Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:26:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082906.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_SRR3082906 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082906.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:26:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082906.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,152,426
Mapped reads	1,930,998 / 89.71%
Unmapped reads	221,428 / 10.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,797 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	97,324 / 4.52%
Duplication rate	4.24%
Clipped reads	854,902 / 39.72%

2.2. ACGT Content

Number/percentage of A's	35,307,580 / 27.44%
Number/percentage of C's	23,758,139 / 18.46%
Number/percentage of T's	40,859,788 / 31.75%
Number/percentage of G's	28,754,342 / 22.34%
Number/percentage of N's	5,776 / 0%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0416

Standard Deviation	0.3355

2.4. Mapping Quality

Mean Mapping Quality	46

2.5. Mismatches and indels

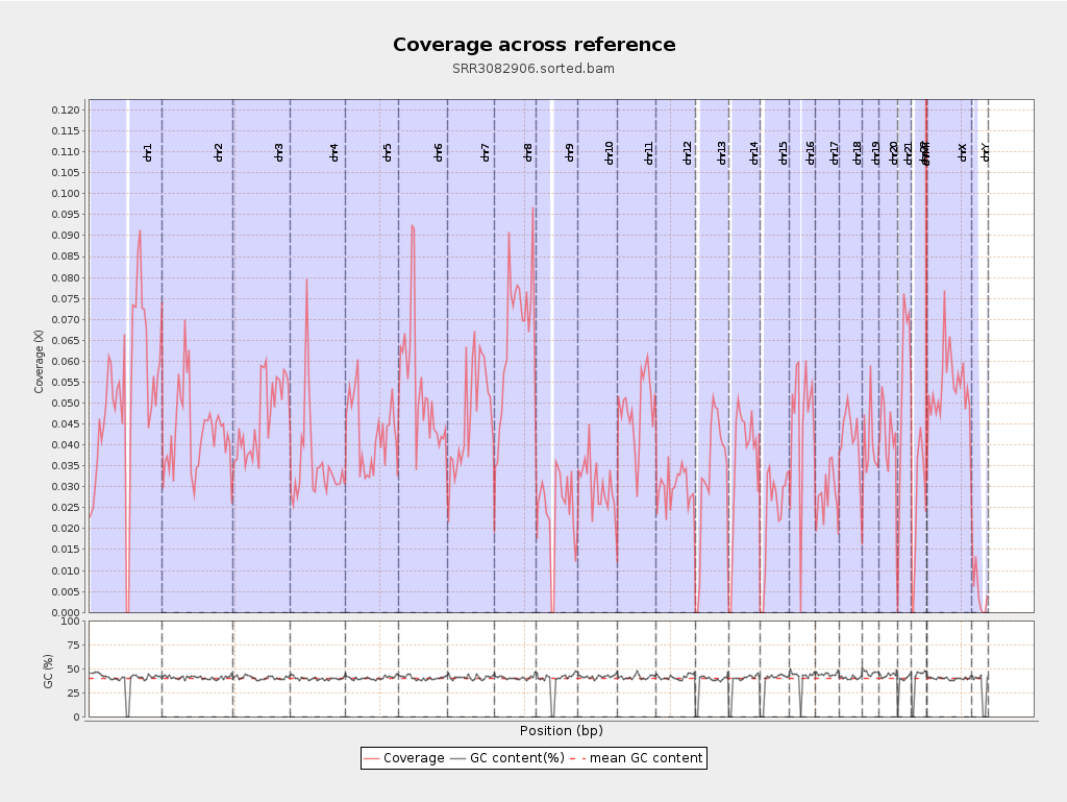
General error rate	0.73%
Mismatches	926,742
Insertions	9,853
Mapped reads with at least one insertion	0.51%
Deletions	30,230
Mapped reads with at least one deletion	1.55%
Homopolymer indels	48.43%

2.6. Chromosome stats

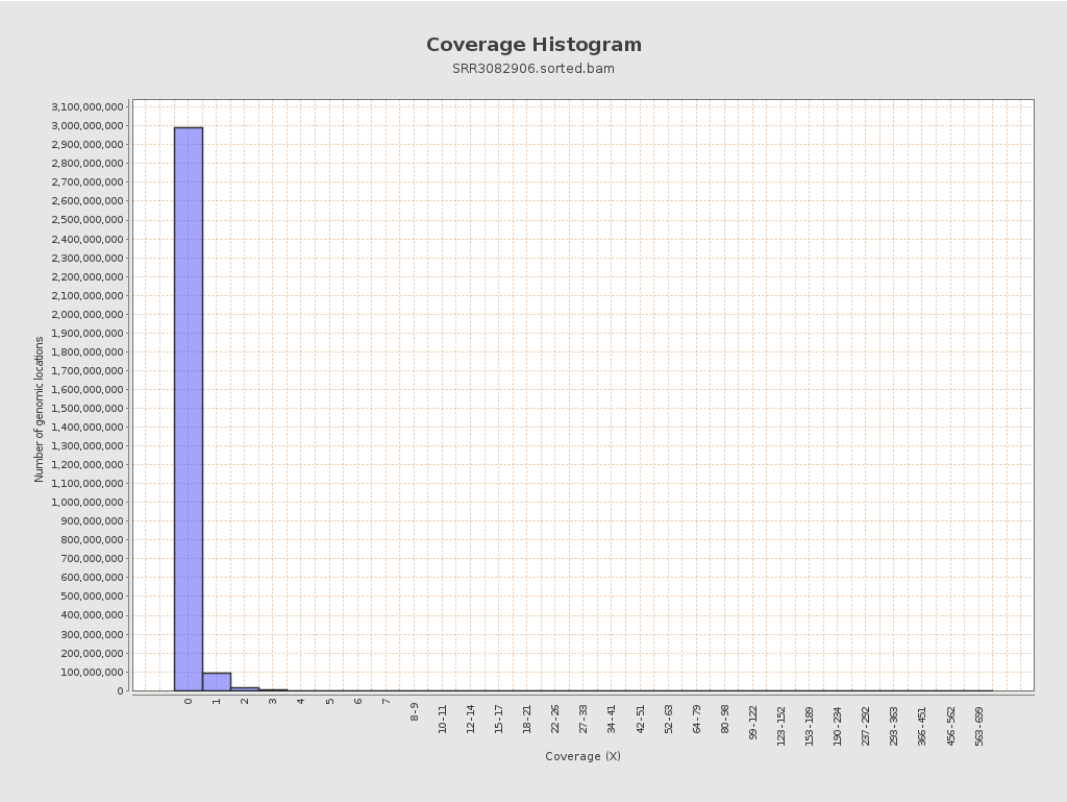
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12772272	0.0512	0.5405
chr2	243199373	10465488	0.043	0.4179
chr3	198022430	9181204	0.0464	0.2489
chr4	191154276	6760135	0.0354	0.2201
chr5	180915260	7746922	0.0428	0.2409
chr6	171115067	9079805	0.0531	0.3249
chr7	159138663	7562321	0.0475	0.4282

chr8	146364022	9681701	0.0661	0.4782
chr9	141213431	3439031	0.0244	0.2547
chr10	135534747	4147036	0.0306	0.2505
chr11	135006516	6488139	0.0481	0.3557
chr12	133851895	3969392	0.0297	0.2026
chr13	115169878	3736802	0.0324	0.2095
chr14	107349540	3851753	0.0359	0.2295
chr15	102531392	2440279	0.0238	0.1821
chr16	90354753	4142986	0.0459	0.2551
chr17	81195210	2260381	0.0278	0.2261
chr18	78077248	3300455	0.0423	0.499
chr19	59128983	2350158	0.0397	0.4118
chr20	63025520	2640899	0.0419	0.2442
chr21	48129895	2571527	0.0534	0.278
chr22	51304566	1327836	0.0259	0.1835
chrMT	16571	211195	12.7449	7.6606
chrX	155270560	8327126	0.0536	0.2866
chrY	59373566	281084	0.0047	0.0971

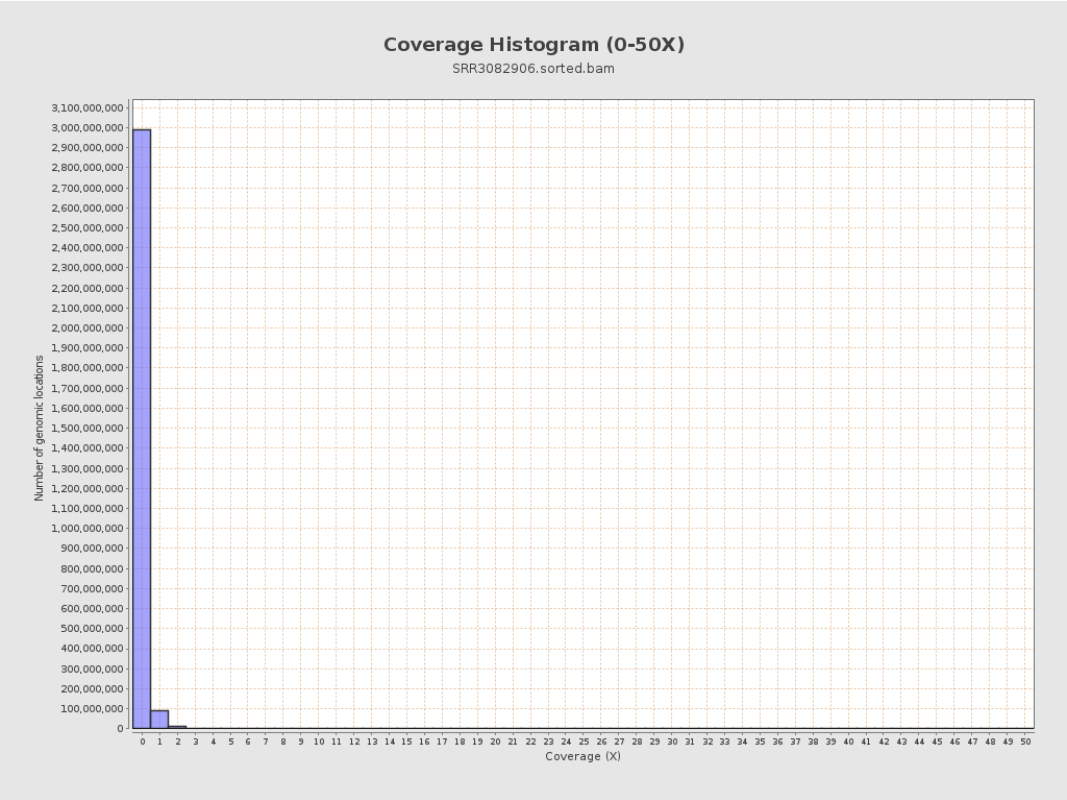
3. Results : Coverage across reference



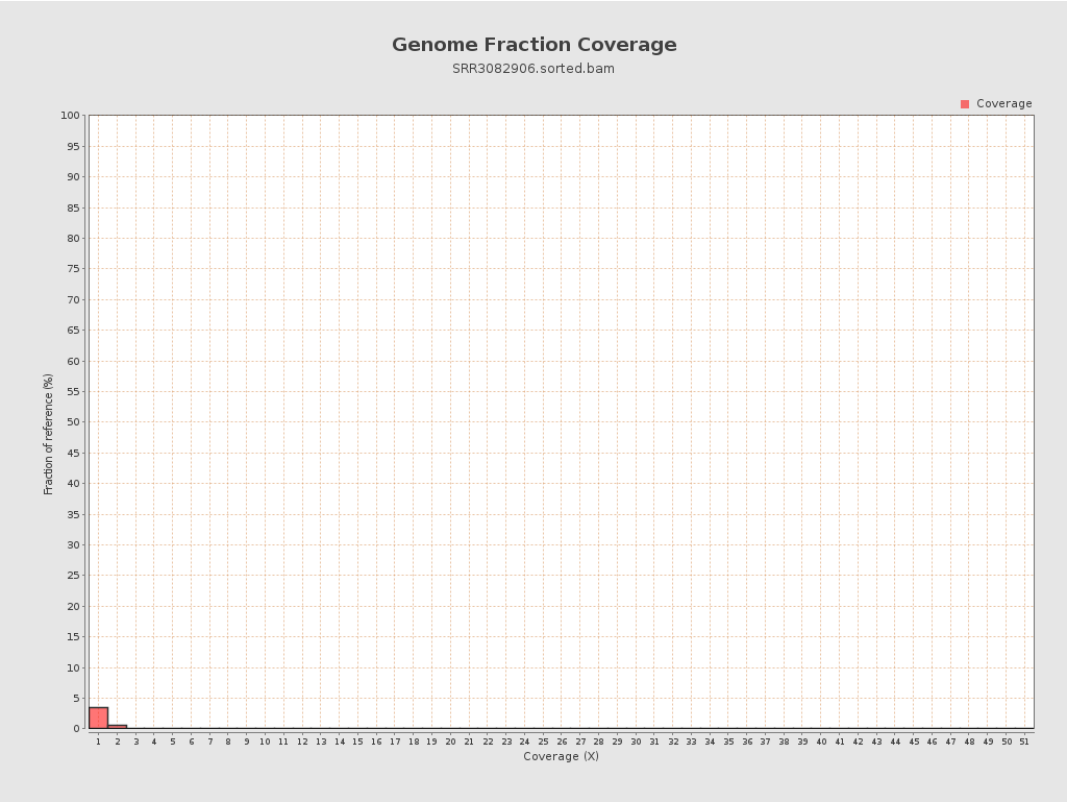
4. Results : Coverage Histogram



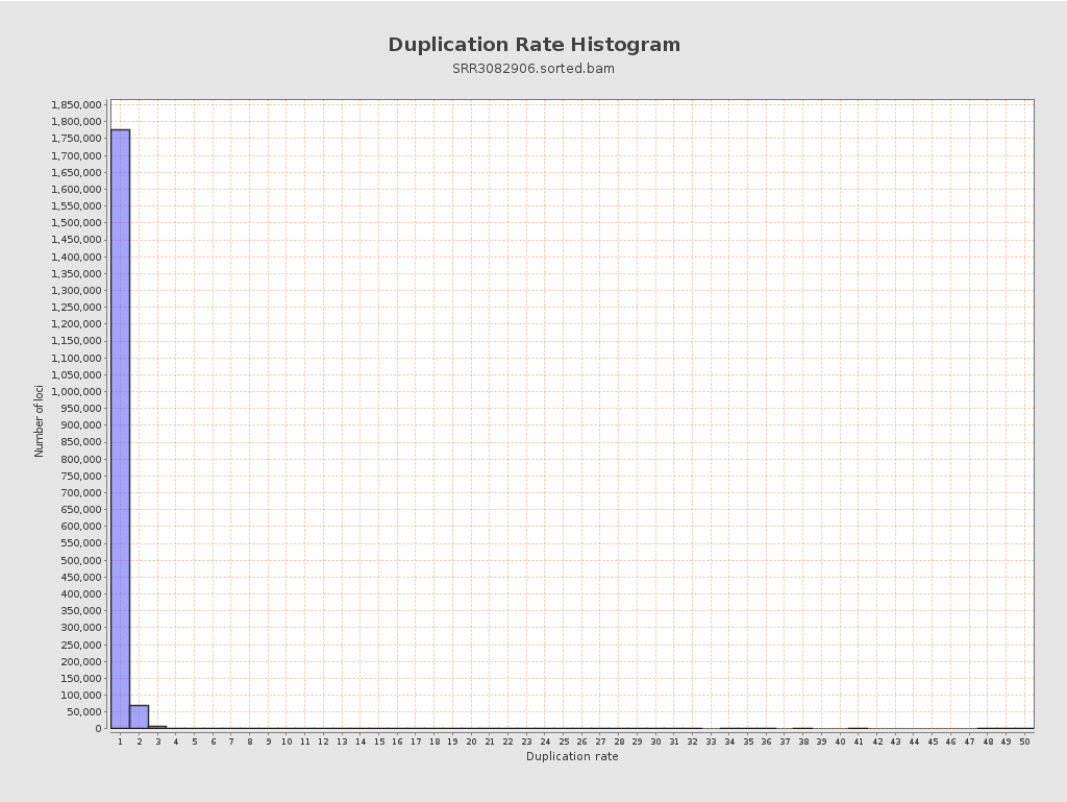
5. Results : Coverage Histogram (0-50X)



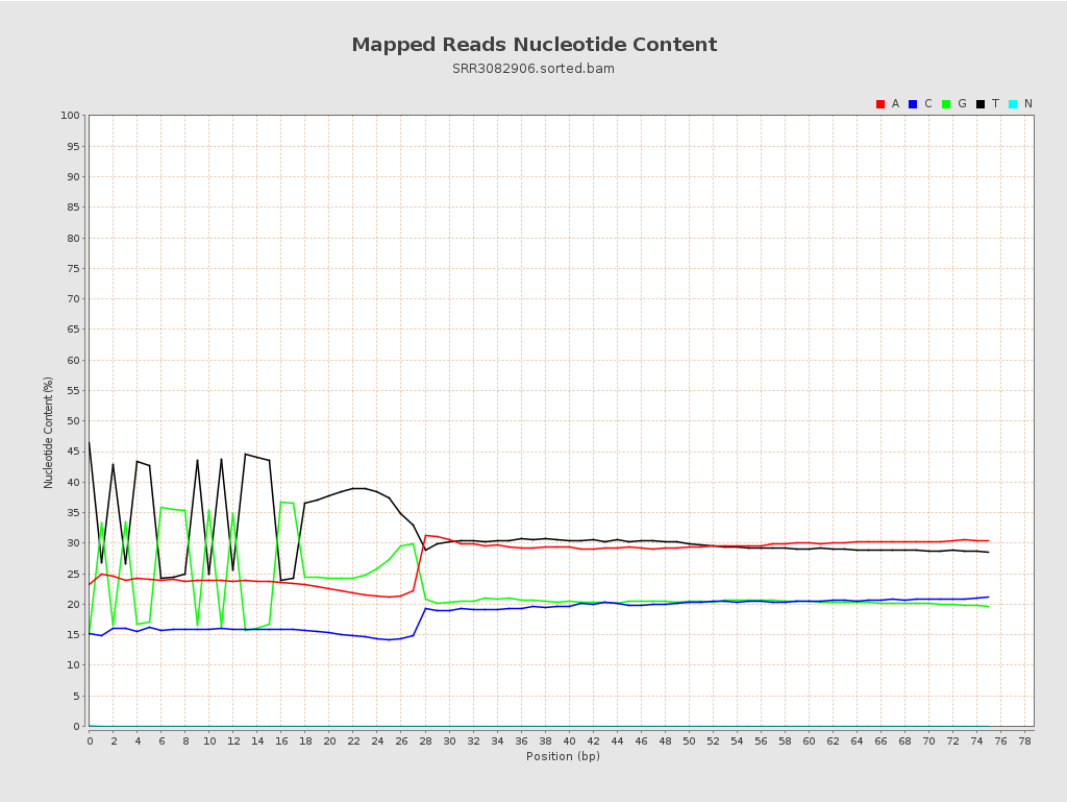
6. Results : Genome Fraction Coverage



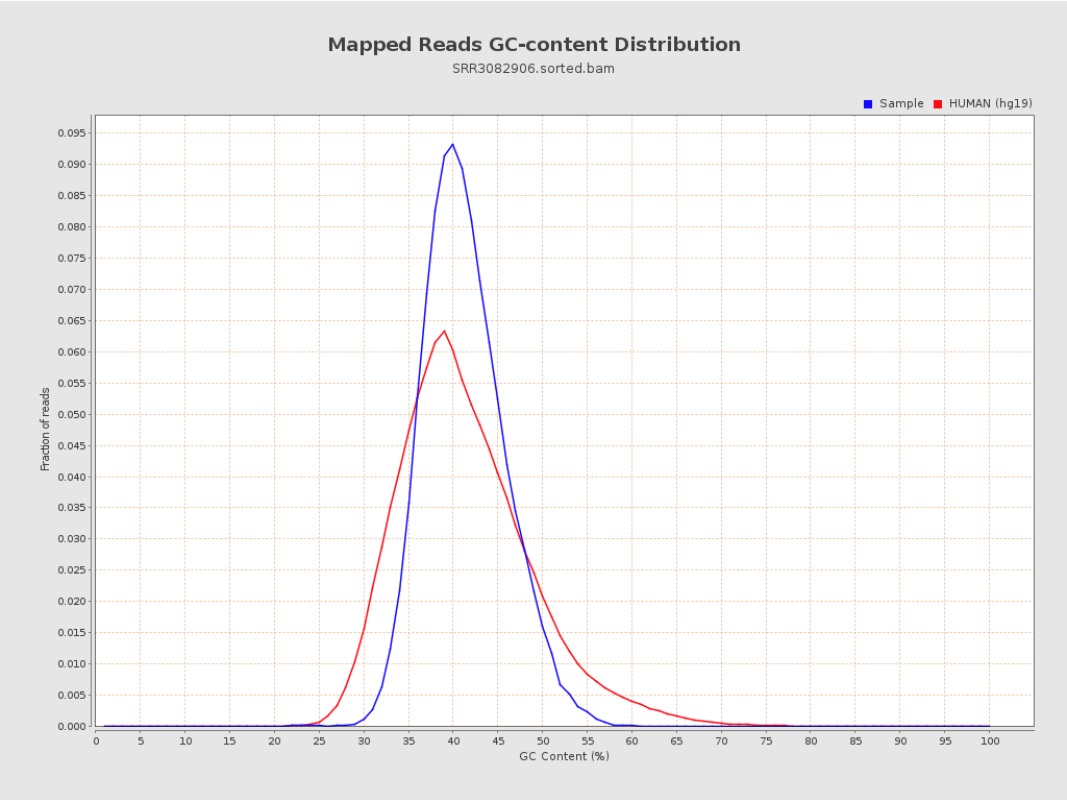
7. Results : Duplication Rate Histogram



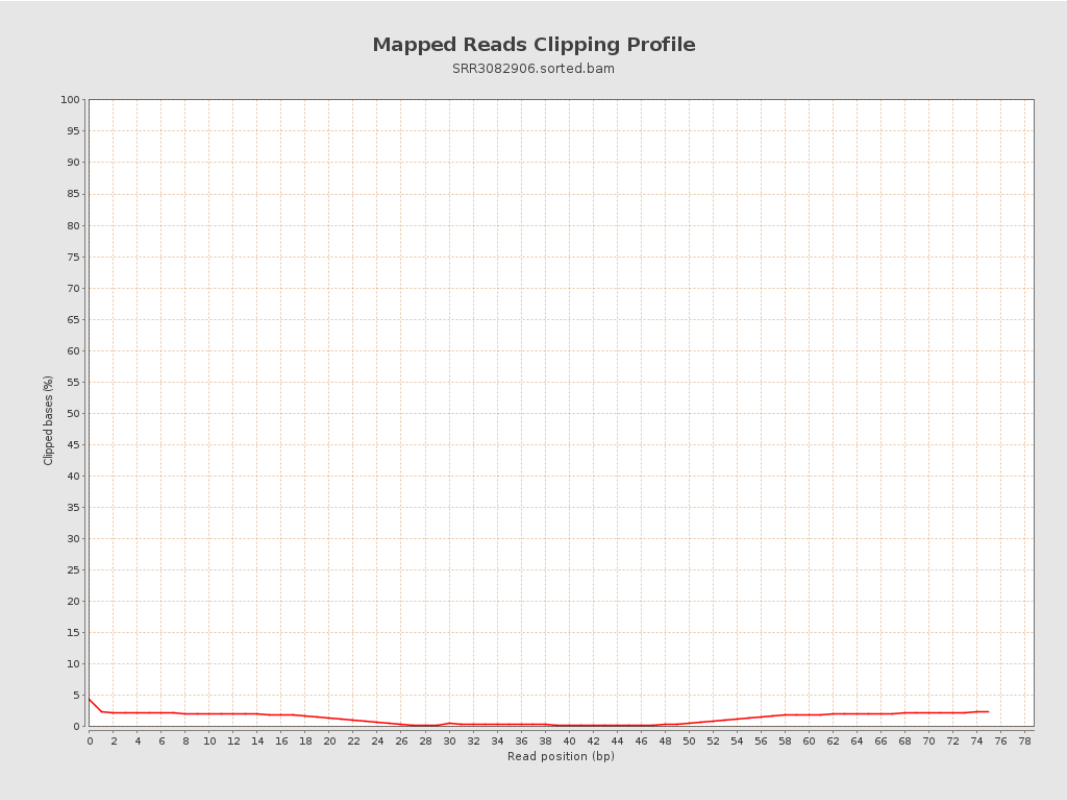
8. Results : Mapped Reads Nucleotide Content



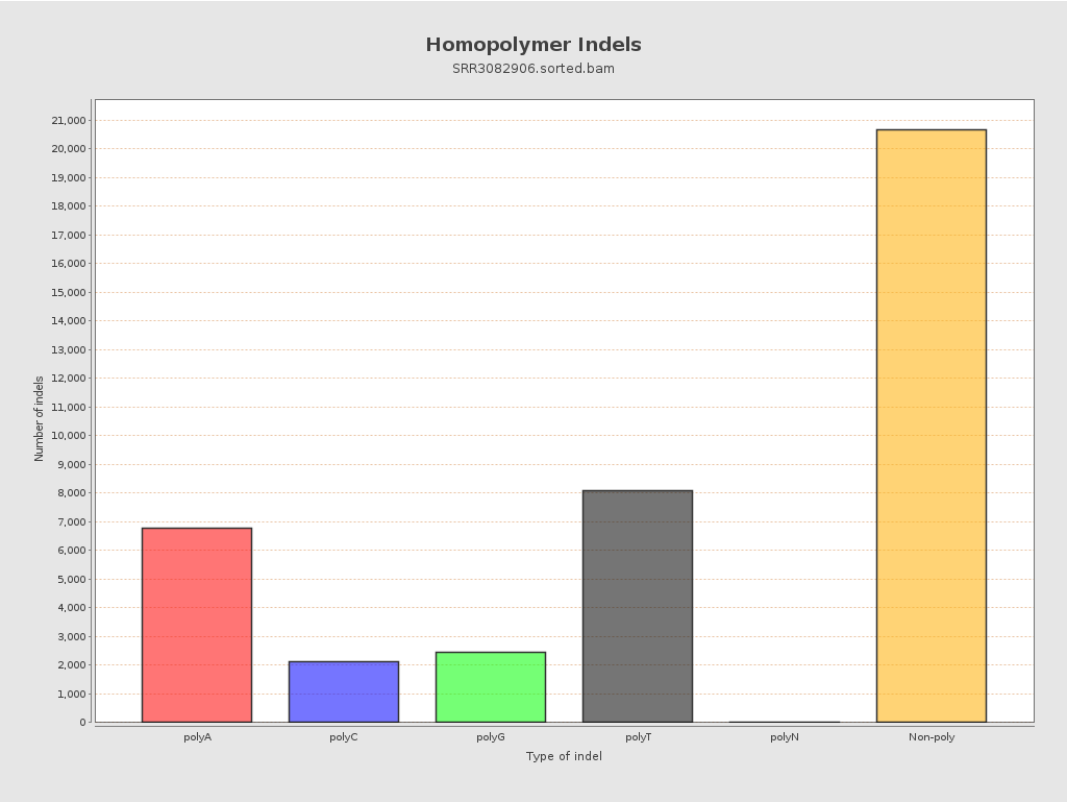
9. Results : Mapped Reads GC-content Distribution



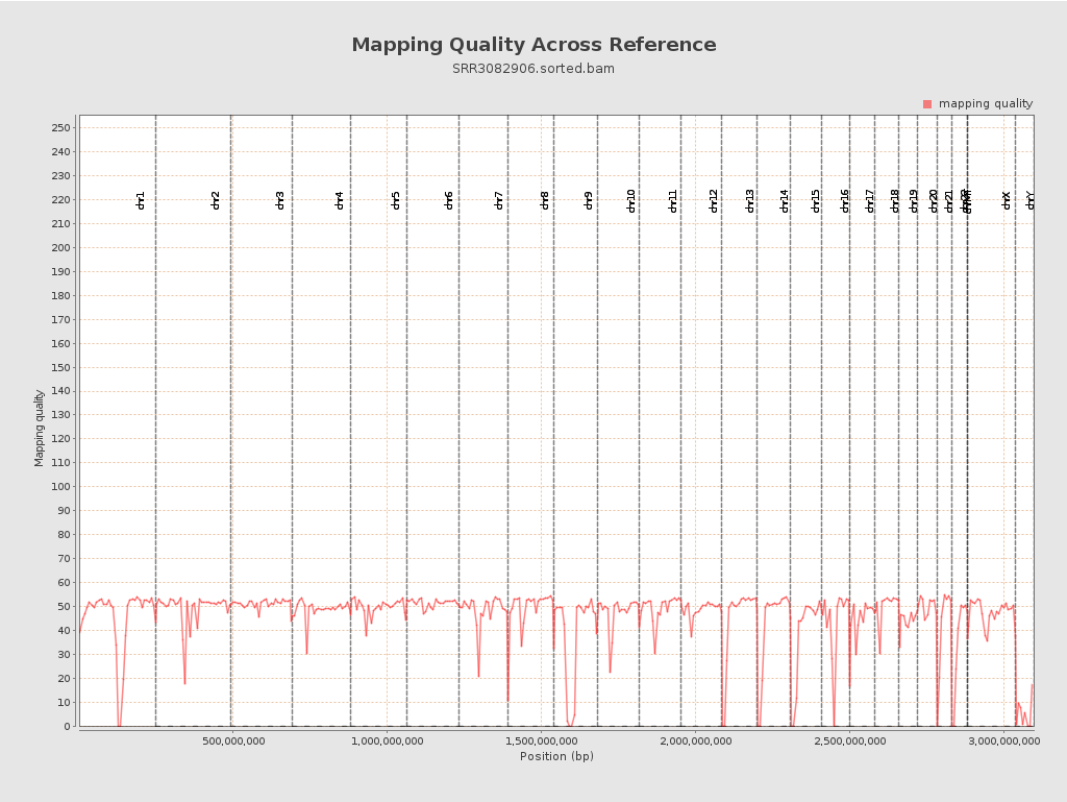
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram