Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:38:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082963.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_SRR3082963 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082963.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:38:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082963.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,076,038
Mapped reads	2,361,094 / 76.76%
Unmapped reads	714,944 / 23.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,425 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	88,515 / 2.88%
Duplication rate	2.75%
Clipped reads	957,990 / 31.14%

2.2. ACGT Content

Number/percentage of A's	45,426,505 / 28.35%
Number/percentage of C's	29,461,819 / 18.38%
Number/percentage of T's	50,997,921 / 31.82%
Number/percentage of G's	34,354,648 / 21.44%
Number/percentage of N's	15,819 / 0.01%
GC Percentage	39.82%

2.3. Coverage

Mean	0.0518

Standard Deviation	0.466

2.4. Mapping Quality

Mean Mapping Quality	45.89

2.5. Mismatches and indels

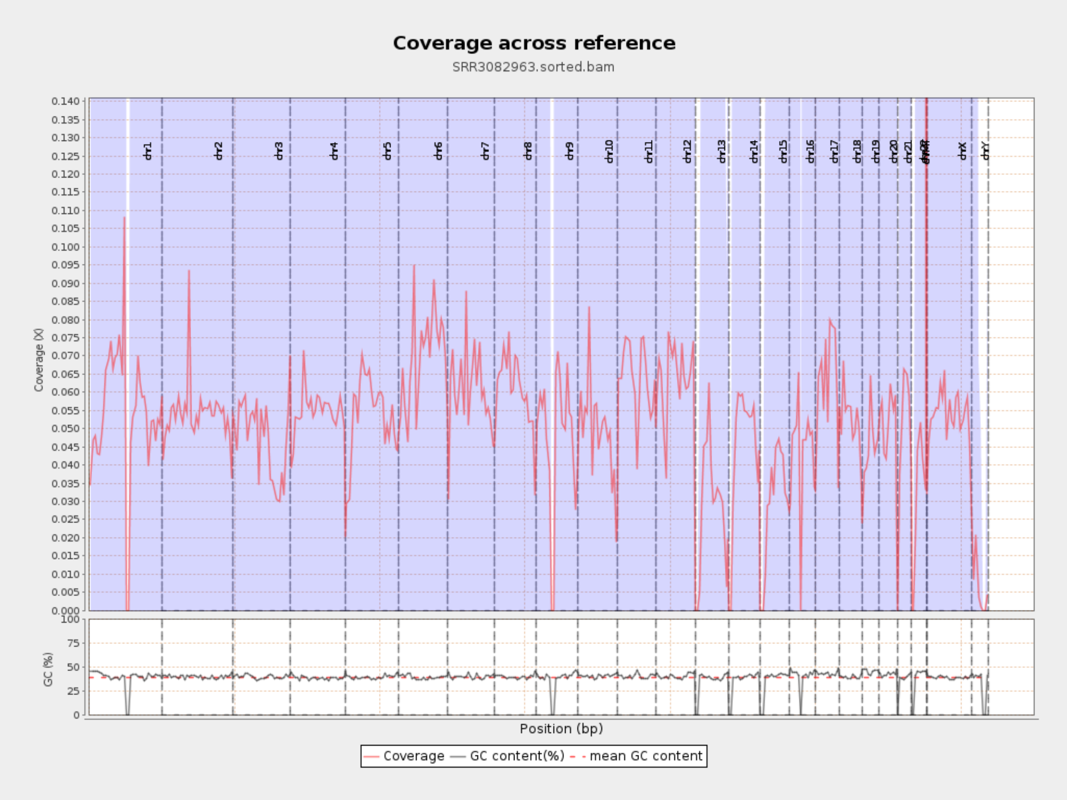
General error rate	0.97%
Mismatches	1,532,491
Insertions	14,475
Mapped reads with at least one insertion	0.61%
Deletions	36,695
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.45%

2.6. Chromosome stats

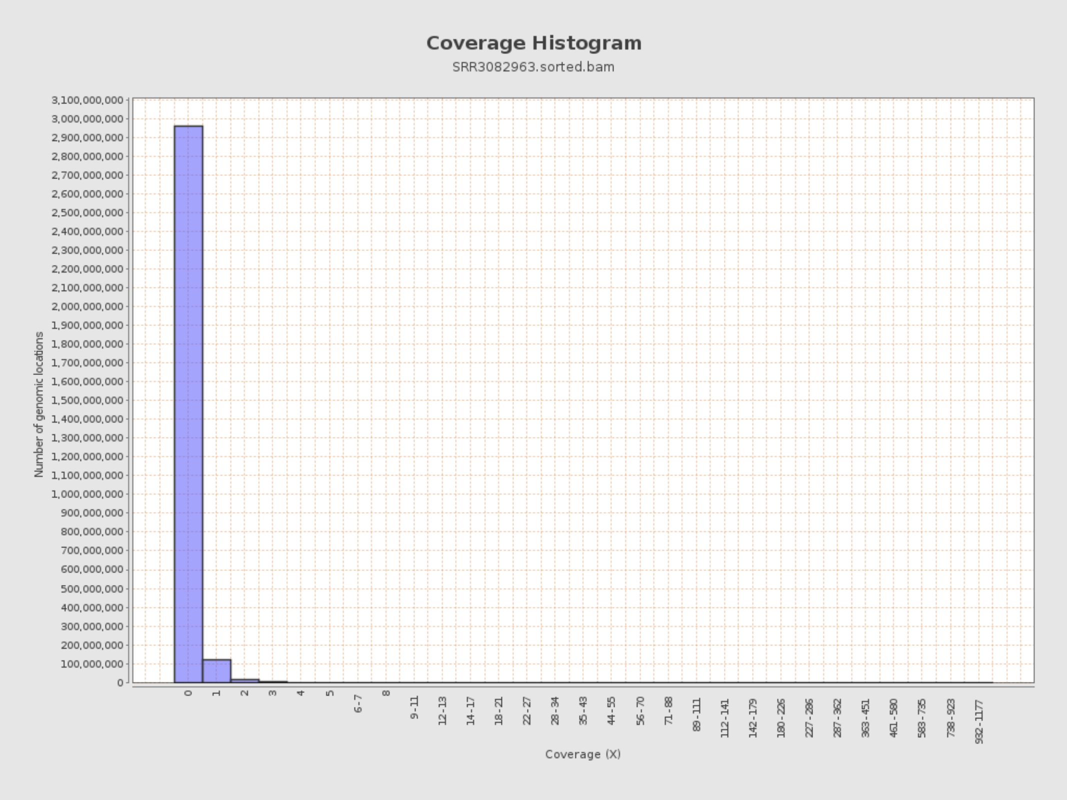
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13545039	0.0543	0.9803
chr2	243199373	13204733	0.0543	0.5019
chr3	198022430	9333468	0.0471	0.2489
chr4	191154276	10471255	0.0548	0.2838
chr5	180915260	9778307	0.054	0.2665
chr6	171115067	11920748	0.0697	0.3774
chr7	159138663	9698522	0.0609	0.5418

chr8	146364022	8863322	0.0606	0.5163
chr9	141213431	6753468	0.0478	0.4427
chr10	135534747	6760192	0.0499	0.3999
chr11	135006516	8578644	0.0635	0.3959
chr12	133851895	8530568	0.0637	0.2926
chr13	115169878	3217649	0.0279	0.1893
chr14	107349540	4780037	0.0445	0.2645
chr15	102531392	3023129	0.0295	0.1947
chr16	90354753	3958017	0.0438	0.3107
chr17	81195210	5169443	0.0637	0.3554
chr18	78077248	4139722	0.053	0.8533
chr19	59128983	2690311	0.0455	0.5986
chr20	63025520	3248130	0.0515	0.2635
chr21	48129895	2351945	0.0489	0.279
chr22	51304566	1555236	0.0303	0.1951
chrMT	16571	37102	2.239	2.1116
chrX	155270560	8328751	0.0536	0.3002
chrY	59373566	382790	0.0064	0.1635

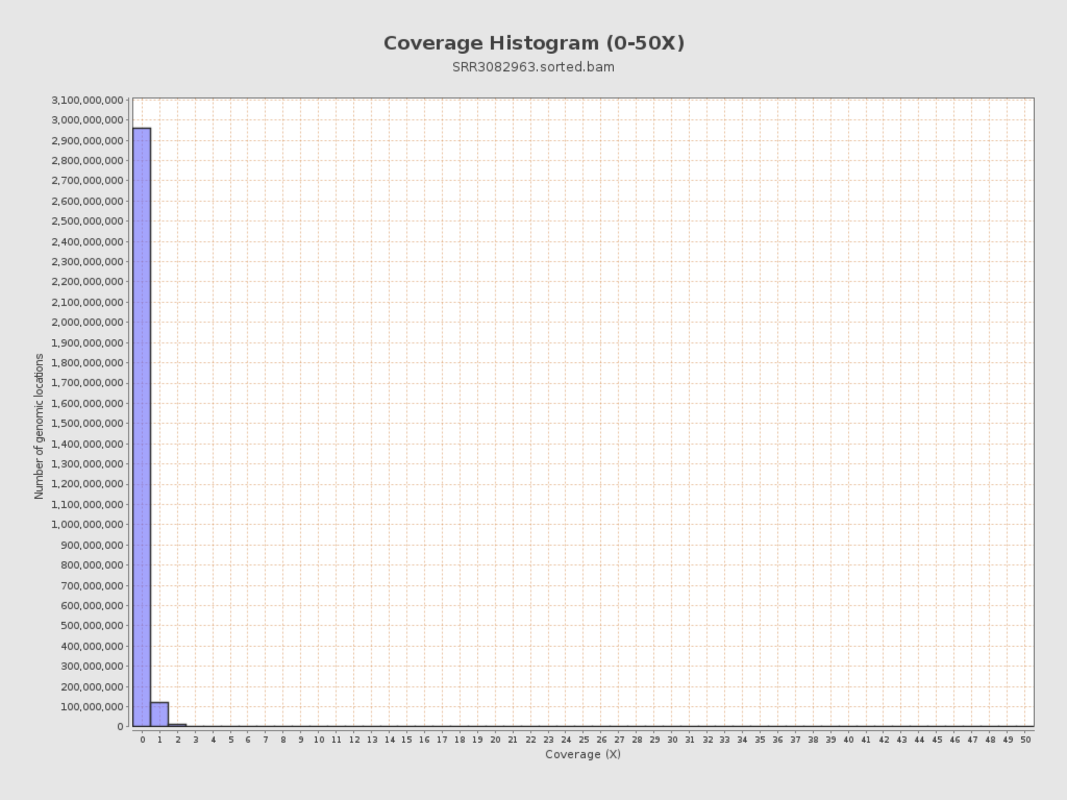
3. Results : Coverage across reference



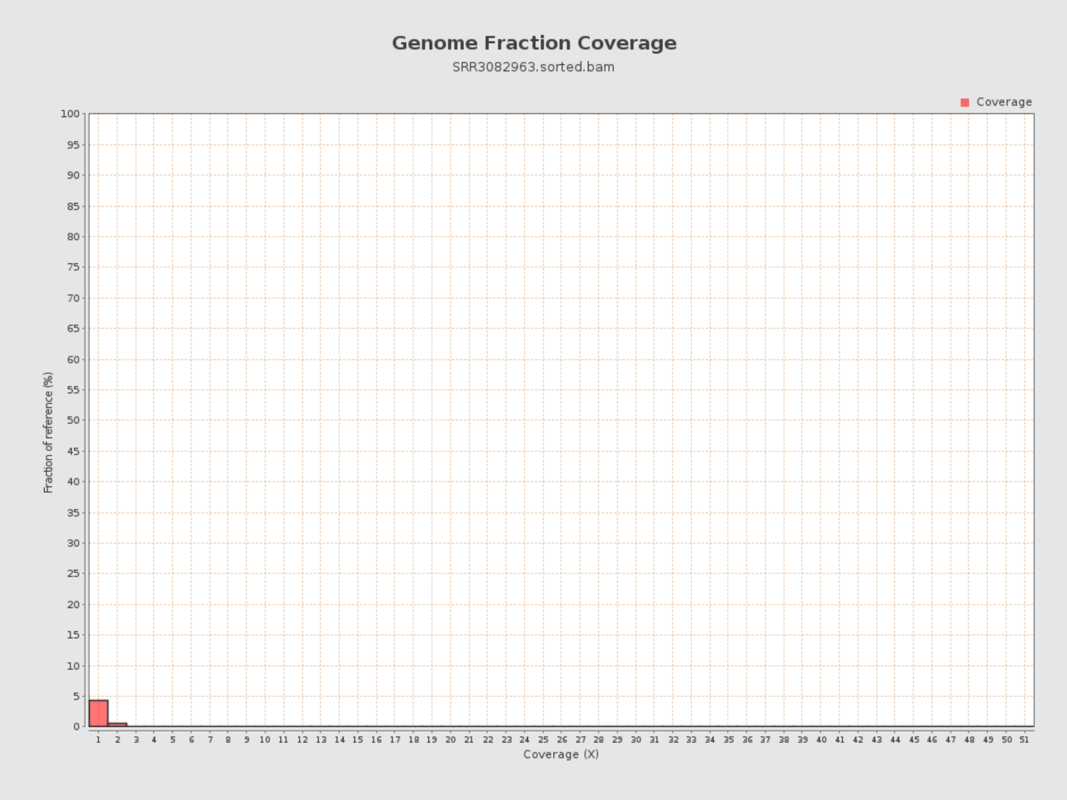
4. Results : Coverage Histogram



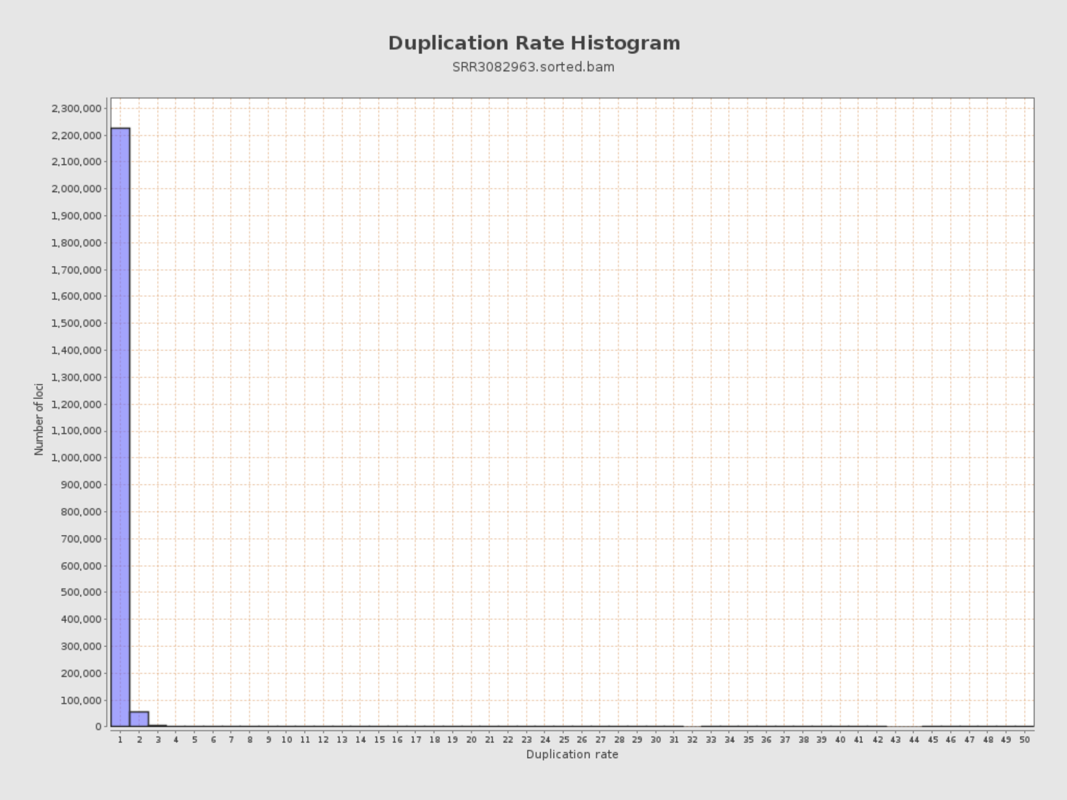
5. Results : Coverage Histogram (0-50X)



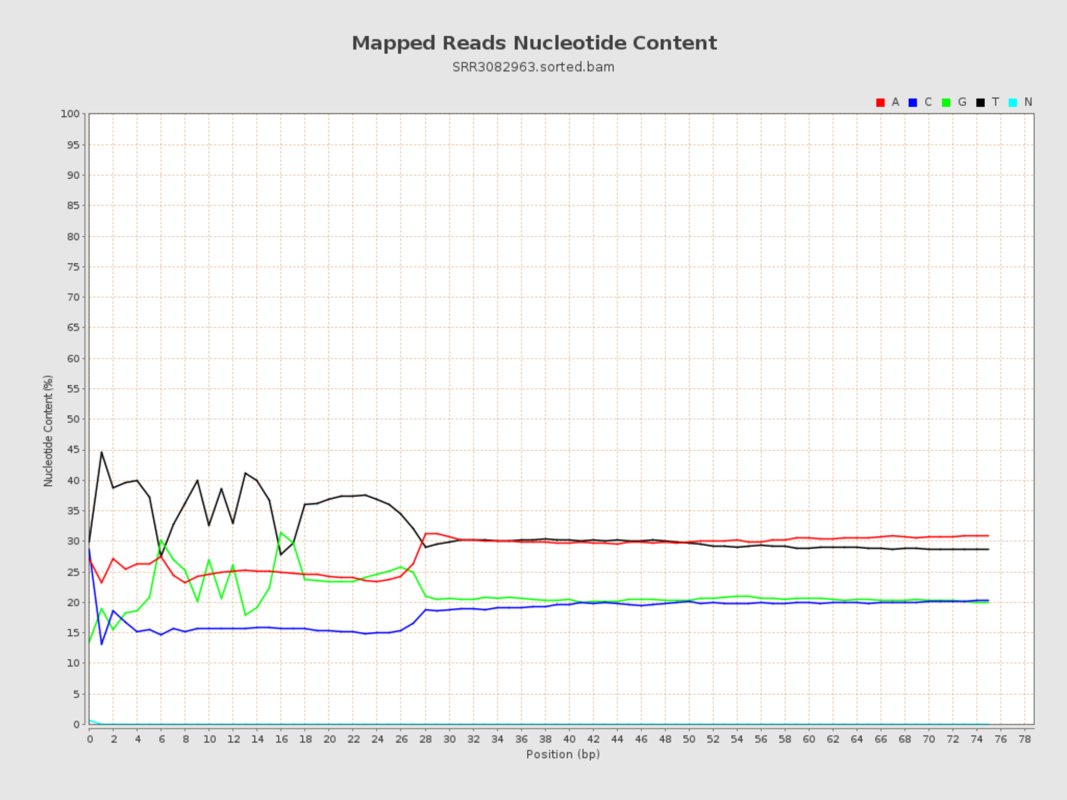
6. Results : Genome Fraction Coverage



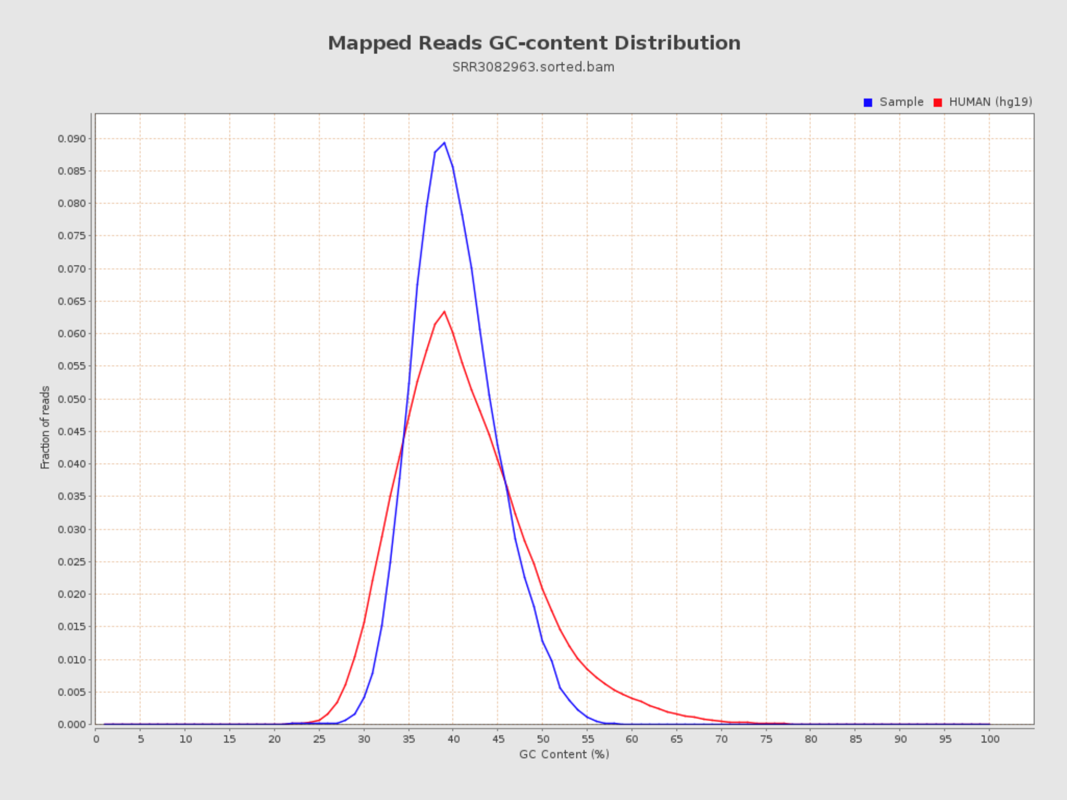
7. Results : Duplication Rate Histogram



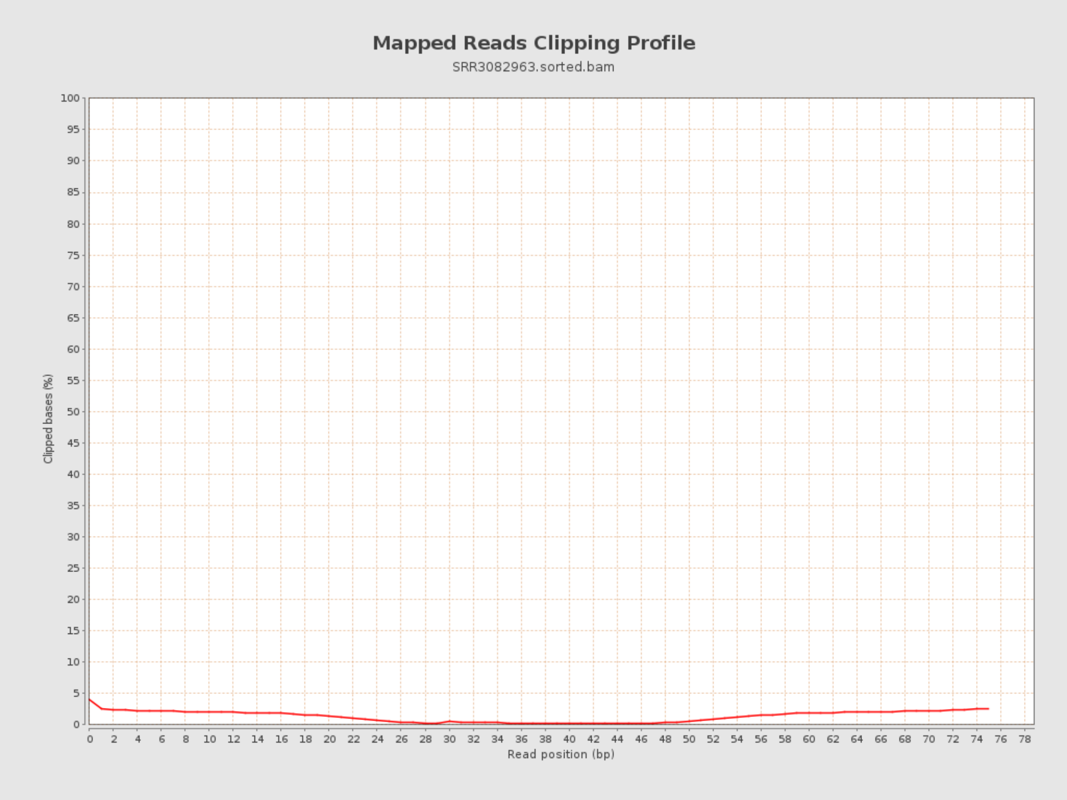
8. Results : Mapped Reads Nucleotide Content



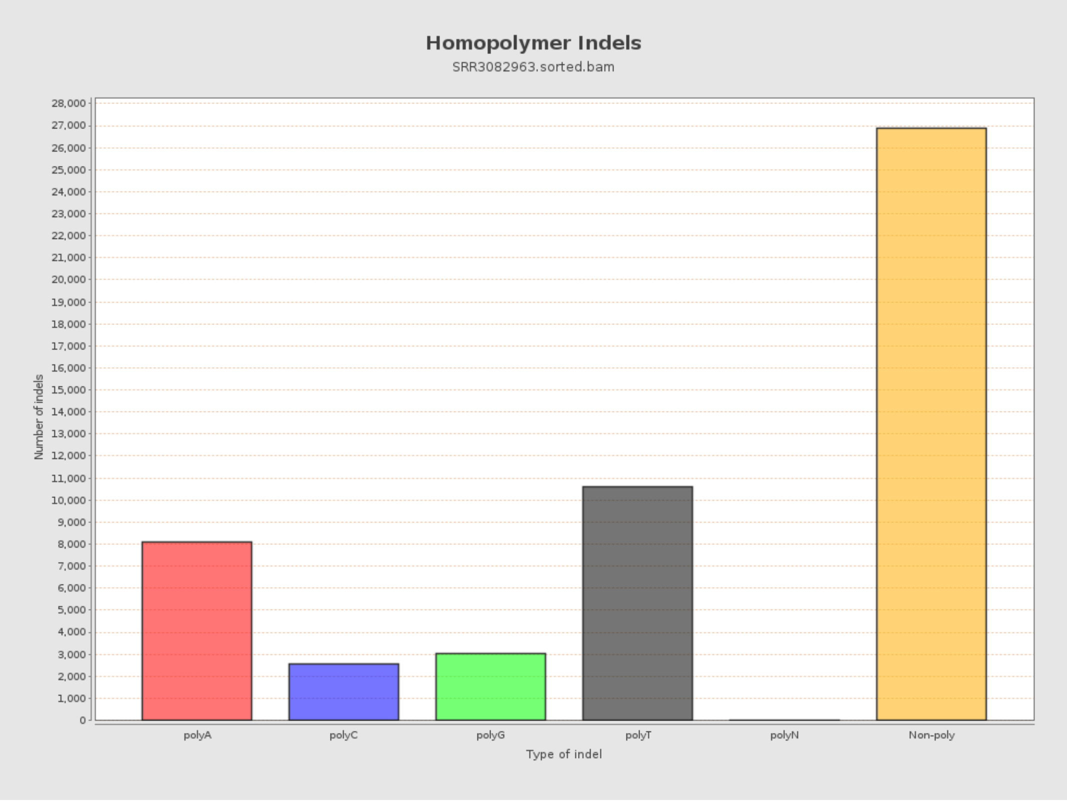
9. Results : Mapped Reads GC-content Distribution



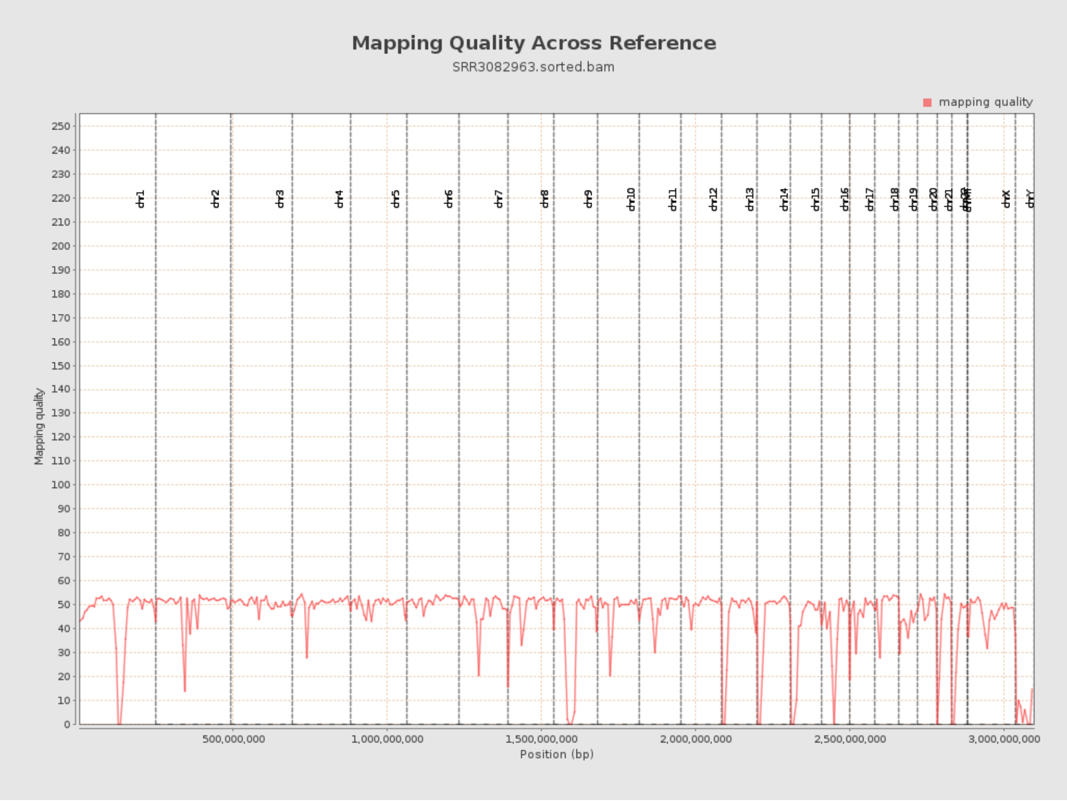
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram