Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:49:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082946.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_SRR3082946 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082946.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:49:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082946.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,054,837
Mapped reads	1,900,811 / 92.5%
Unmapped reads	154,026 / 7.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,872 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	92,468 / 4.5%
Duplication rate	4.07%
Clipped reads	774,743 / 37.7%

2.2. ACGT Content

Number/percentage of A's	36,206,747 / 28.19%
Number/percentage of C's	23,234,419 / 18.09%
Number/percentage of T's	41,460,055 / 32.28%
Number/percentage of G's	27,544,889 / 21.44%
Number/percentage of N's	6,149 / 0%
GC Percentage	39.53%

2.3. Coverage

Mean	0.0415

Standard Deviation	0.3192

2.4. Mapping Quality

Mean Mapping Quality	46.42

2.5. Mismatches and indels

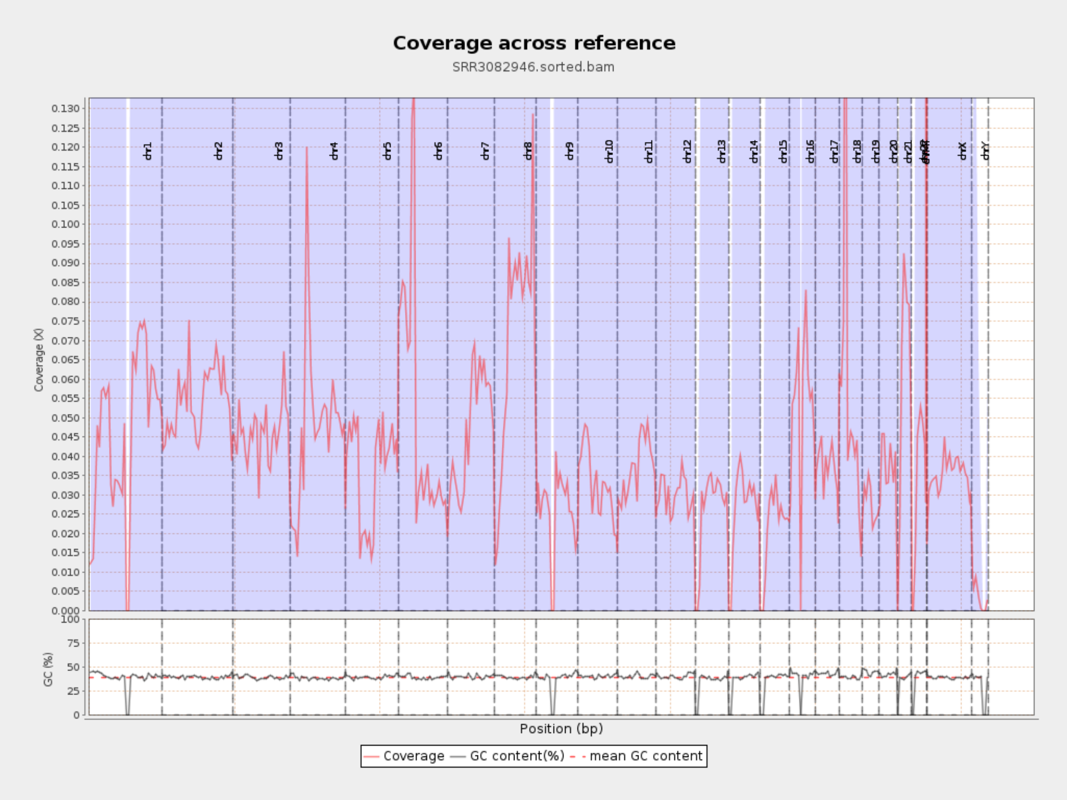
General error rate	0.73%
Mismatches	913,247
Insertions	10,779
Mapped reads with at least one insertion	0.56%
Deletions	30,250
Mapped reads with at least one deletion	1.58%
Homopolymer indels	49.23%

2.6. Chromosome stats

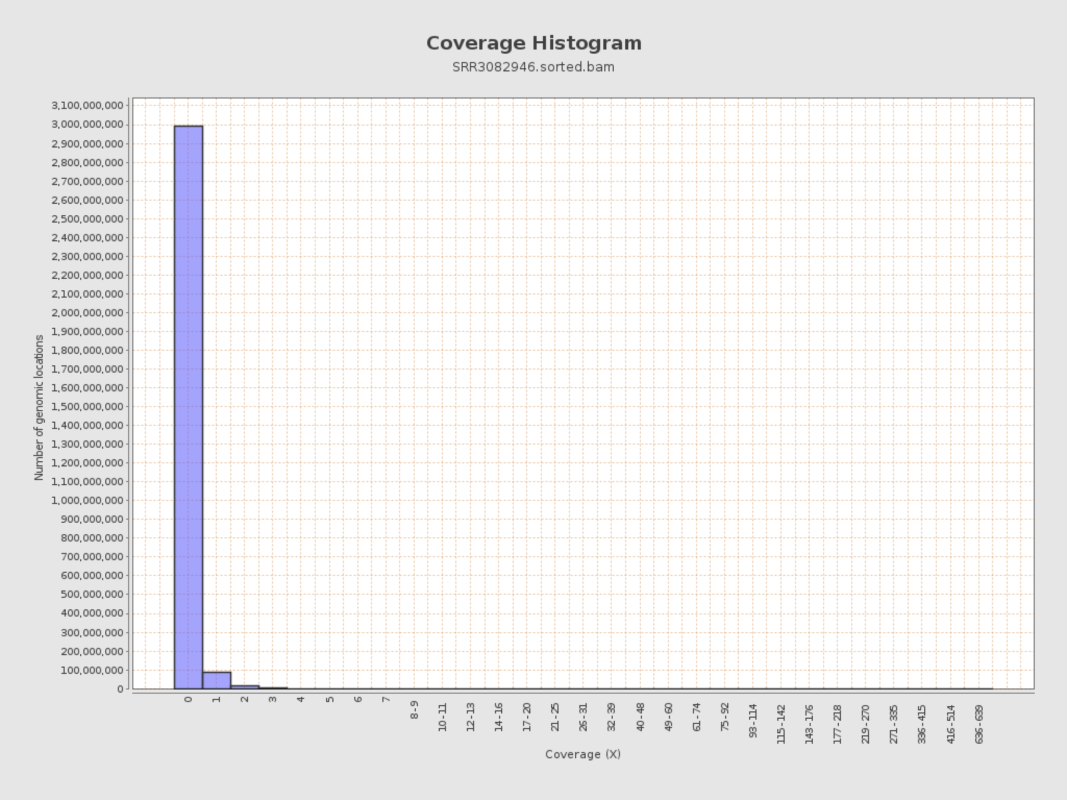
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11566702	0.0464	0.4413
chr2	243199373	13240781	0.0544	0.4732
chr3	198022430	9150818	0.0462	0.25
chr4	191154276	9199196	0.0481	0.262
chr5	180915260	6556581	0.0362	0.2236
chr6	171115067	8794335	0.0514	0.3356
chr7	159138663	7567058	0.0476	0.3301

chr8	146364022	10331312	0.0706	0.4551
chr9	141213431	3654114	0.0259	0.2957
chr10	135534747	4544359	0.0335	0.2377
chr11	135006516	4974154	0.0368	0.2767
chr12	133851895	3987445	0.0298	0.2051
chr13	115169878	2986547	0.0259	0.1899
chr14	107349540	2848598	0.0265	0.2034
chr15	102531392	2198044	0.0214	0.176
chr16	90354753	4833835	0.0535	0.2818
chr17	81195210	2989318	0.0368	0.2432
chr18	78077248	4765064	0.061	0.5478
chr19	59128983	1655464	0.028	0.3335
chr20	63025520	2347279	0.0372	0.23
chr21	48129895	2886159	0.06	0.2903
chr22	51304566	1648113	0.0321	0.2066
chrMT	16571	149091	8.9971	5.7386
chrX	155270560	5420526	0.0349	0.2391
chrY	59373566	206866	0.0035	0.0803

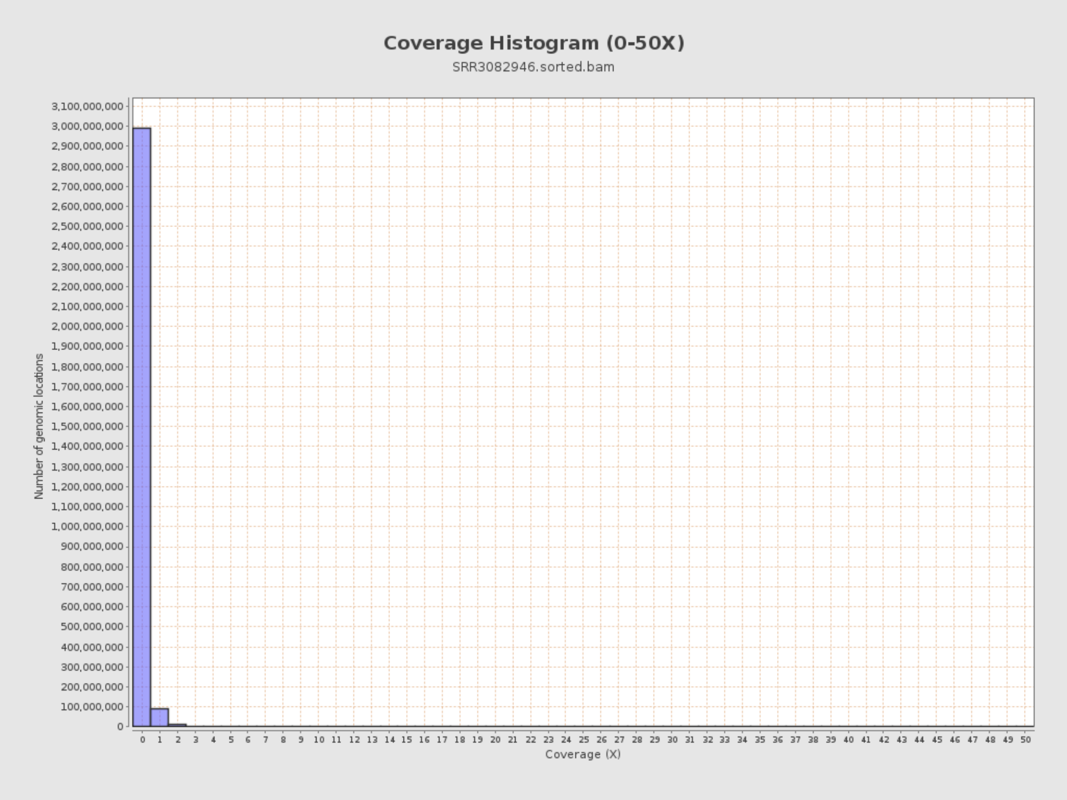
3. Results : Coverage across reference



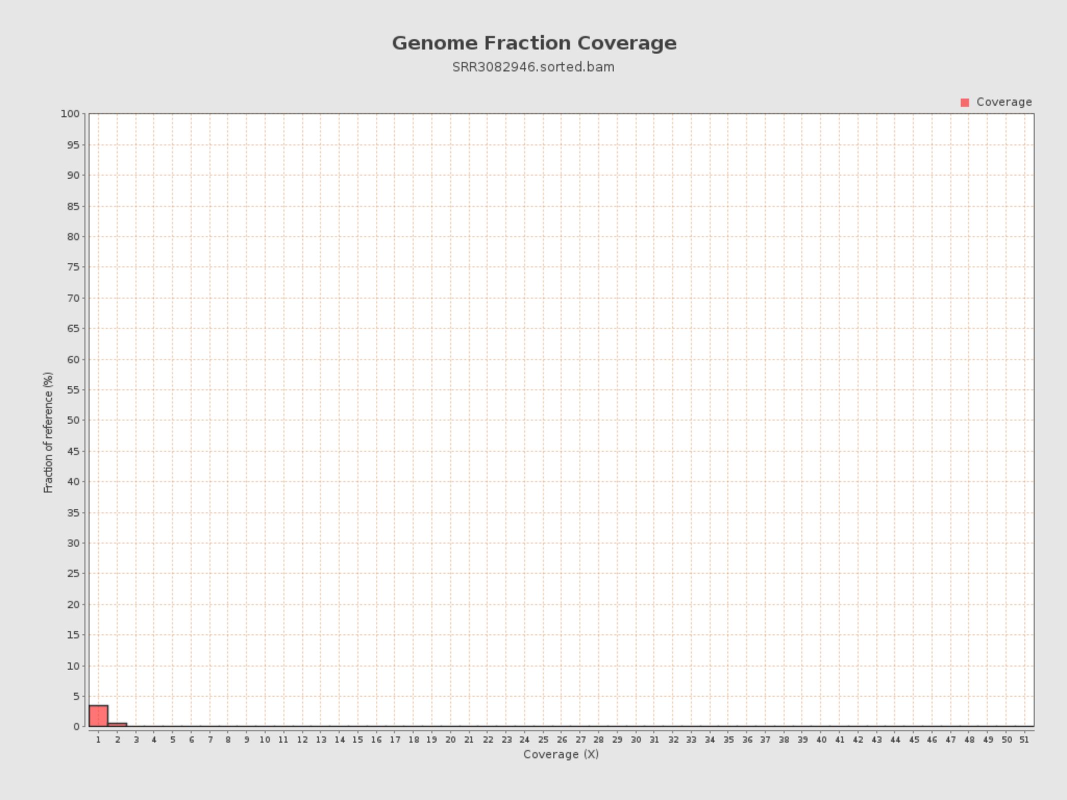
4. Results : Coverage Histogram



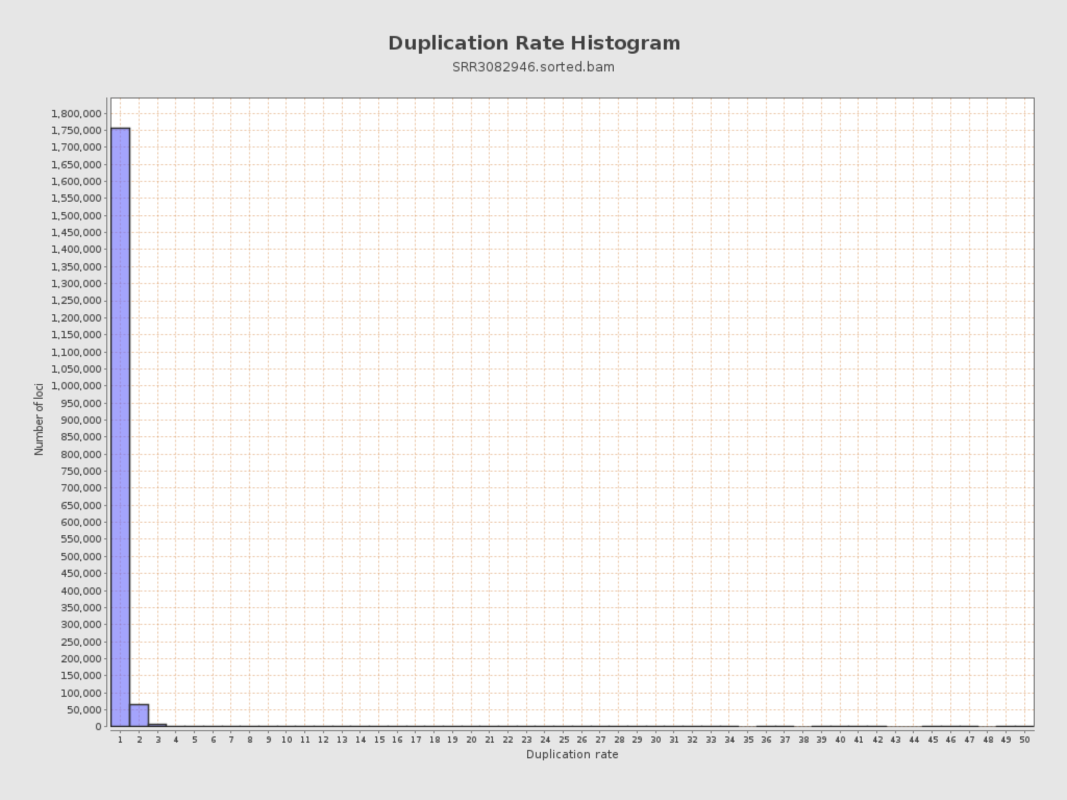
5. Results : Coverage Histogram (0-50X)



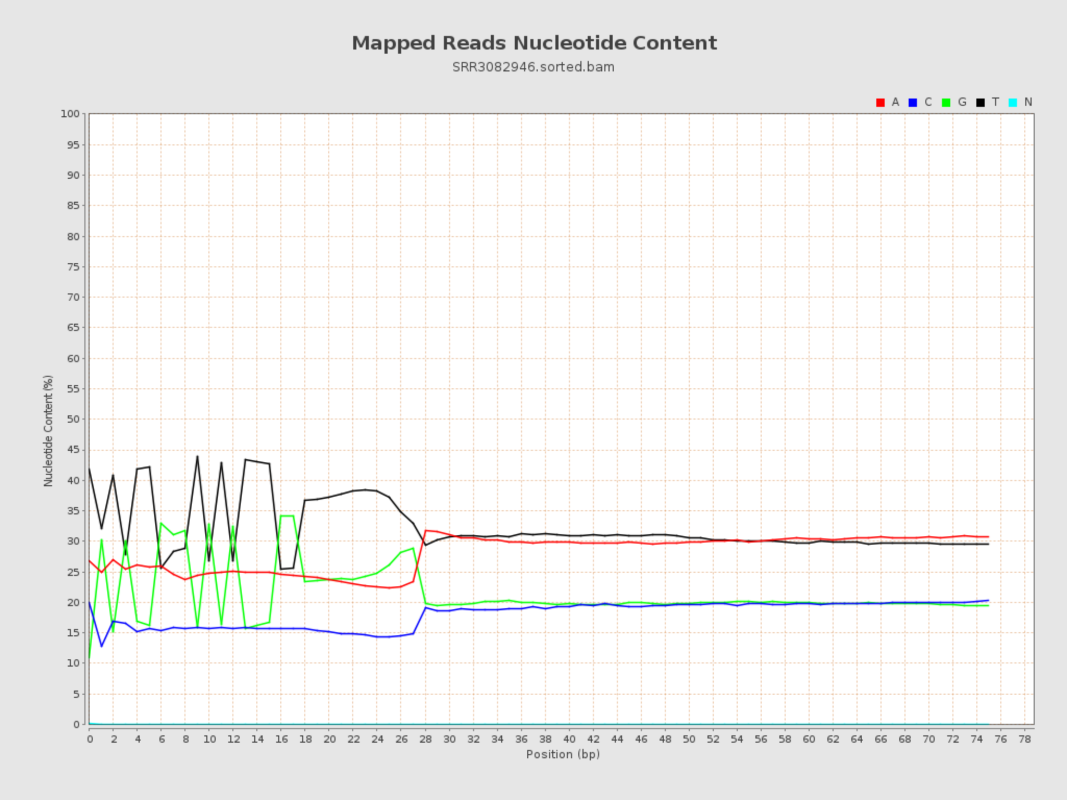
6. Results : Genome Fraction Coverage



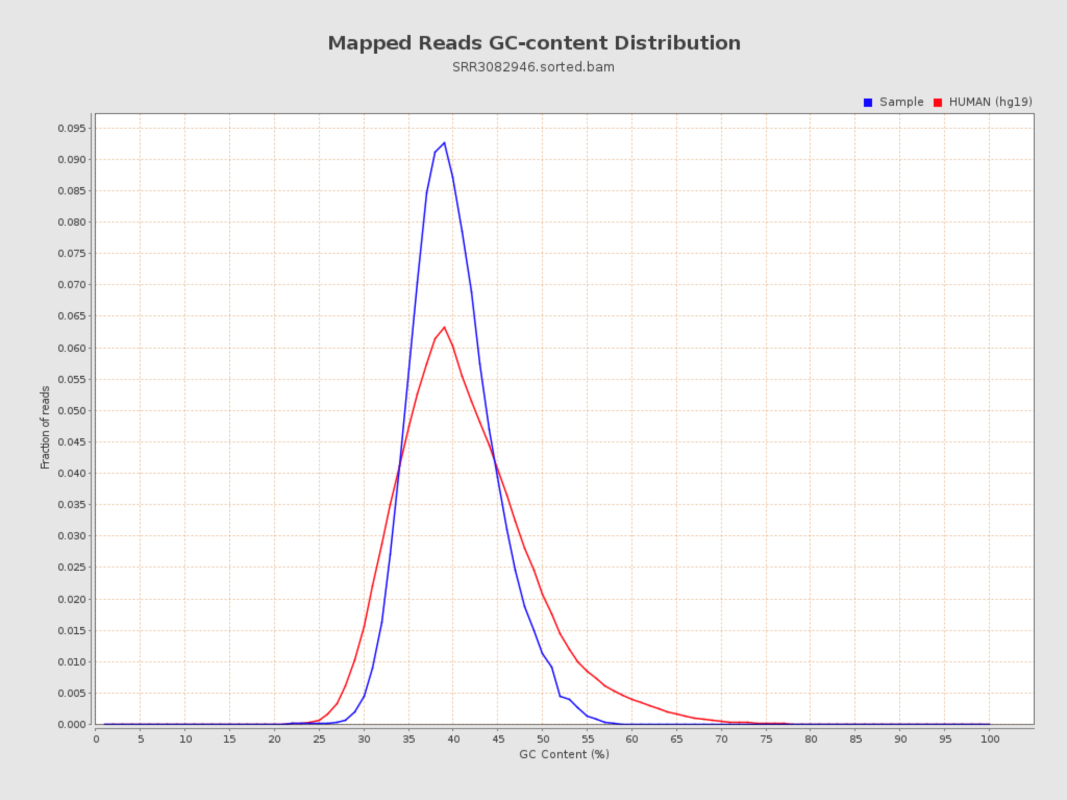
7. Results : Duplication Rate Histogram



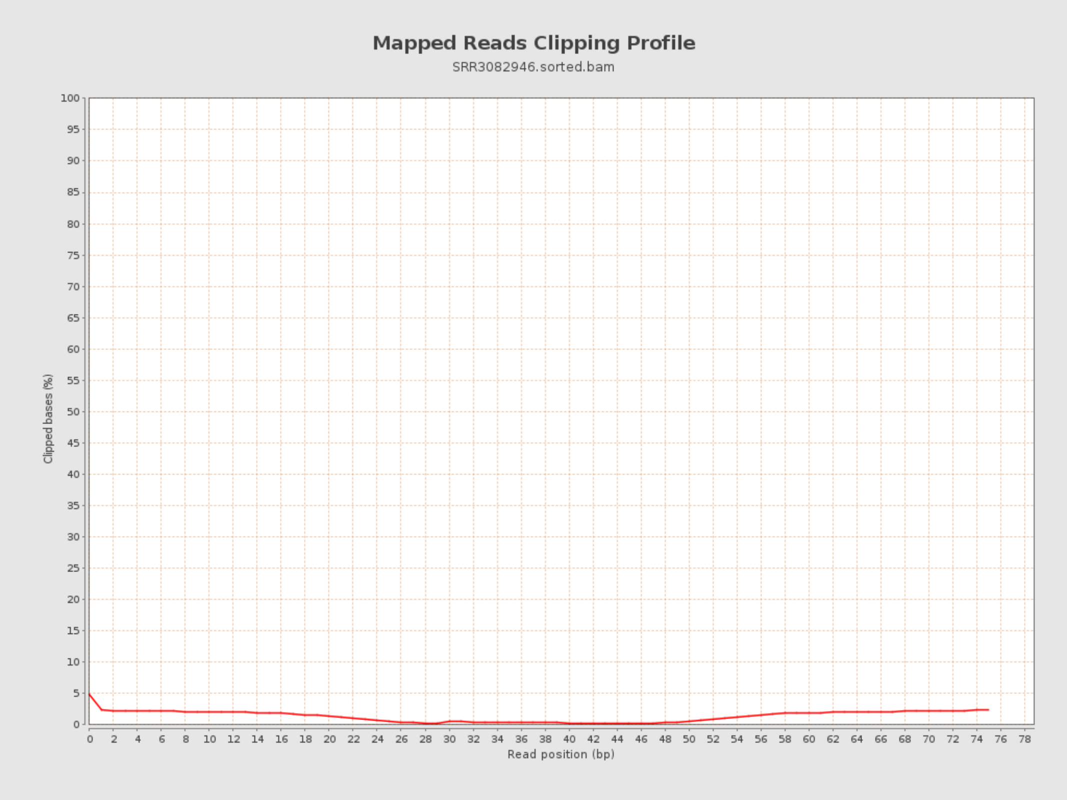
8. Results : Mapped Reads Nucleotide Content



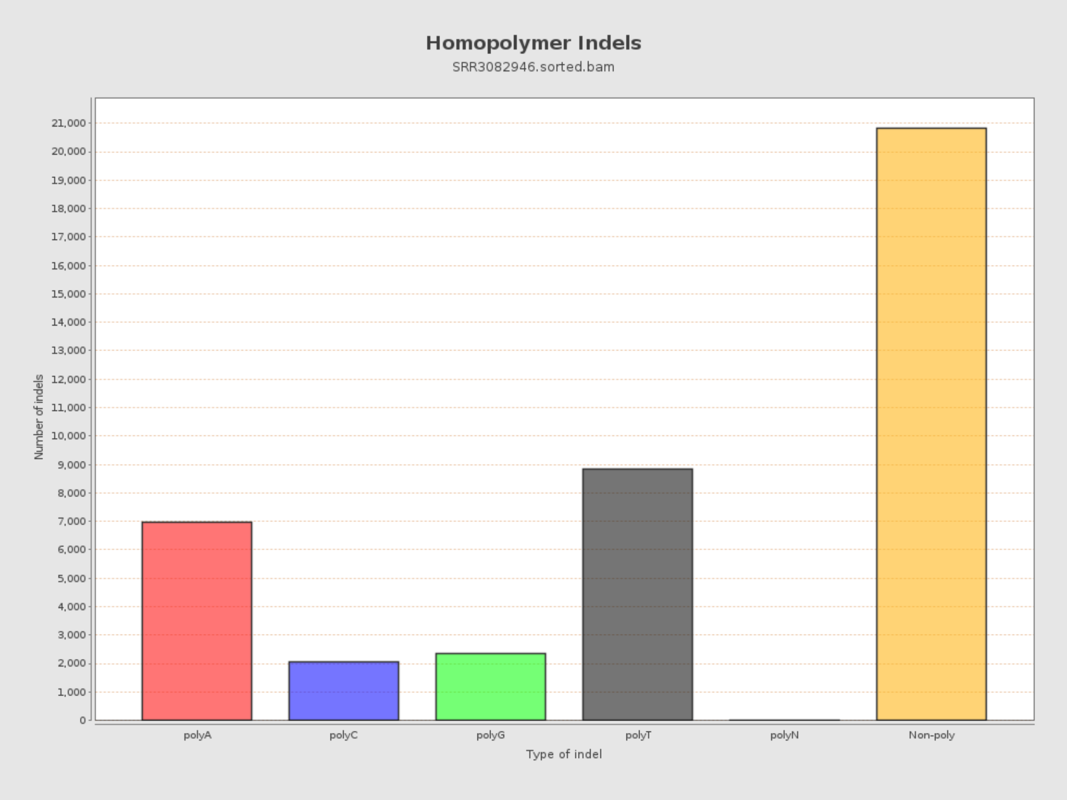
9. Results : Mapped Reads GC-content Distribution



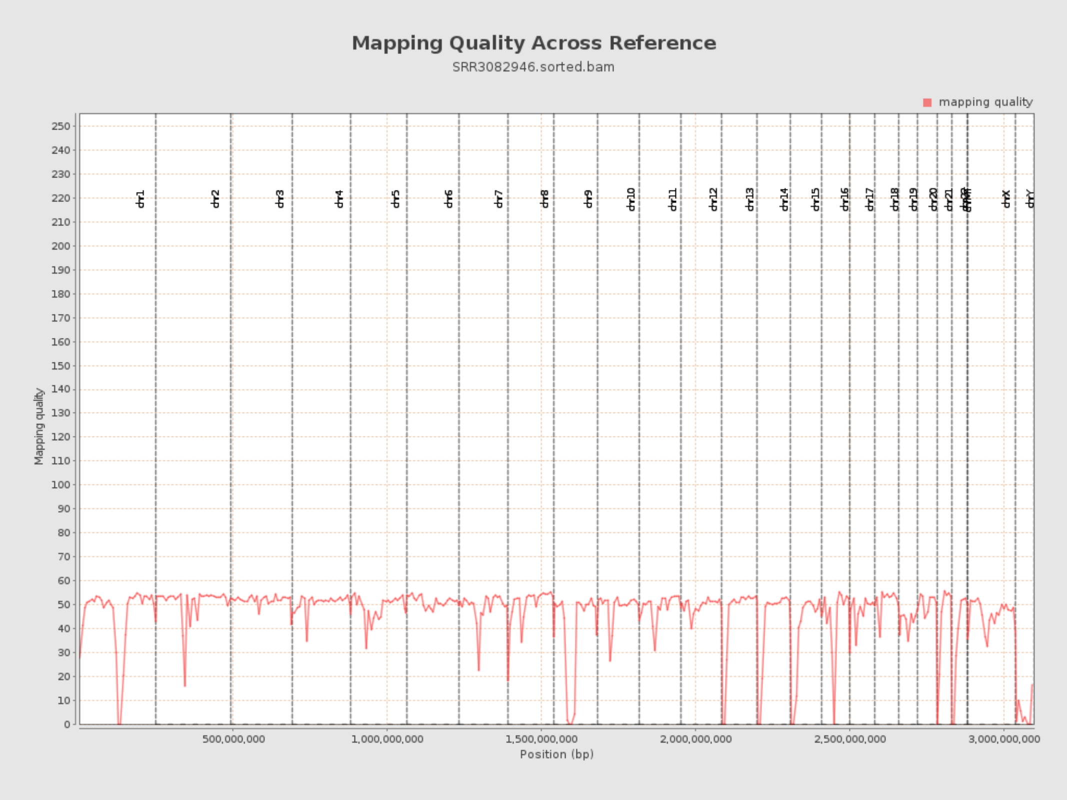
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram