Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:44:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080683.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_SRR3080683 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080683.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:44:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080683.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,253,538
Mapped reads	1,152,848 / 91.97%
Unmapped reads	100,690 / 8.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,450 / 0.99%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	40,386 / 3.22%
Duplication rate	3.06%
Clipped reads	524,971 / 41.88%

2.2. ACGT Content

Number/percentage of A's	21,094,170 / 27.54%
Number/percentage of C's	13,986,635 / 18.26%
Number/percentage of T's	24,449,175 / 31.92%
Number/percentage of G's	17,057,696 / 22.27%
Number/percentage of N's	3,584 / 0%
GC Percentage	40.53%

2.3. Coverage

Mean	0.0248

Standard Deviation	0.2085

2.4. Mapping Quality

Mean Mapping Quality	45.94

2.5. Mismatches and indels

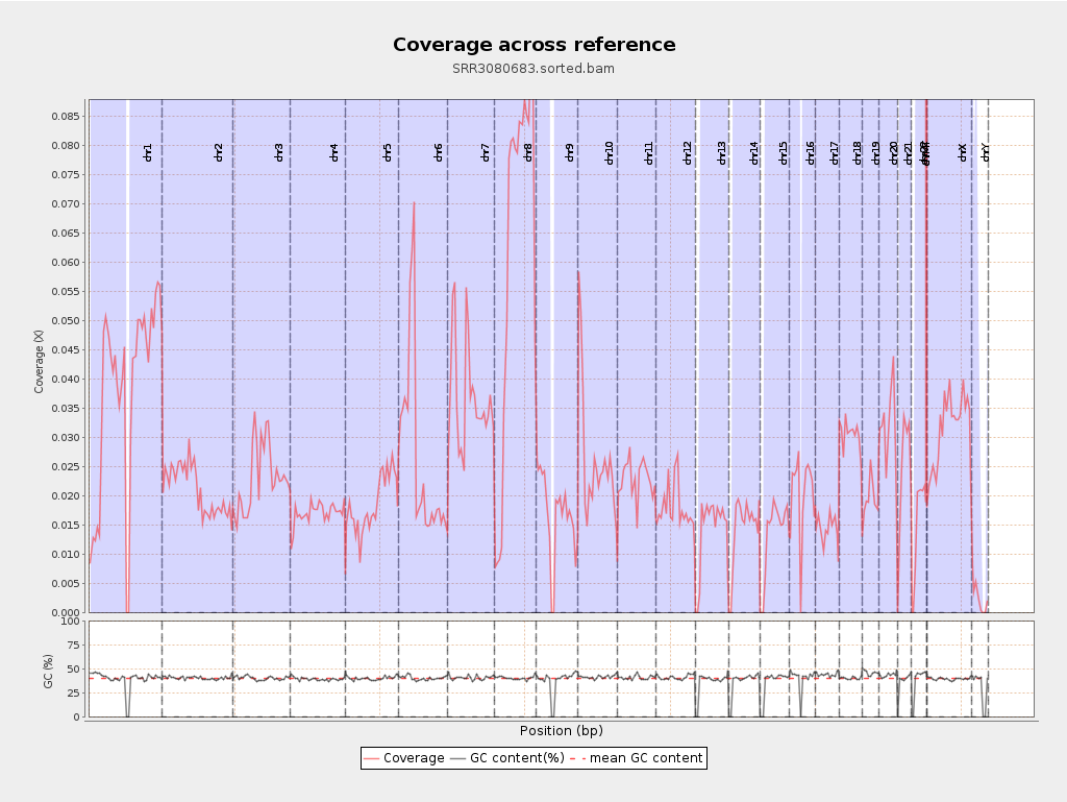
General error rate	0.68%
Mismatches	513,555
Insertions	5,736
Mapped reads with at least one insertion	0.49%
Deletions	17,449
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.9%

2.6. Chromosome stats

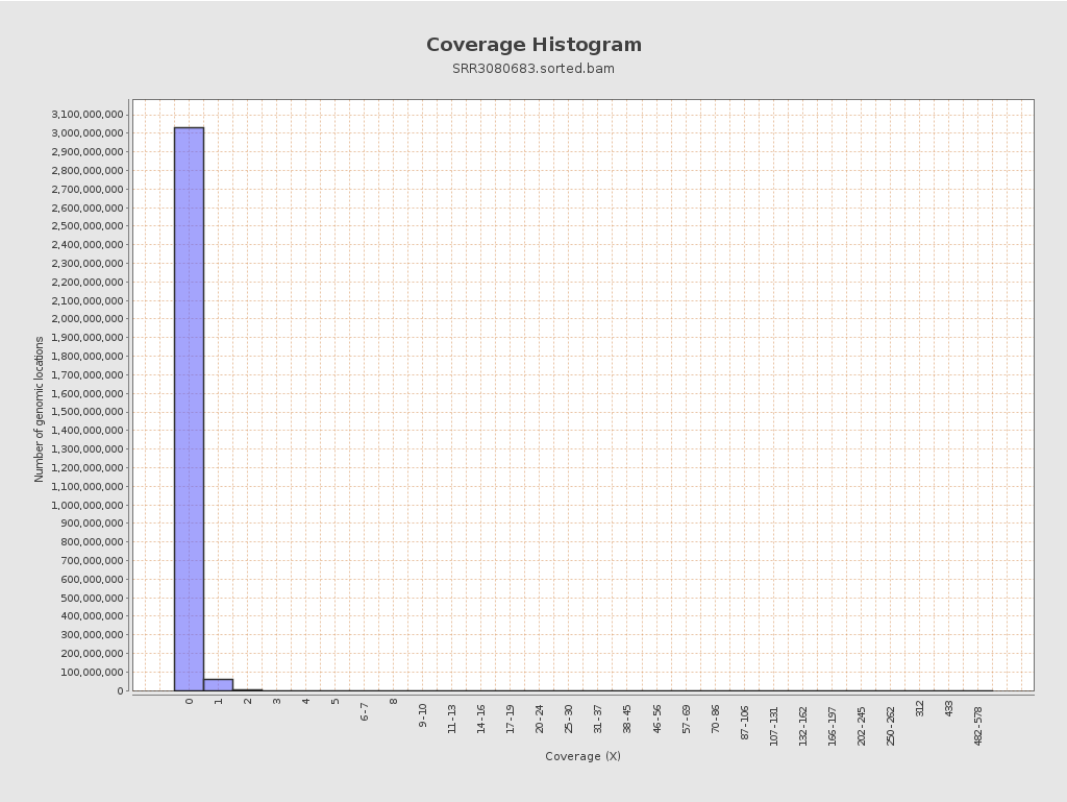
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9377254	0.0376	0.2464
chr2	243199373	5100484	0.021	0.2948
chr3	198022430	4592117	0.0232	0.1667
chr4	191154276	3247506	0.017	0.1455
chr5	180915260	3366174	0.0186	0.1495
chr6	171115067	4551722	0.0266	0.2107
chr7	159138663	5932336	0.0373	0.3696

chr8	146364022	9092245	0.0621	0.3037
chr9	141213431	2331796	0.0165	0.1598
chr10	135534747	3583696	0.0264	0.1853
chr11	135006516	3066635	0.0227	0.1769
chr12	133851895	2396053	0.0179	0.1474
chr13	115169878	1619510	0.0141	0.1311
chr14	107349540	1504907	0.014	0.1309
chr15	102531392	1376189	0.0134	0.1334
chr16	90354753	1846361	0.0204	0.1585
chr17	81195210	1152689	0.0142	0.132
chr18	78077248	2387436	0.0306	0.2192
chr19	59128983	1180411	0.02	0.1759
chr20	63025520	1991354	0.0316	0.1964
chr21	48129895	1148268	0.0239	0.1717
chr22	51304566	751186	0.0146	0.1312
chrMT	16571	12608	0.7608	0.9885
chrX	155270560	4867663	0.0313	0.1989
chrY	59373566	143069	0.0024	0.0574

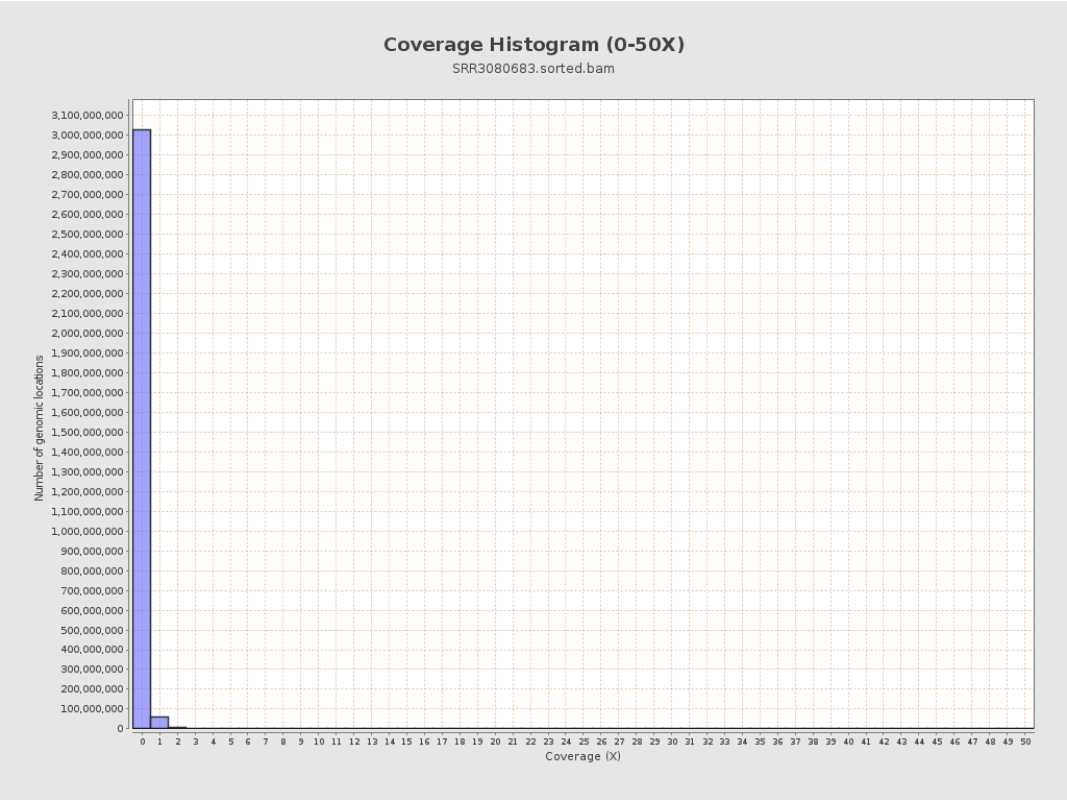
3. Results : Coverage across reference



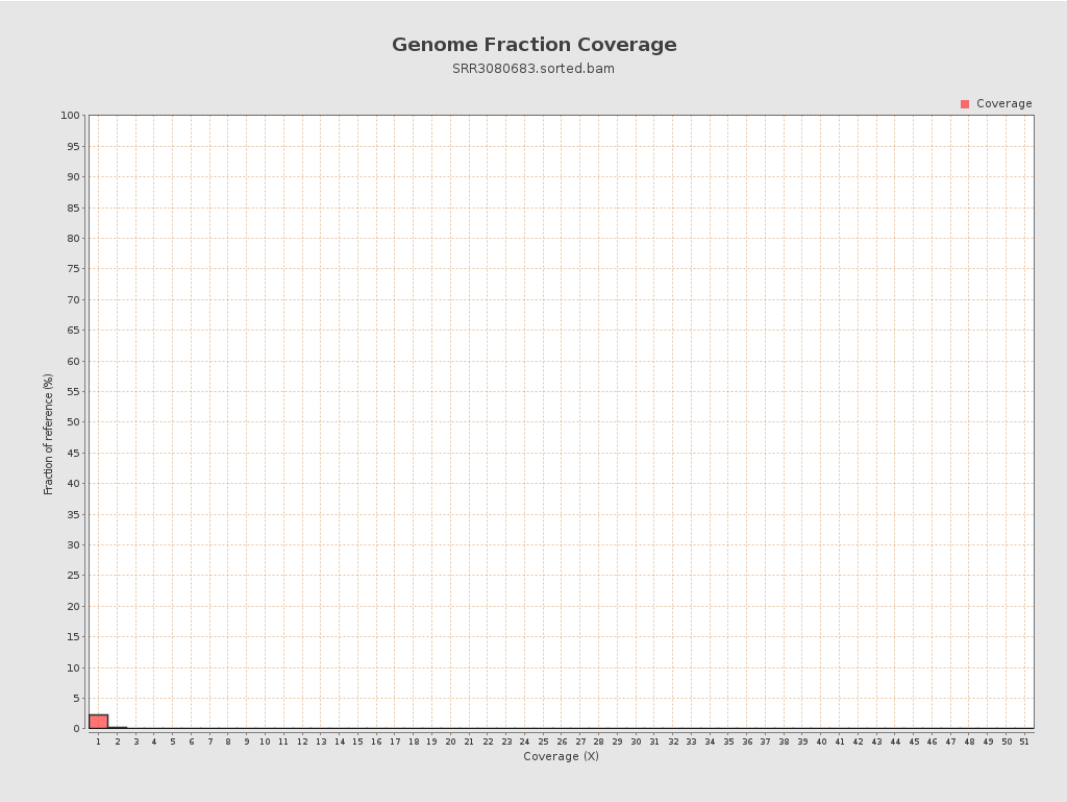
4. Results : Coverage Histogram



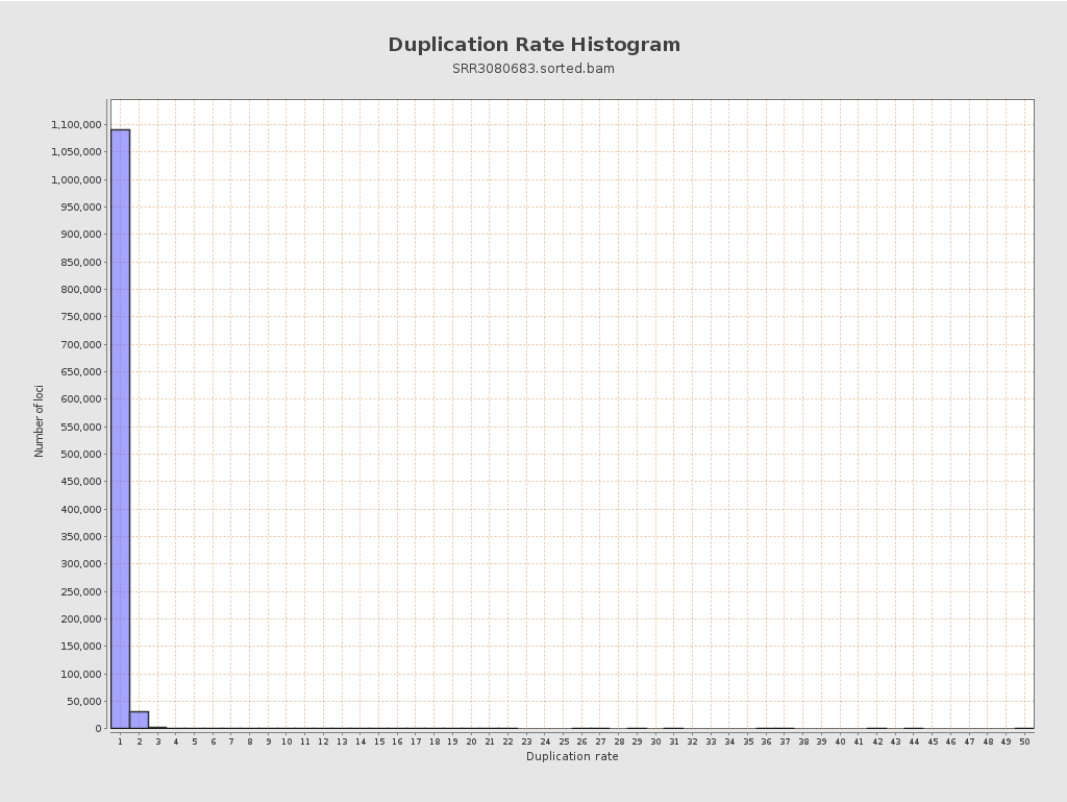
5. Results : Coverage Histogram (0-50X)



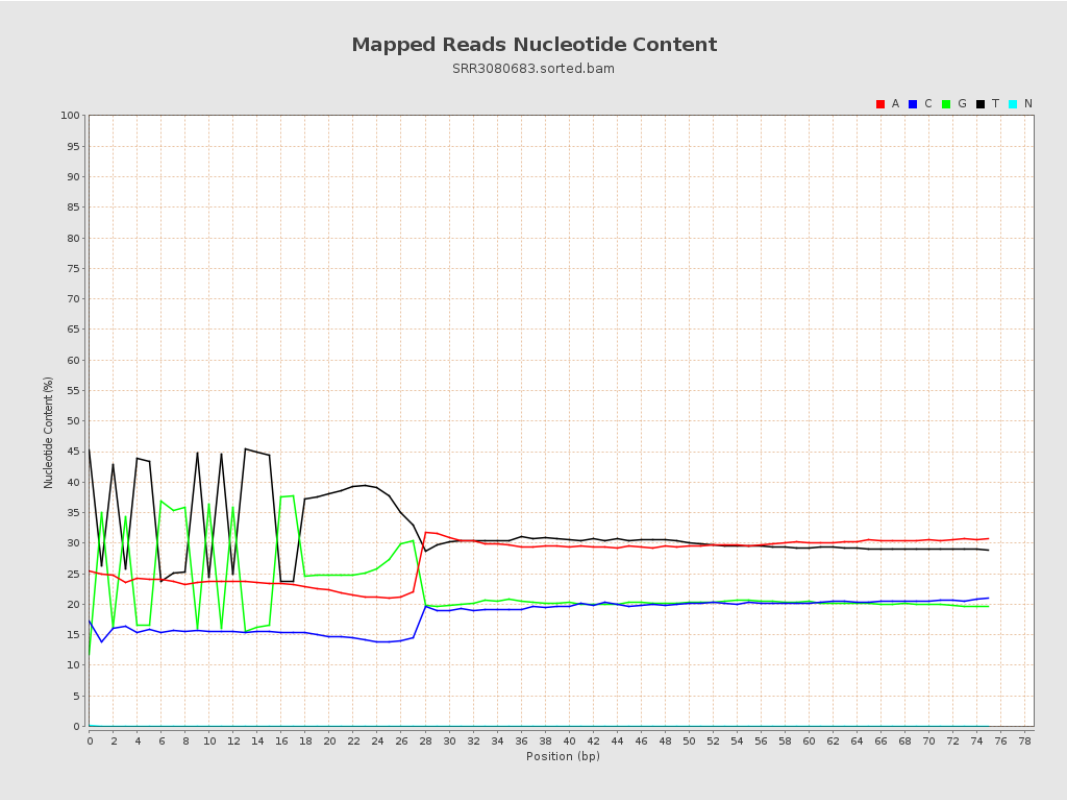
6. Results : Genome Fraction Coverage



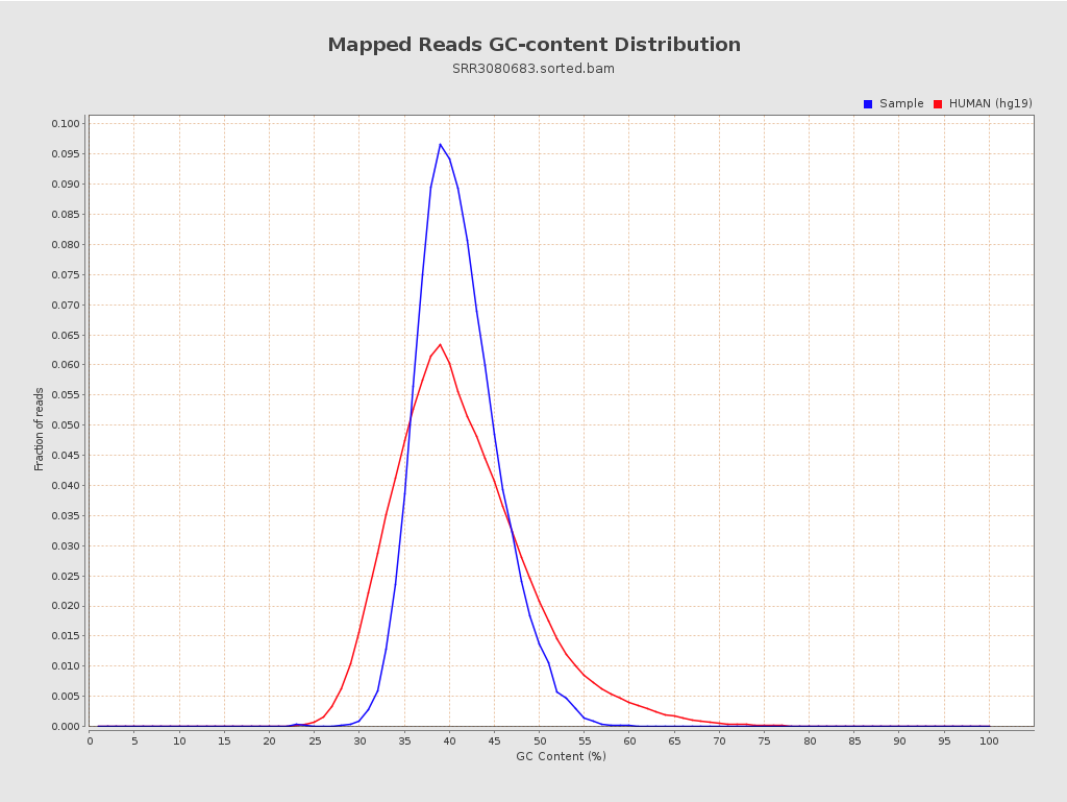
7. Results : Duplication Rate Histogram



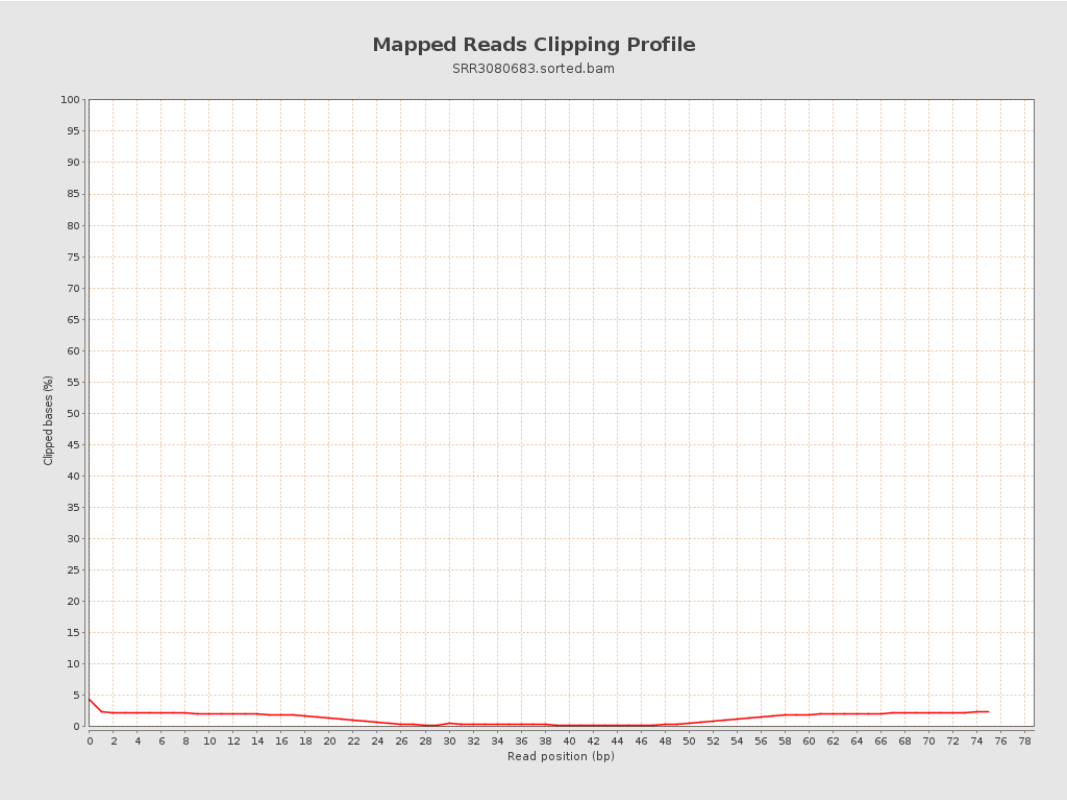
8. Results : Mapped Reads Nucleotide Content



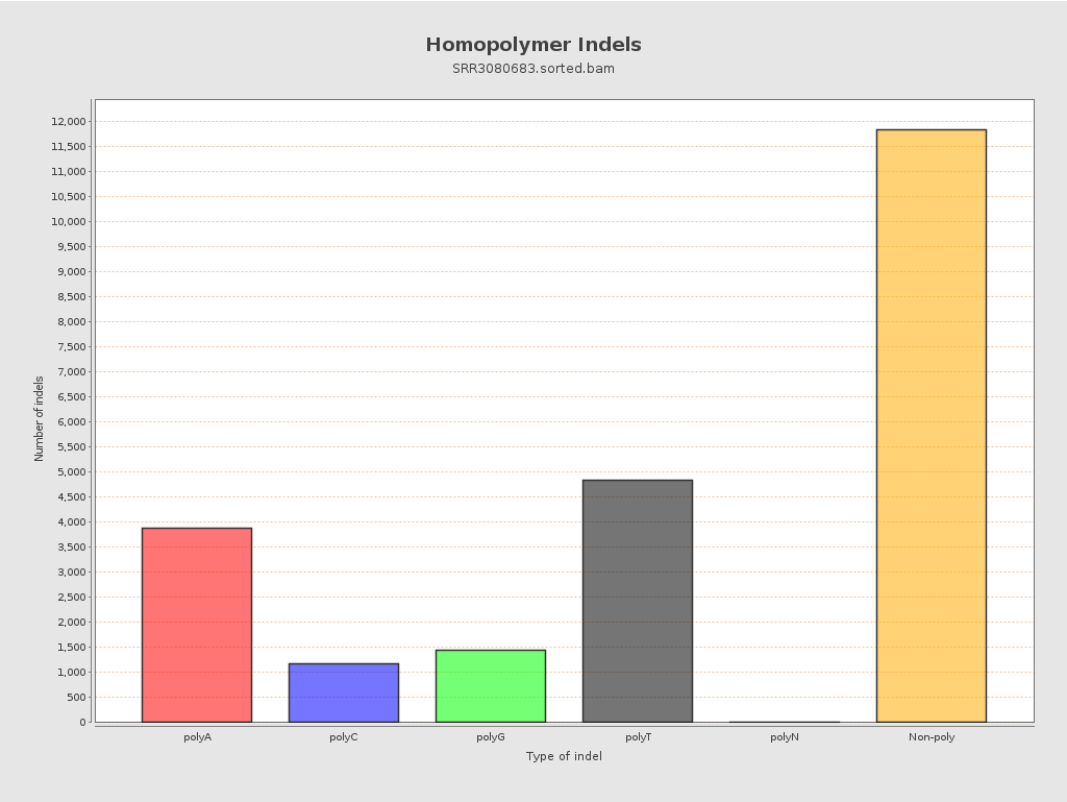
9. Results : Mapped Reads GC-content Distribution



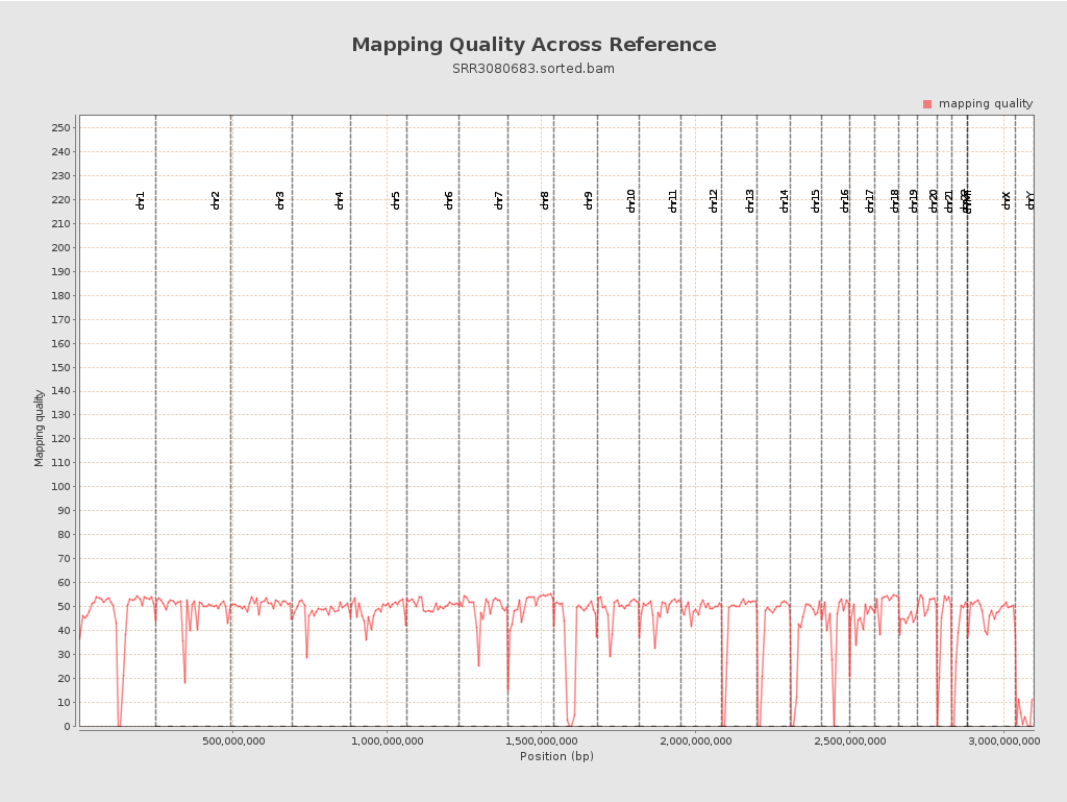
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram