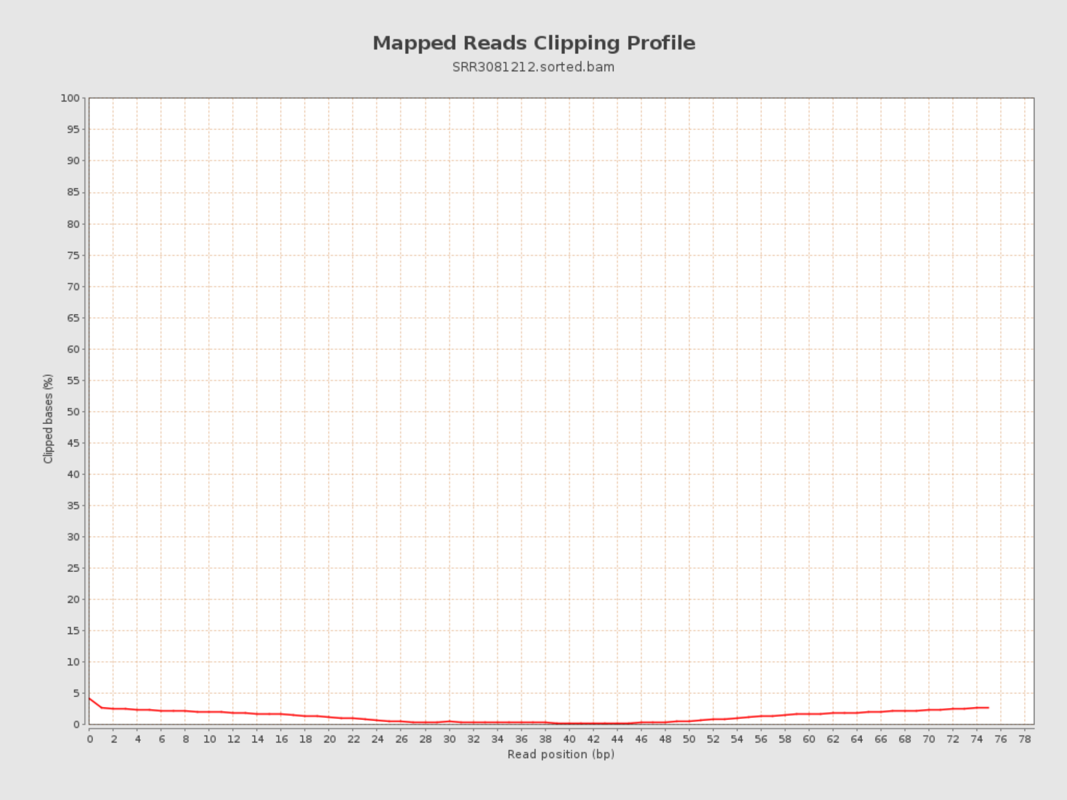
8. Results : Mapped Reads Nucleotide Content



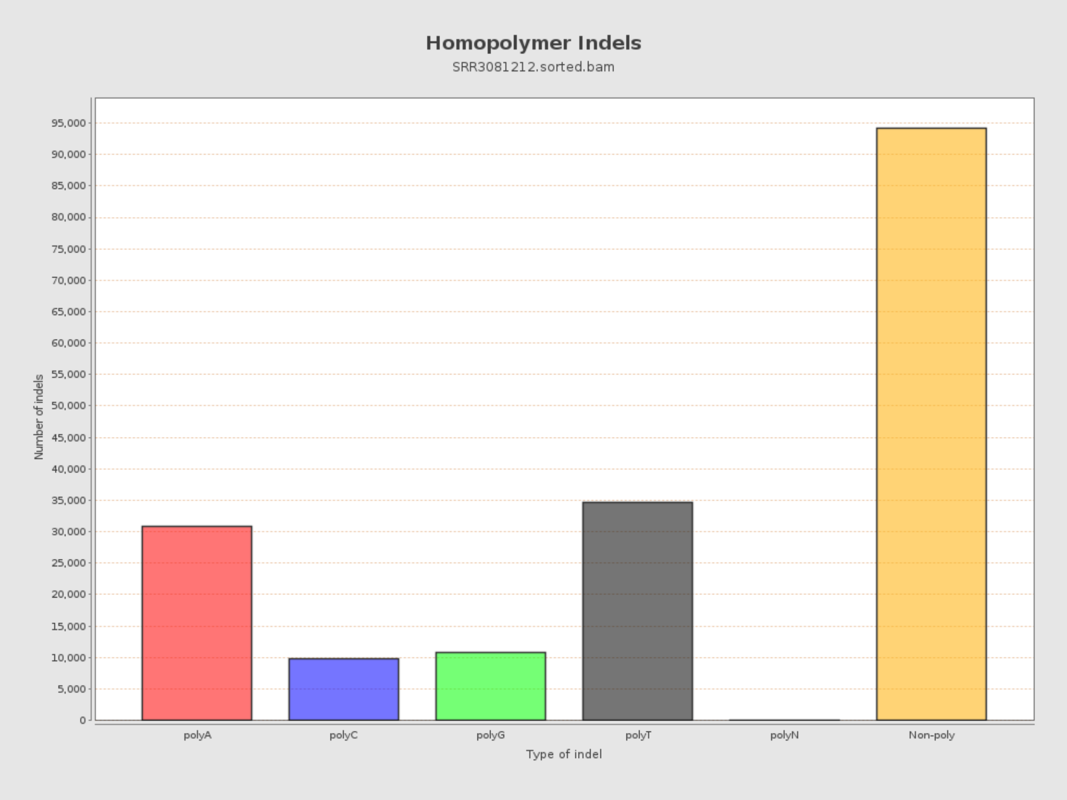
9. Results : Mapped Reads GC-content Distribution



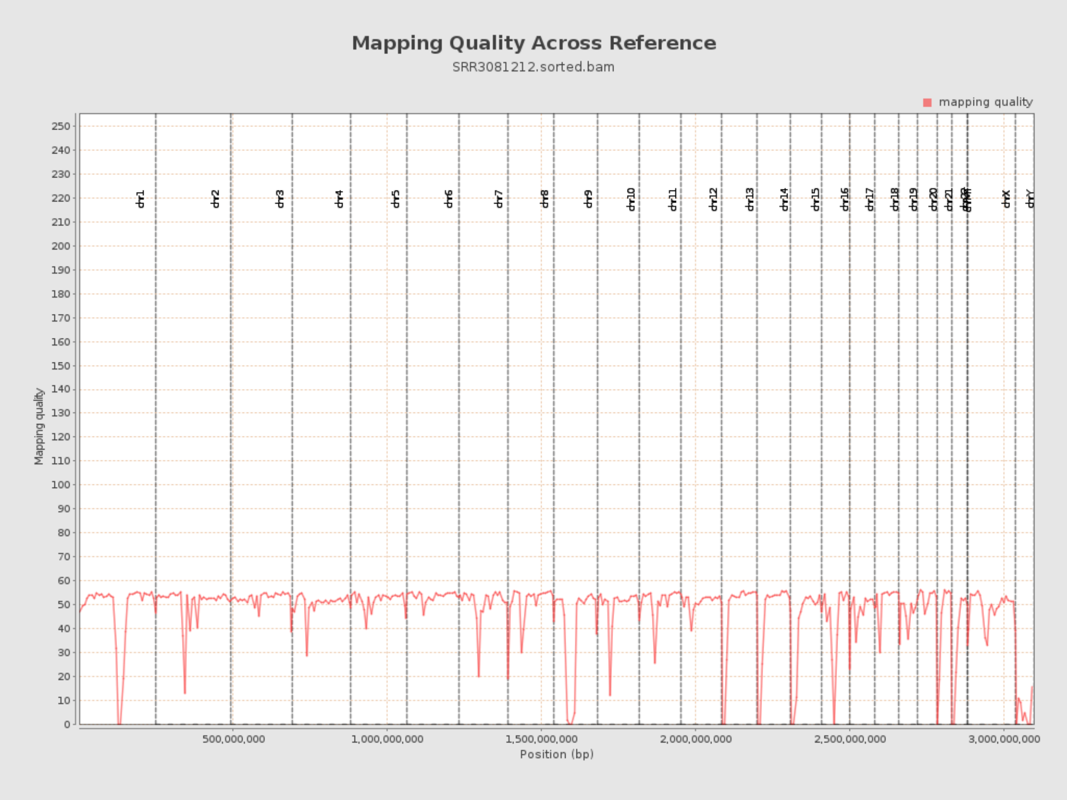
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram