Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 13:10:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867852.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_SRR9867852 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867852.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 13:10:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867852.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,986,976
Mapped reads	1,836,483 / 92.43%
Unmapped reads	150,493 / 7.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,946 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	89,559 / 4.51%
Duplication rate	3.59%
Clipped reads	1,837,105 / 92.46%

2.2. ACGT Content

Number/percentage of A's	27,393,369 / 25.27%
Number/percentage of C's	20,210,890 / 18.64%
Number/percentage of T's	34,812,929 / 32.12%
Number/percentage of G's	25,967,540 / 23.96%
Number/percentage of N's	15,111 / 0.01%
GC Percentage	42.6%

2.3. Coverage

Mean	0.035

Standard Deviation	0.3367

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

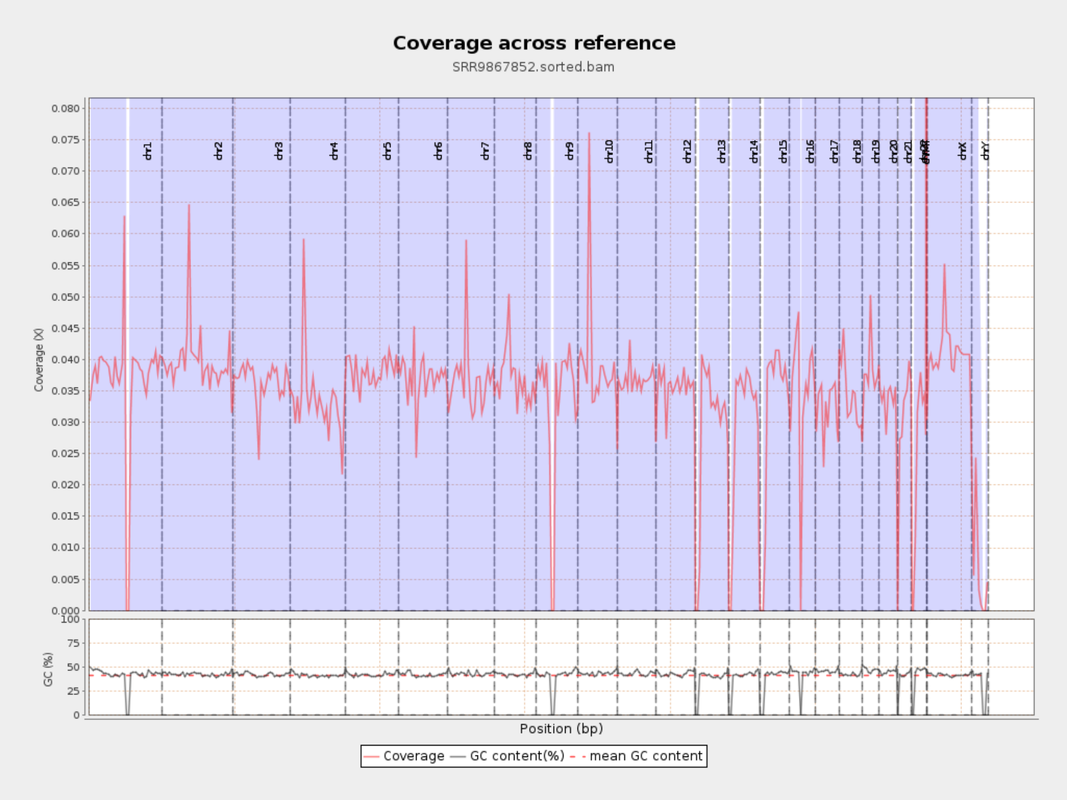
General error rate	0.52%
Mismatches	546,932
Insertions	9,201
Mapped reads with at least one insertion	0.5%
Deletions	21,149
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.3%

2.6. Chromosome stats

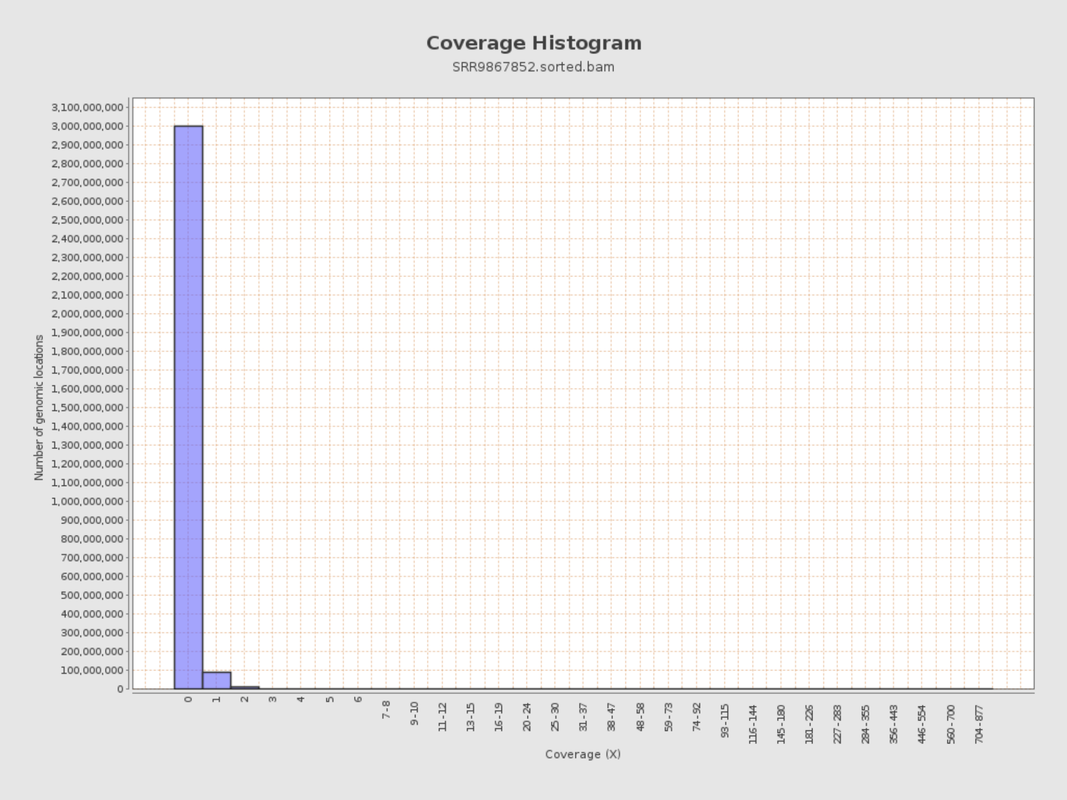
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9104410	0.0365	0.6208
chr2	243199373	9703655	0.0399	0.4545
chr3	198022430	7214915	0.0364	0.2115
chr4	191154276	6360057	0.0333	0.2416
chr5	180915260	6899802	0.0381	0.2196
chr6	171115067	6344583	0.0371	0.2511
chr7	159138663	5864942	0.0369	0.3876

chr8	146364022	5414398	0.037	0.3702
chr9	141213431	4630546	0.0328	0.2889
chr10	135534747	5332831	0.0393	0.3564
chr11	135006516	4940807	0.0366	0.2852
chr12	133851895	4767550	0.0356	0.212
chr13	115169878	3302329	0.0287	0.1893
chr14	107349540	3121047	0.0291	0.1978
chr15	102531392	3176150	0.031	0.1965
chr16	90354753	3171314	0.0351	0.2312
chr17	81195210	2578770	0.0318	0.211
chr18	78077248	2717512	0.0348	0.5235
chr19	59128983	2270749	0.0384	0.4658
chr20	63025520	2102539	0.0334	0.2087
chr21	48129895	1444823	0.03	0.2353
chr22	51304566	1208317	0.0236	0.1709
chrMT	16571	8866	0.535	0.8206
chrX	155270560	6379517	0.0411	0.2502
chrY	59373566	373138	0.0063	0.2434

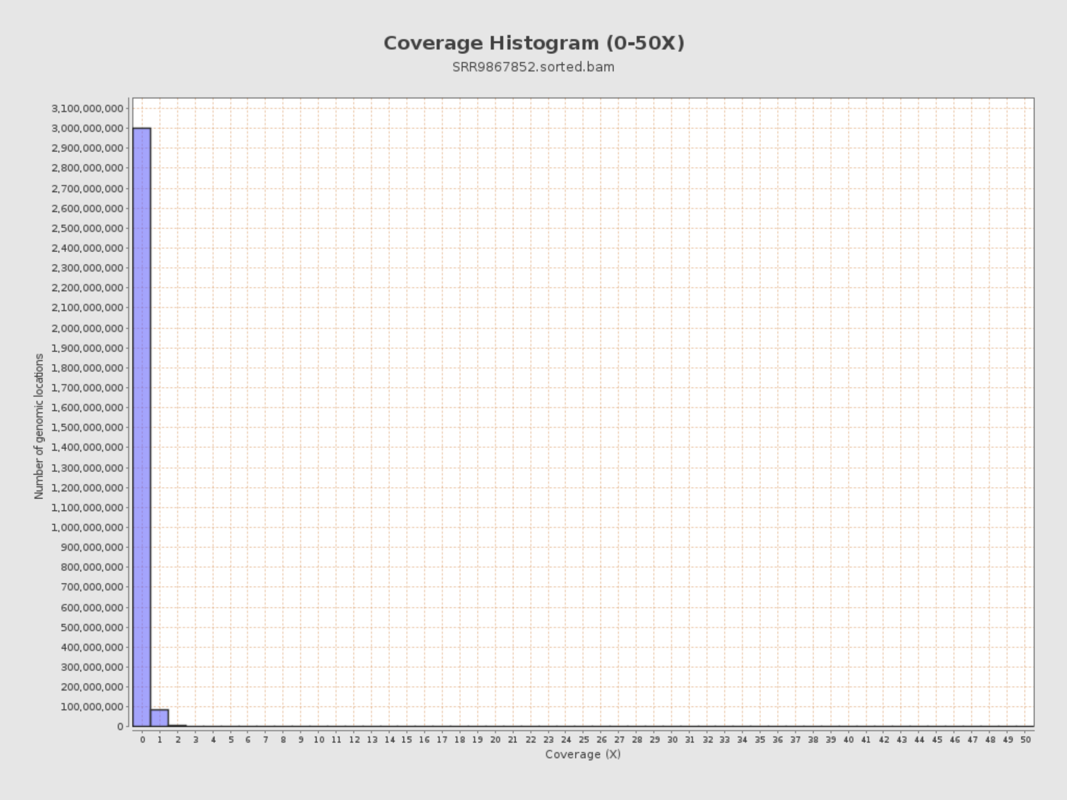
3. Results : Coverage across reference



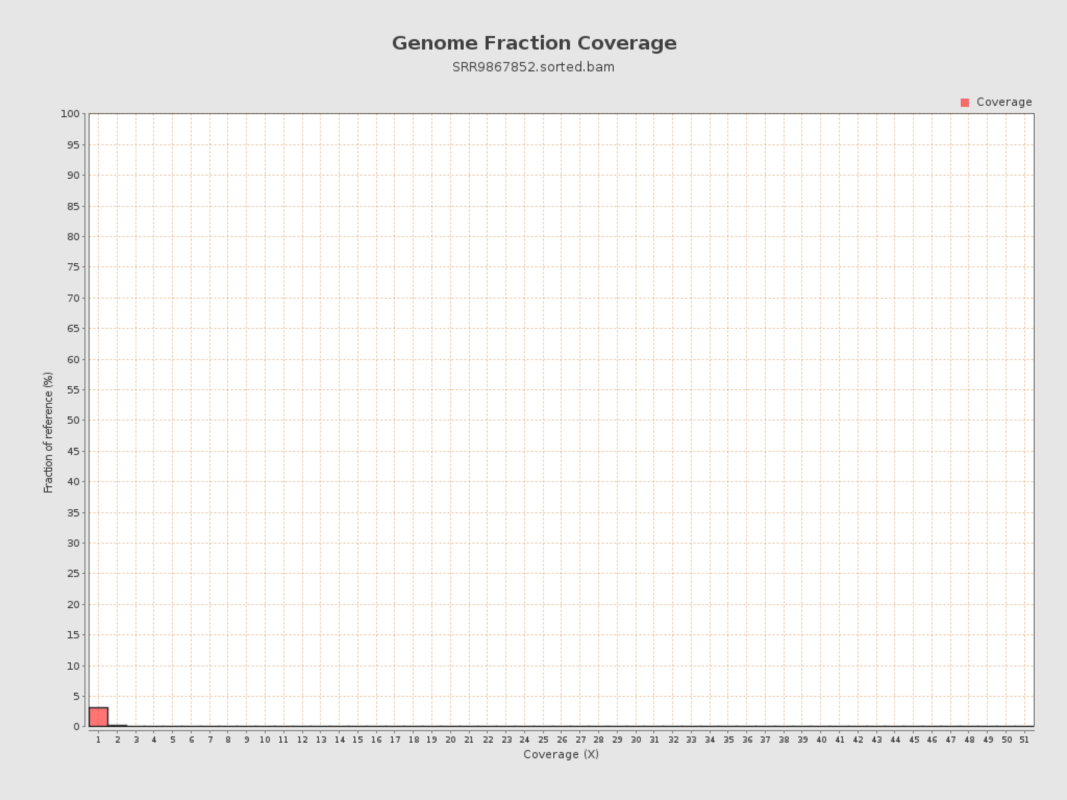
4. Results : Coverage Histogram



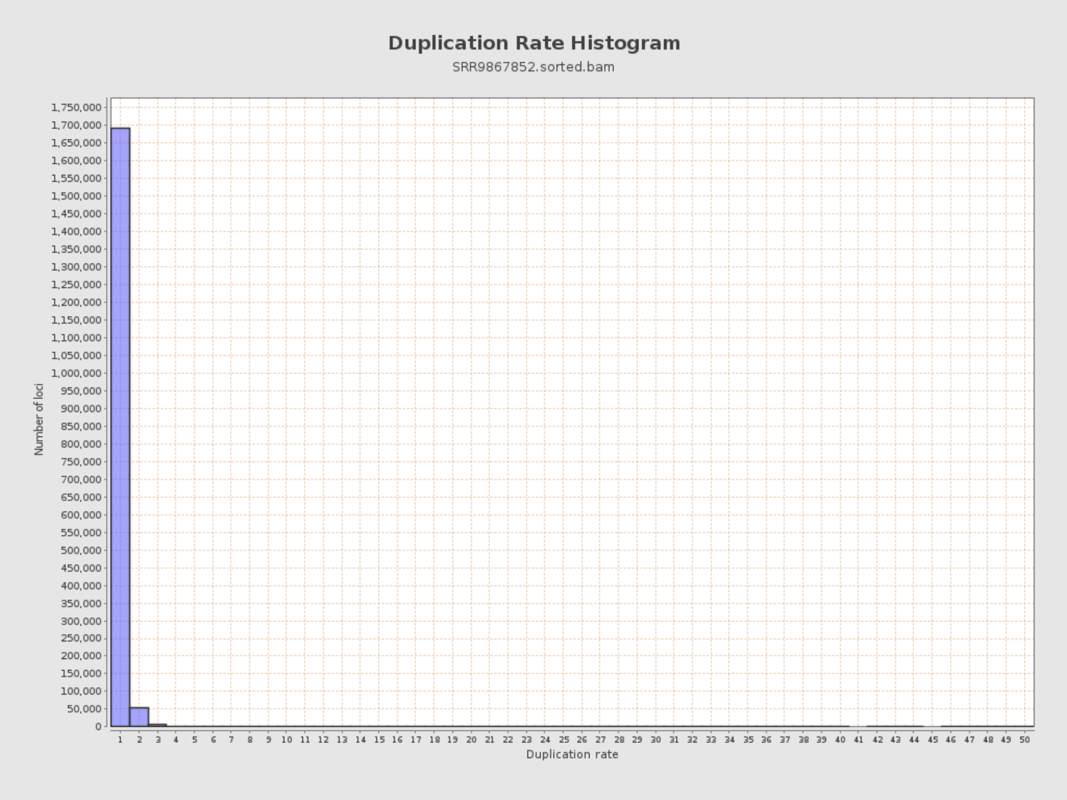
5. Results : Coverage Histogram (0-50X)



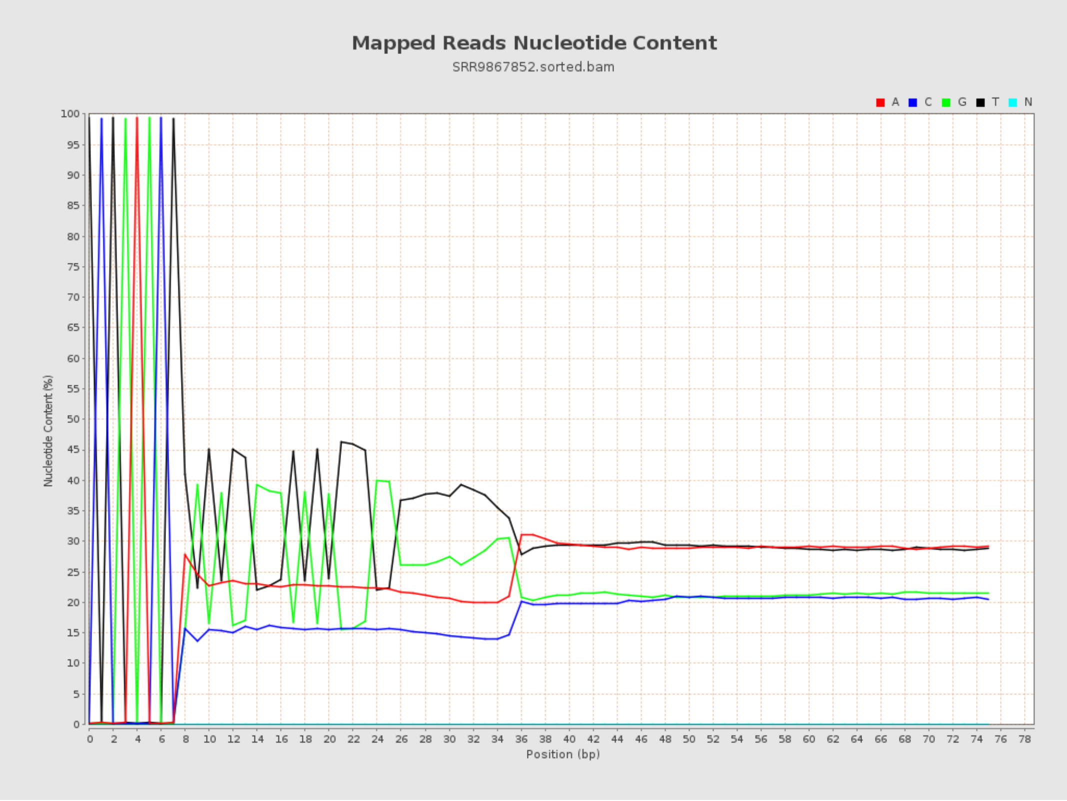
6. Results : Genome Fraction Coverage



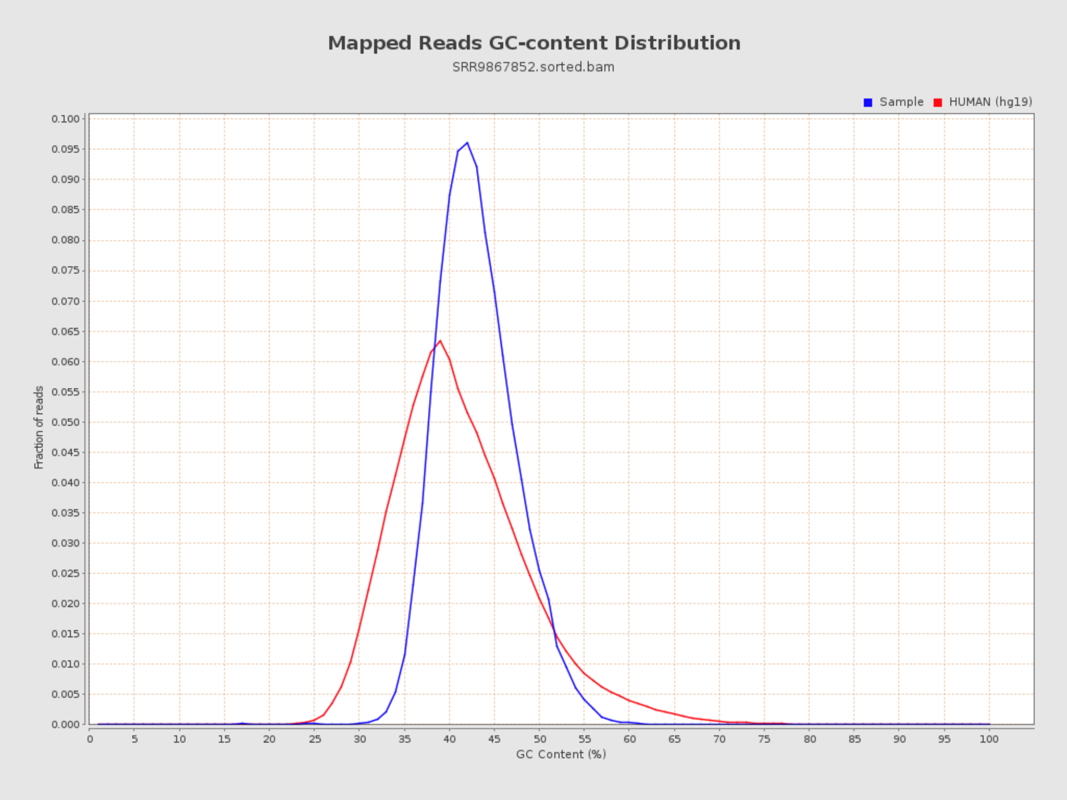
7. Results : Duplication Rate Histogram



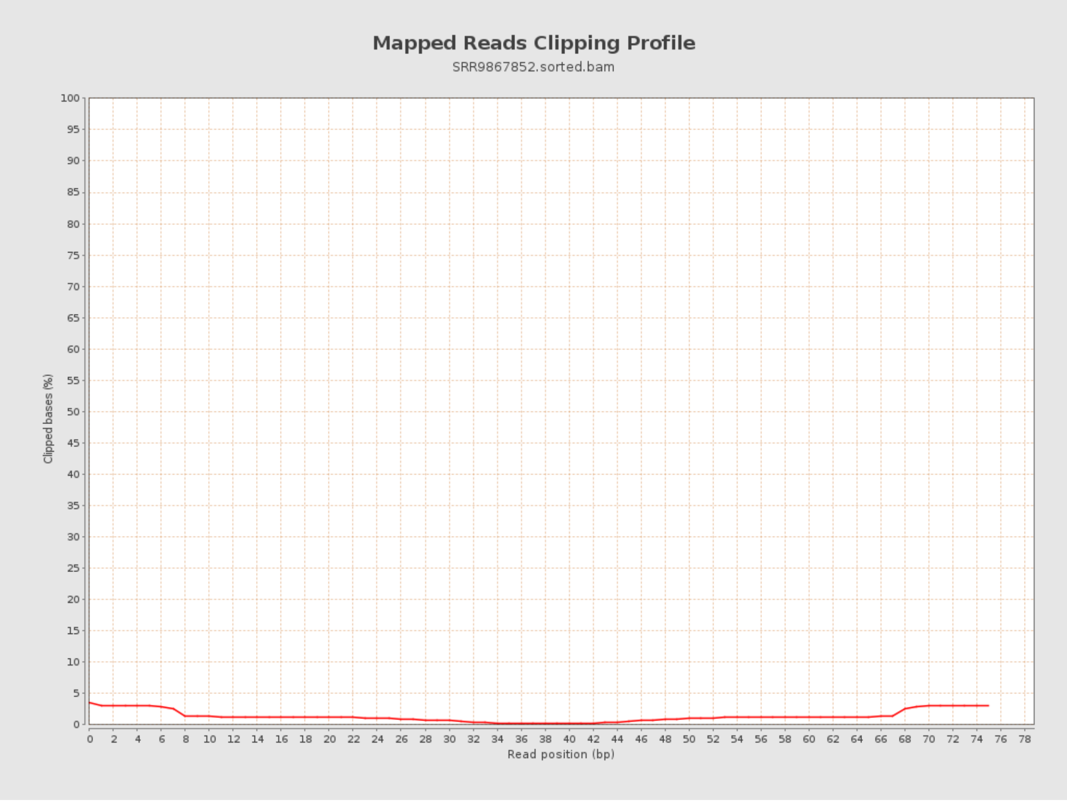
8. Results : Mapped Reads Nucleotide Content



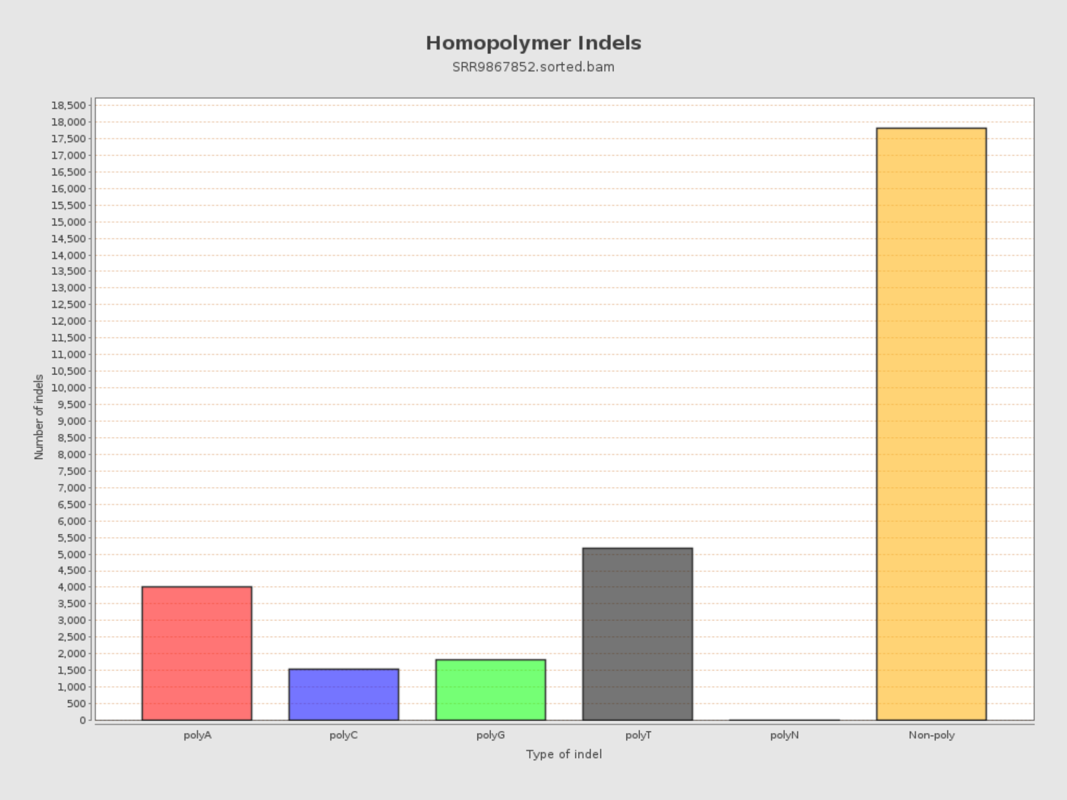
9. Results : Mapped Reads GC-content Distribution



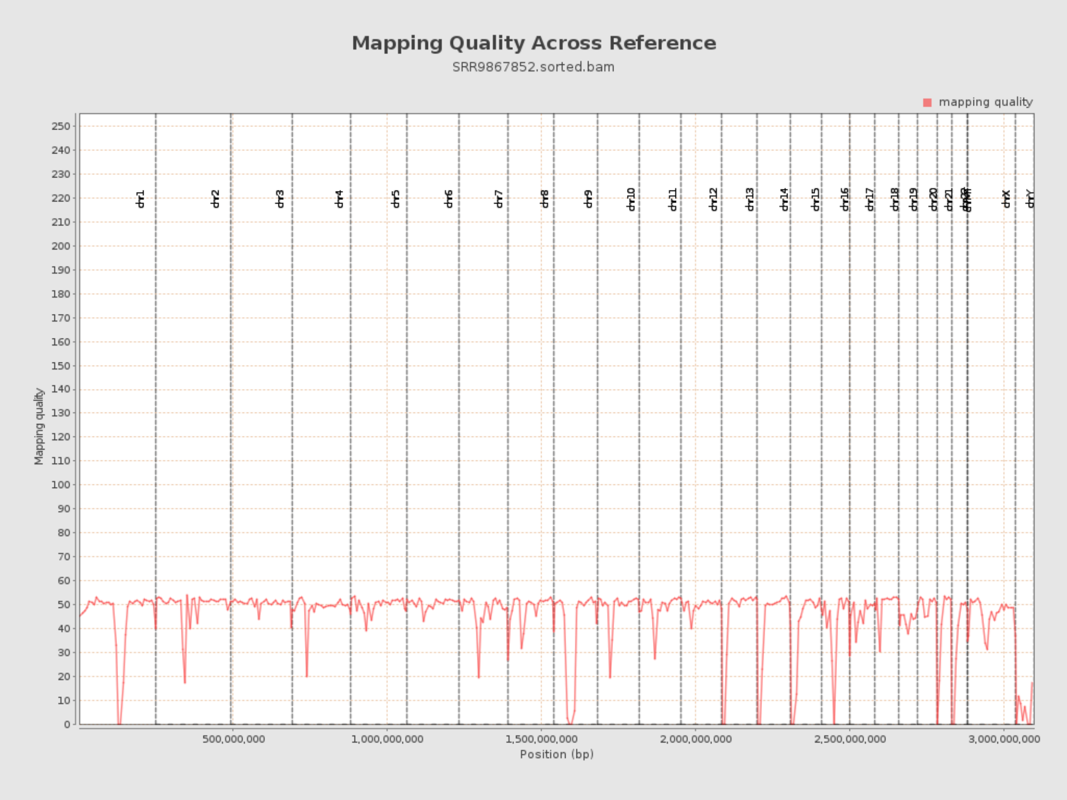
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram