Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:05:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081906.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_SRR3081906 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081906.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:05:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081906.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,782,661
Mapped reads	2,582,114 / 92.79%
Unmapped reads	200,547 / 7.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,356 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	91,760 / 3.3%
Duplication rate	2.7%
Clipped reads	940,029 / 33.78%

2.2. ACGT Content

Number/percentage of A's	51,356,179 / 28.91%
Number/percentage of C's	33,512,347 / 18.87%
Number/percentage of T's	55,344,648 / 31.16%
Number/percentage of G's	37,410,907 / 21.06%
Number/percentage of N's	2,068 / 0%
GC Percentage	39.93%

2.3. Coverage

Mean	0.0574

Standard Deviation	0.4504

2.4. Mapping Quality

Mean Mapping Quality	47.02

2.5. Mismatches and indels

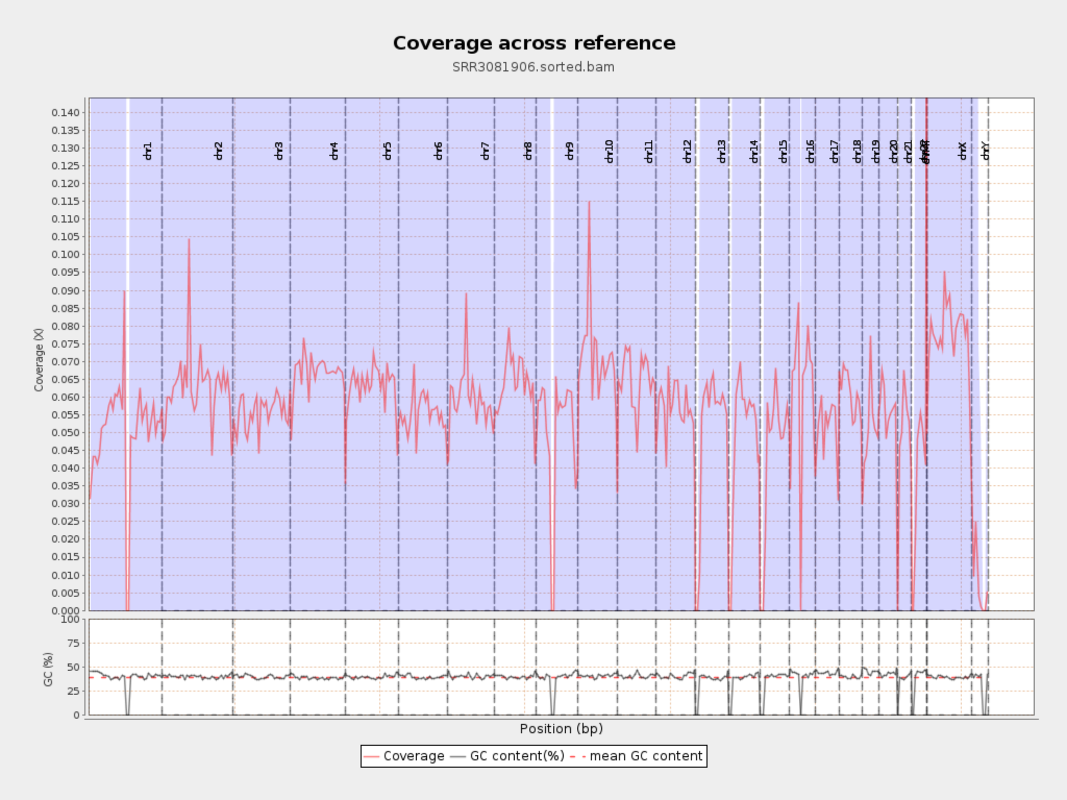
General error rate	0.81%
Mismatches	1,413,112
Insertions	12,874
Mapped reads with at least one insertion	0.49%
Deletions	35,571
Mapped reads with at least one deletion	1.36%
Homopolymer indels	47.18%

2.6. Chromosome stats

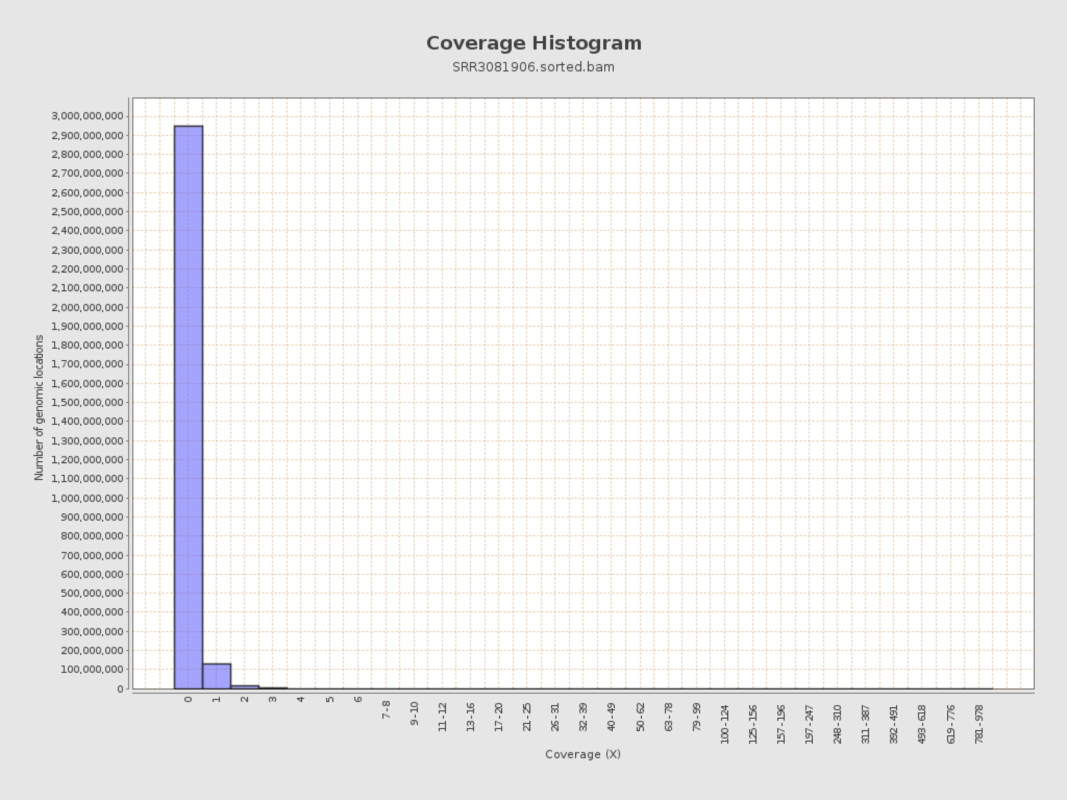
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12556216	0.0504	0.8397
chr2	243199373	15337087	0.0631	0.5023
chr3	198022430	10996428	0.0555	0.2714
chr4	191154276	12792695	0.0669	0.3209
chr5	180915260	11469588	0.0634	0.2896
chr6	171115067	9473600	0.0554	0.3054
chr7	159138663	9536365	0.0599	0.506

chr8	146364022	9335691	0.0638	0.6613
chr9	141213431	7040649	0.0499	0.395
chr10	135534747	9764413	0.072	0.5187
chr11	135006516	8701383	0.0645	0.3827
chr12	133851895	7598414	0.0568	0.2743
chr13	115169878	5693560	0.0494	0.2524
chr14	107349540	5210648	0.0485	0.2687
chr15	102531392	4520898	0.0441	0.2423
chr16	90354753	5610262	0.0621	0.3411
chr17	81195210	4117289	0.0507	0.2885
chr18	78077248	4774682	0.0612	0.6925
chr19	59128983	3058533	0.0517	0.6374
chr20	63025520	3546908	0.0563	0.2774
chr21	48129895	2311378	0.048	0.2783
chr22	51304566	1773682	0.0346	0.2102
chrMT	16571	4653	0.2808	0.6158
chrX	155270560	11994395	0.0772	0.3527
chrY	59373566	470137	0.0079	0.1788

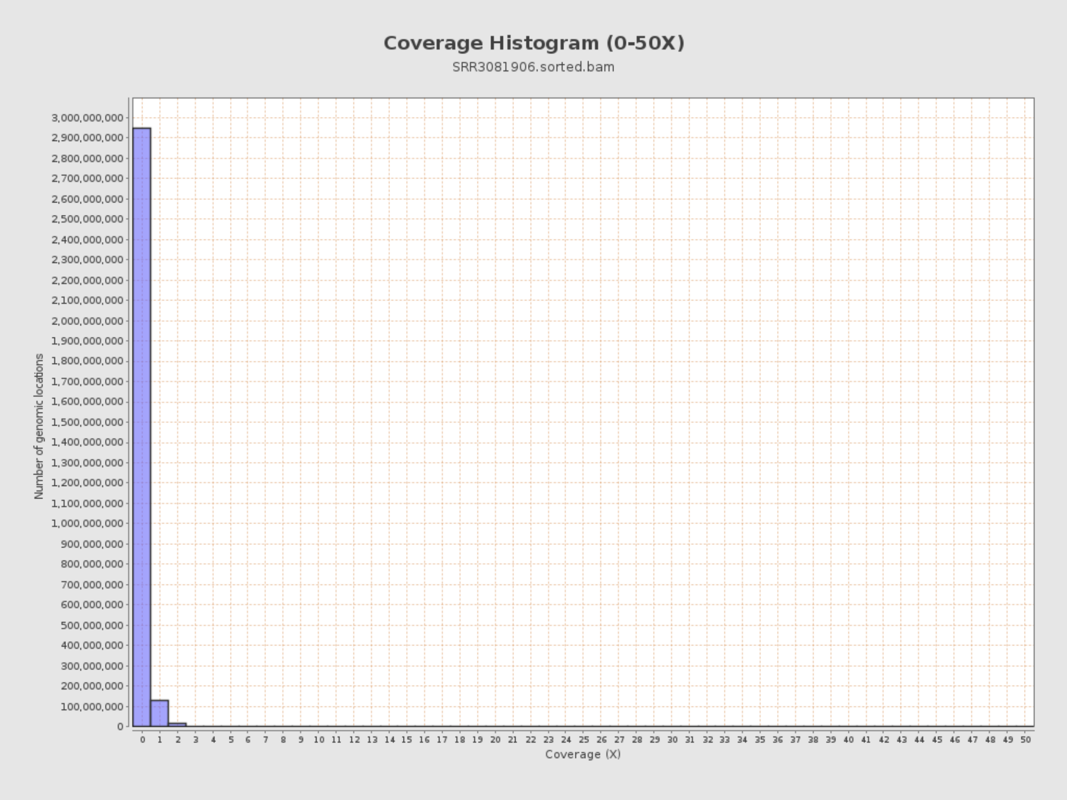
3. Results : Coverage across reference



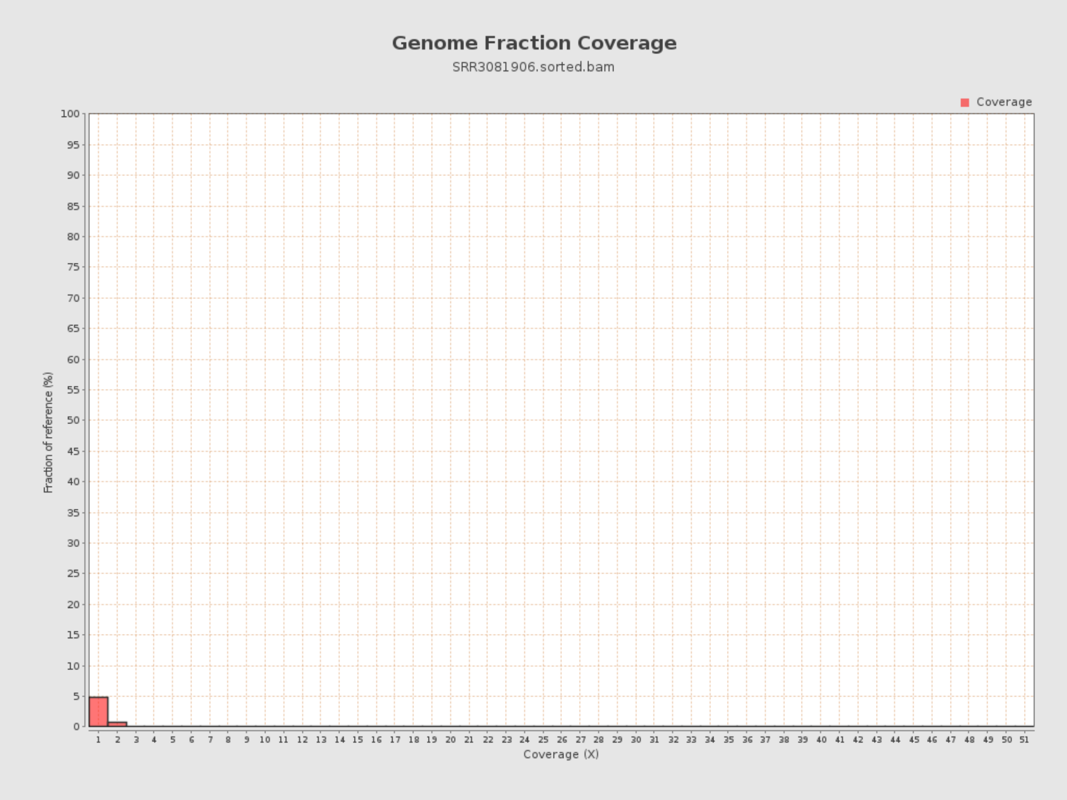
4. Results : Coverage Histogram



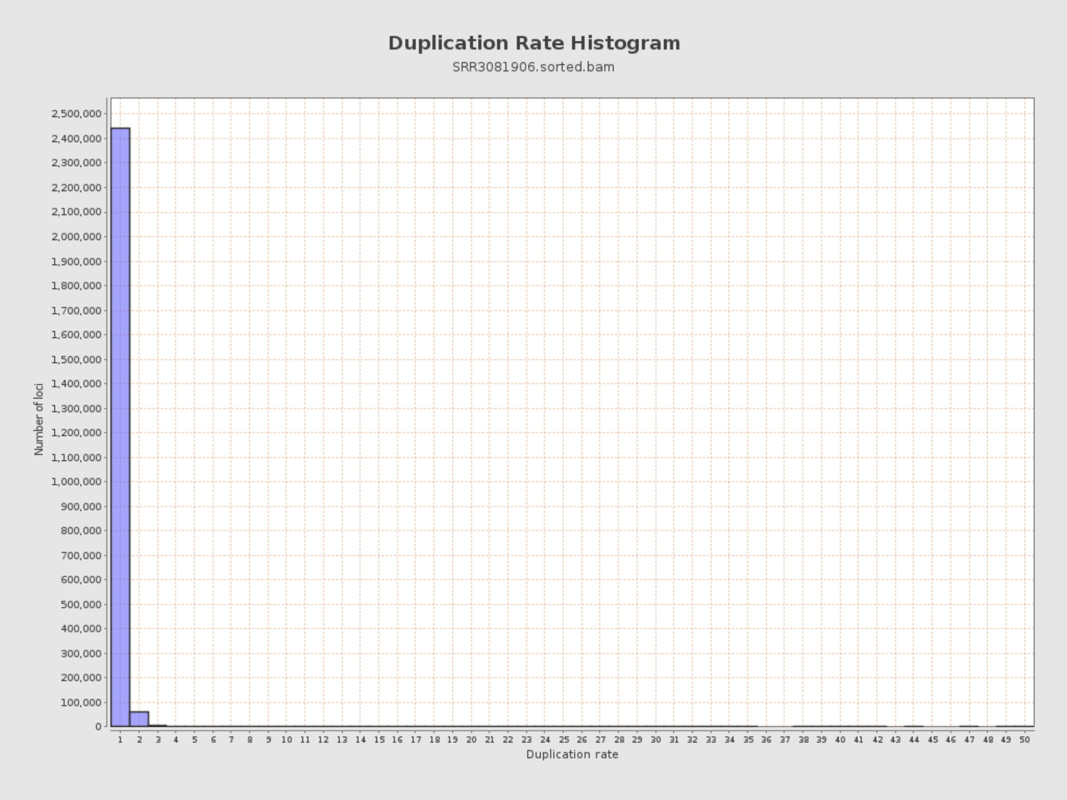
5. Results : Coverage Histogram (0-50X)



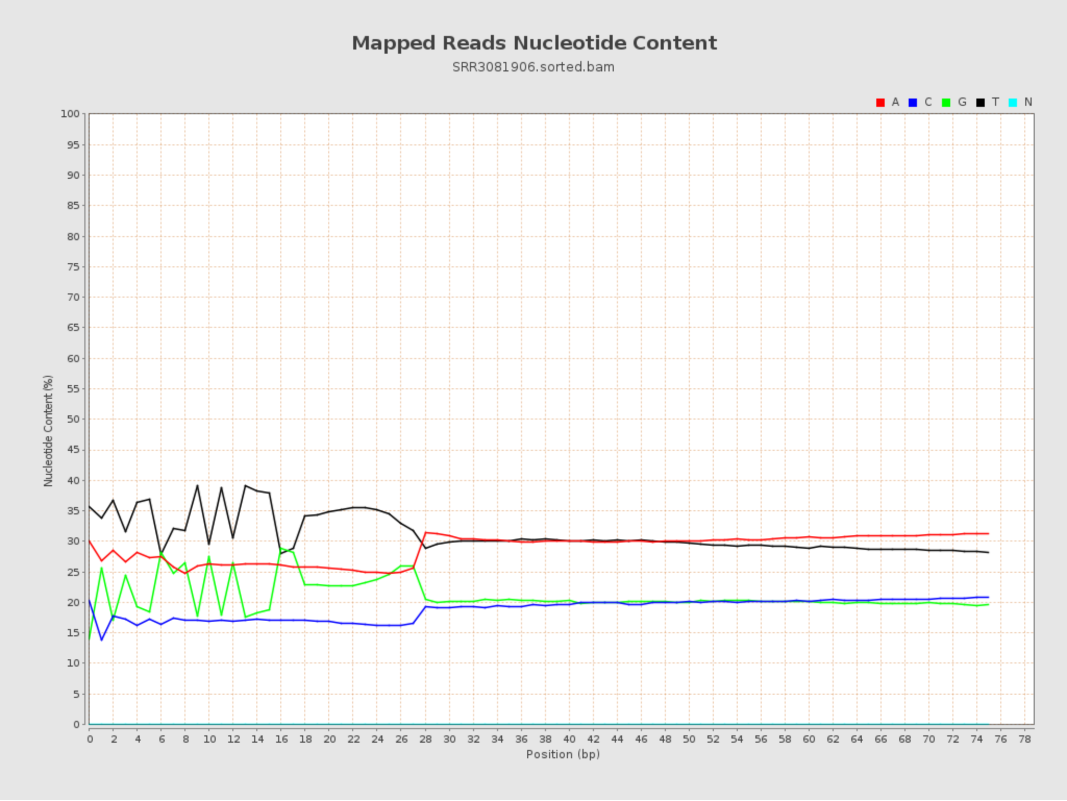
6. Results : Genome Fraction Coverage



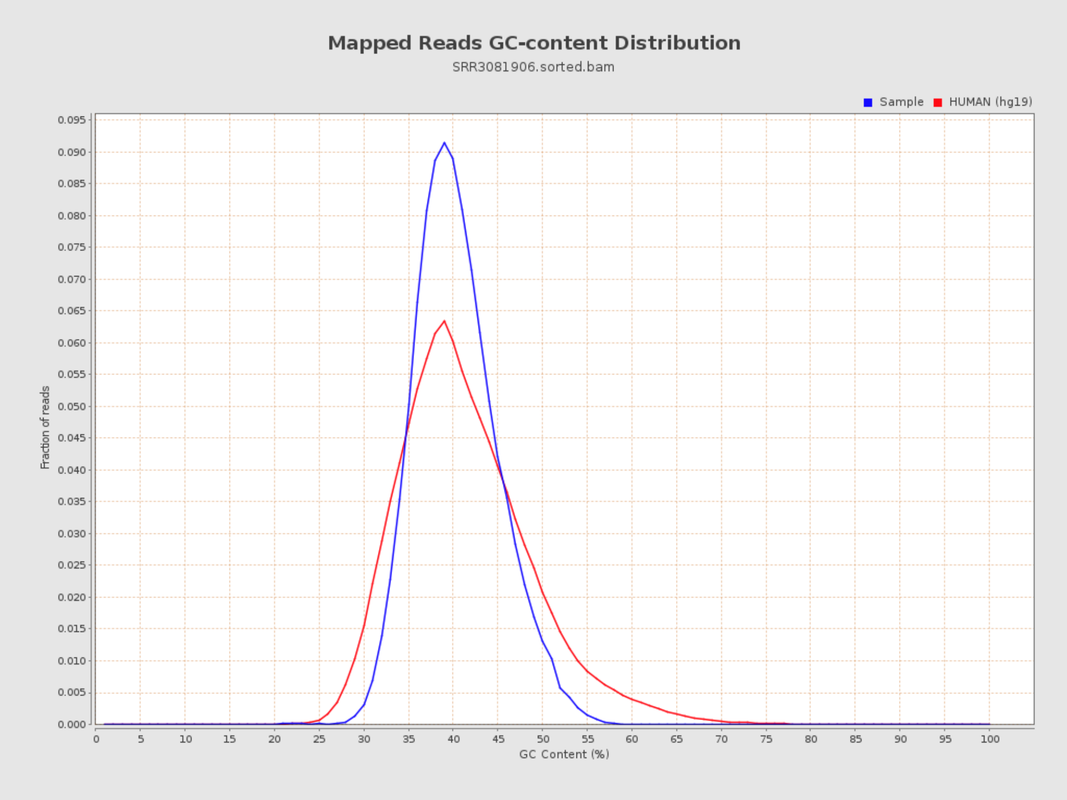
7. Results : Duplication Rate Histogram



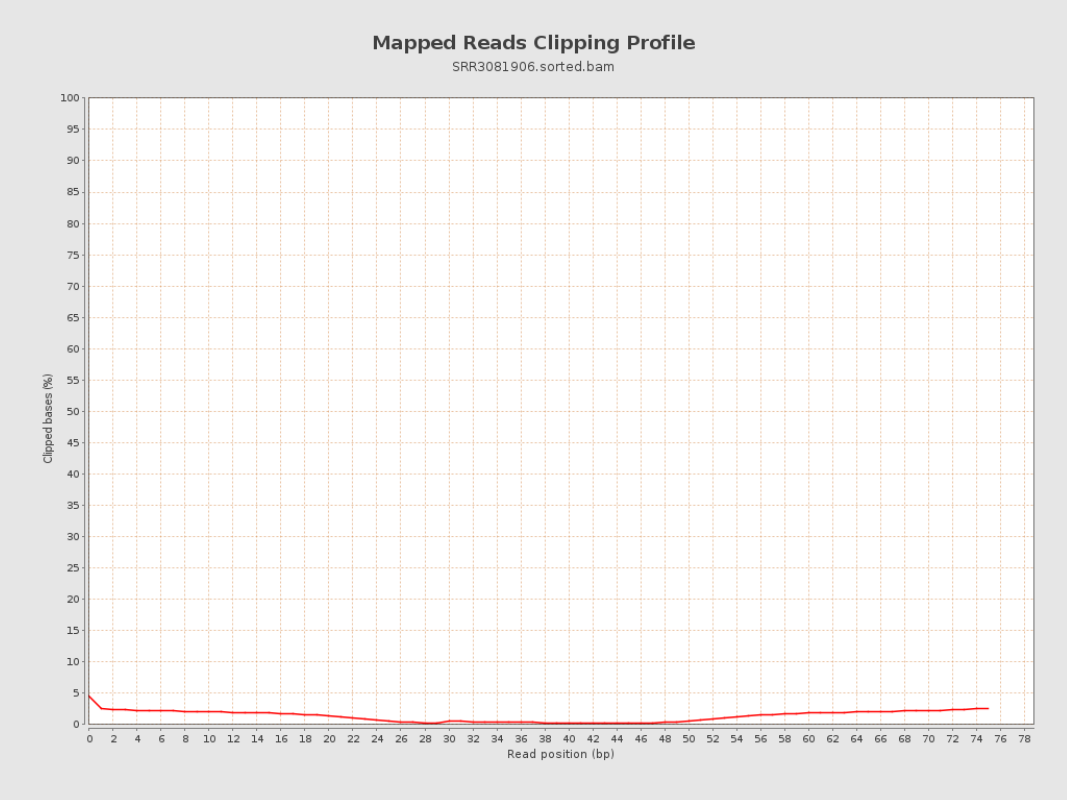
8. Results : Mapped Reads Nucleotide Content



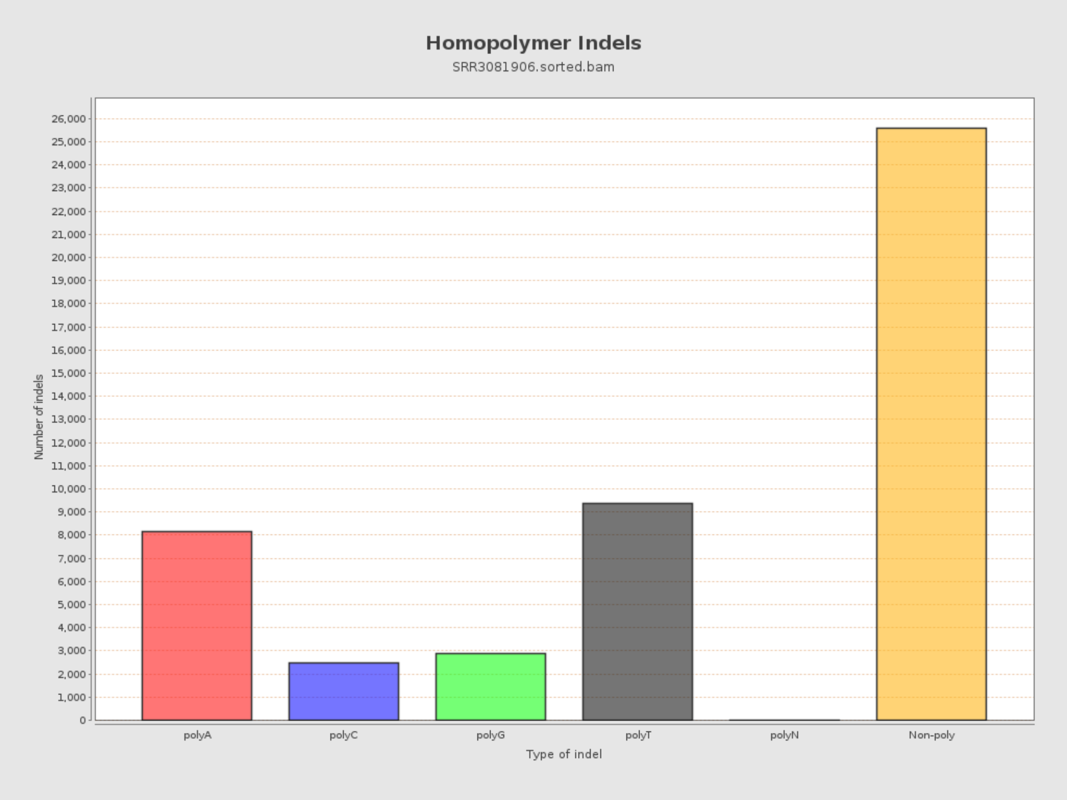
9. Results : Mapped Reads GC-content Distribution



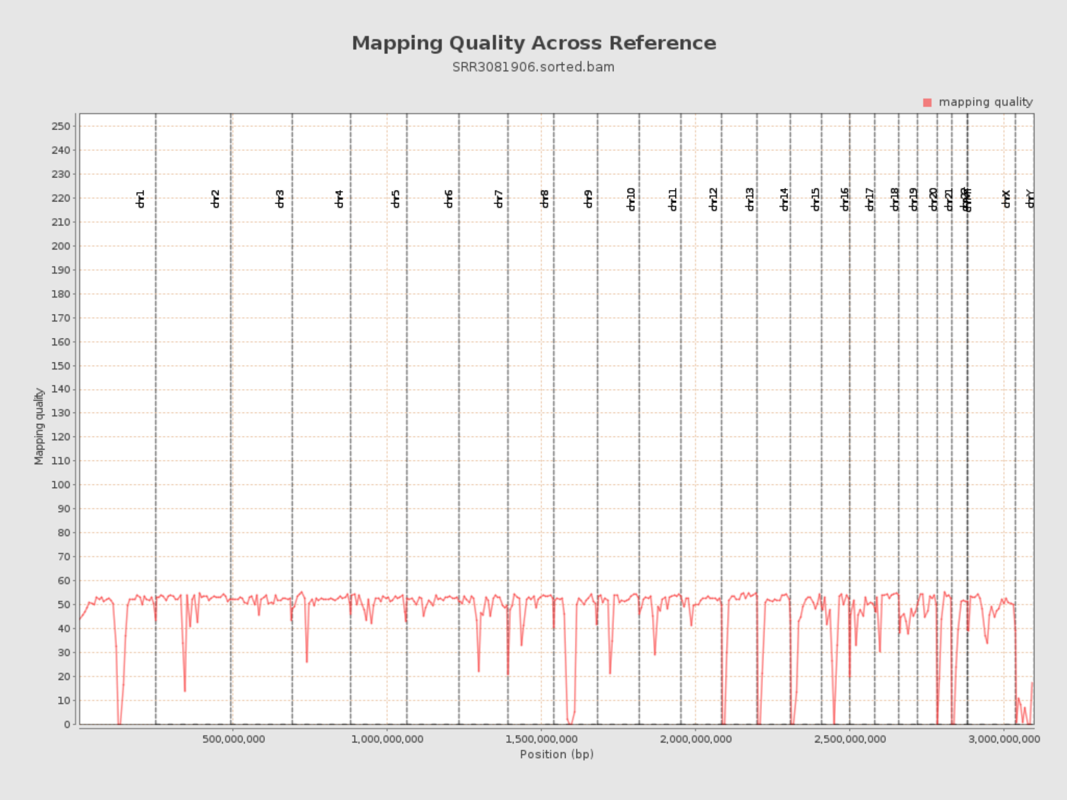
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram