Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 13:40:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867853.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_SRR9867853 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867853.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 13:40:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867853.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,269,208
Mapped reads	2,089,262 / 92.07%
Unmapped reads	179,946 / 7.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,726 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	101,940 / 4.49%
Duplication rate	3.57%
Clipped reads	2,091,996 / 92.19%

2.2. ACGT Content

Number/percentage of A's	30,057,051 / 24.36%
Number/percentage of C's	22,106,081 / 17.91%
Number/percentage of T's	40,489,830 / 32.81%
Number/percentage of G's	30,737,461 / 24.91%
Number/percentage of N's	16,312 / 0.01%
GC Percentage	42.82%

2.3. Coverage

Mean	0.0399

Standard Deviation	0.3708

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

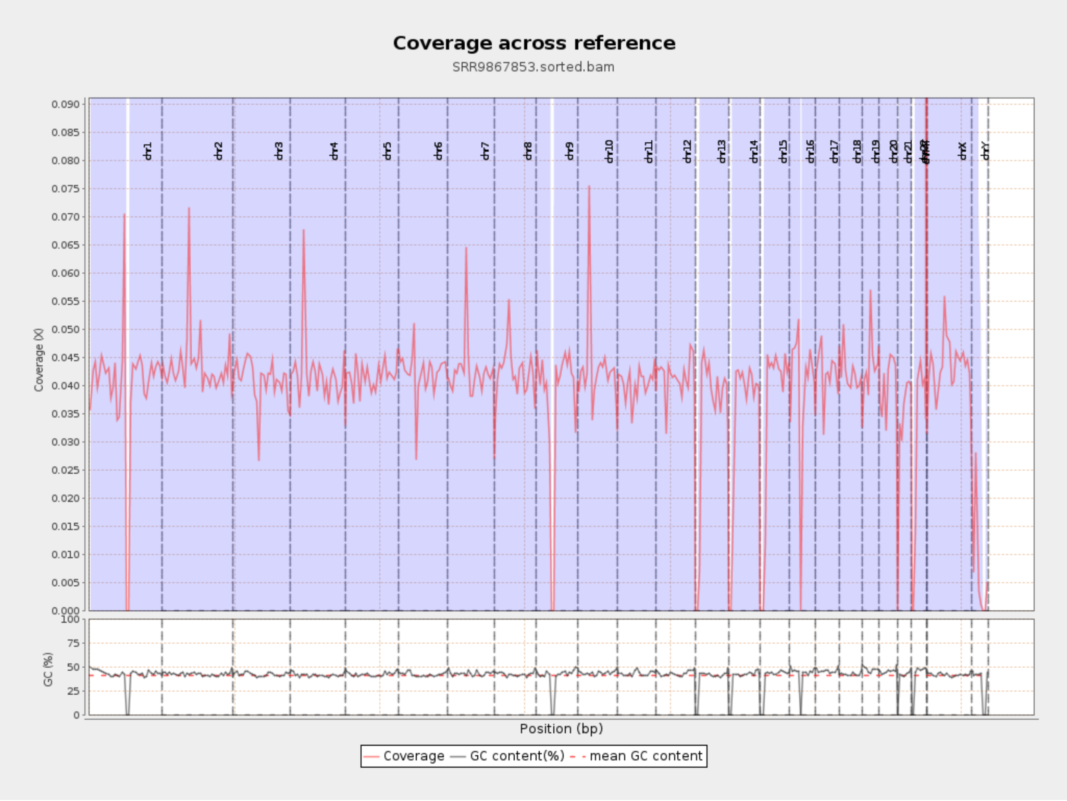
General error rate	0.52%
Mismatches	620,080
Insertions	9,082
Mapped reads with at least one insertion	0.43%
Deletions	23,625
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.87%

2.6. Chromosome stats

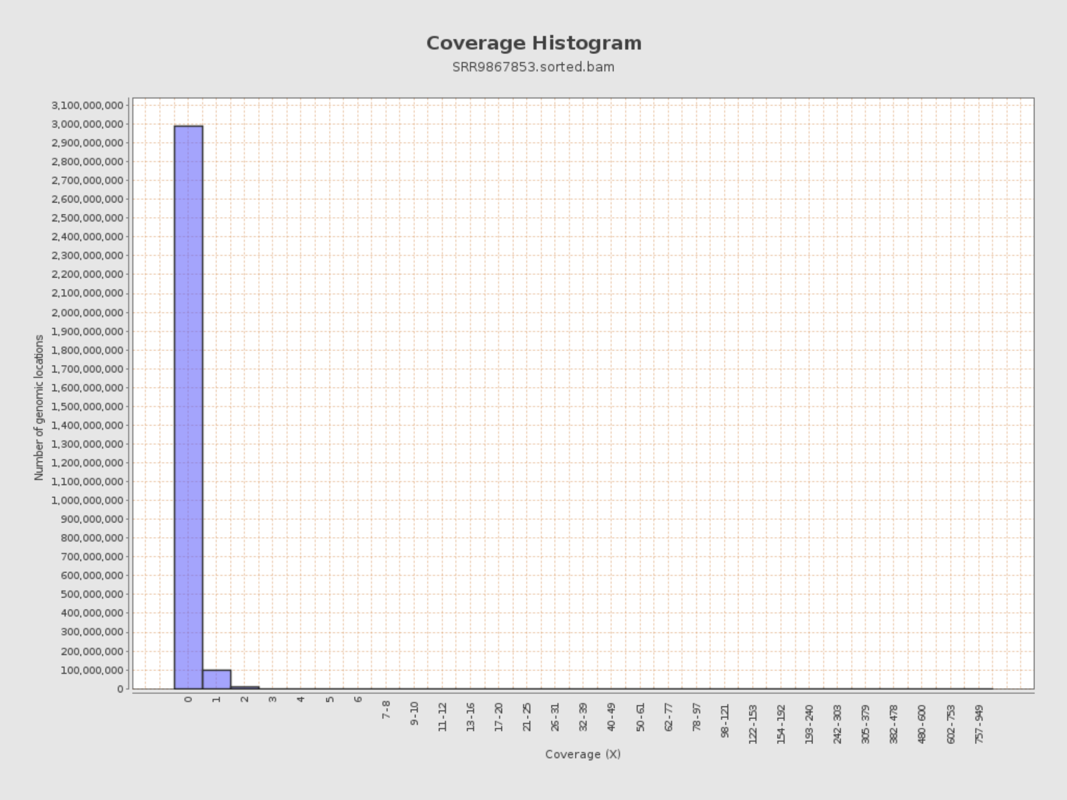
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9933973	0.0399	0.7115
chr2	243199373	10641553	0.0438	0.4972
chr3	198022430	8099684	0.0409	0.2252
chr4	191154276	8052483	0.0421	0.2671
chr5	180915260	7522499	0.0416	0.2283
chr6	171115067	7259513	0.0424	0.262
chr7	159138663	6814245	0.0428	0.4321

chr8	146364022	6215083	0.0425	0.395
chr9	141213431	5180475	0.0367	0.3028
chr10	135534747	5884068	0.0434	0.3764
chr11	135006516	5444218	0.0403	0.3036
chr12	133851895	5568294	0.0416	0.2299
chr13	115169878	3887908	0.0338	0.2029
chr14	107349540	3650620	0.034	0.2119
chr15	102531392	3577349	0.0349	0.2074
chr16	90354753	3588125	0.0397	0.2436
chr17	81195210	3404830	0.0419	0.2436
chr18	78077248	3314832	0.0425	0.5777
chr19	59128983	2596693	0.0439	0.526
chr20	63025520	2530804	0.0402	0.2306
chr21	48129895	1601087	0.0333	0.2493
chr22	51304566	1466399	0.0286	0.1869
chrMT	16571	26197	1.5809	1.581
chrX	155270560	6751440	0.0435	0.2622
chrY	59373566	432181	0.0073	0.2815

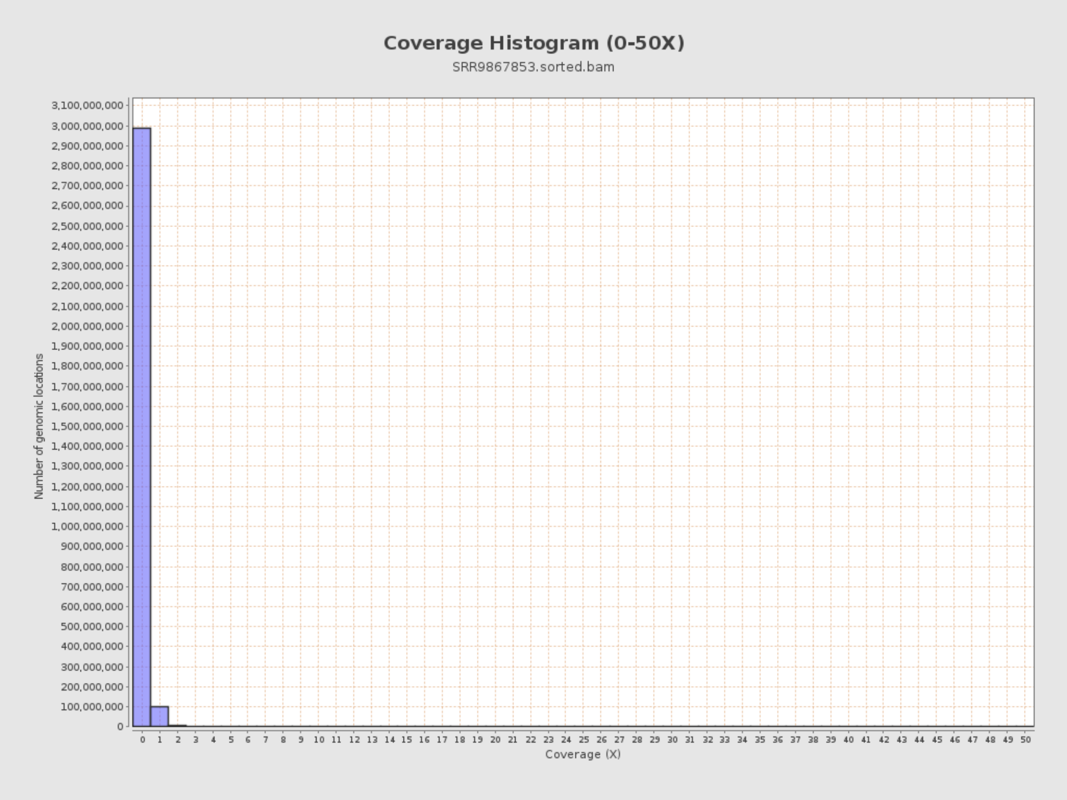
3. Results : Coverage across reference



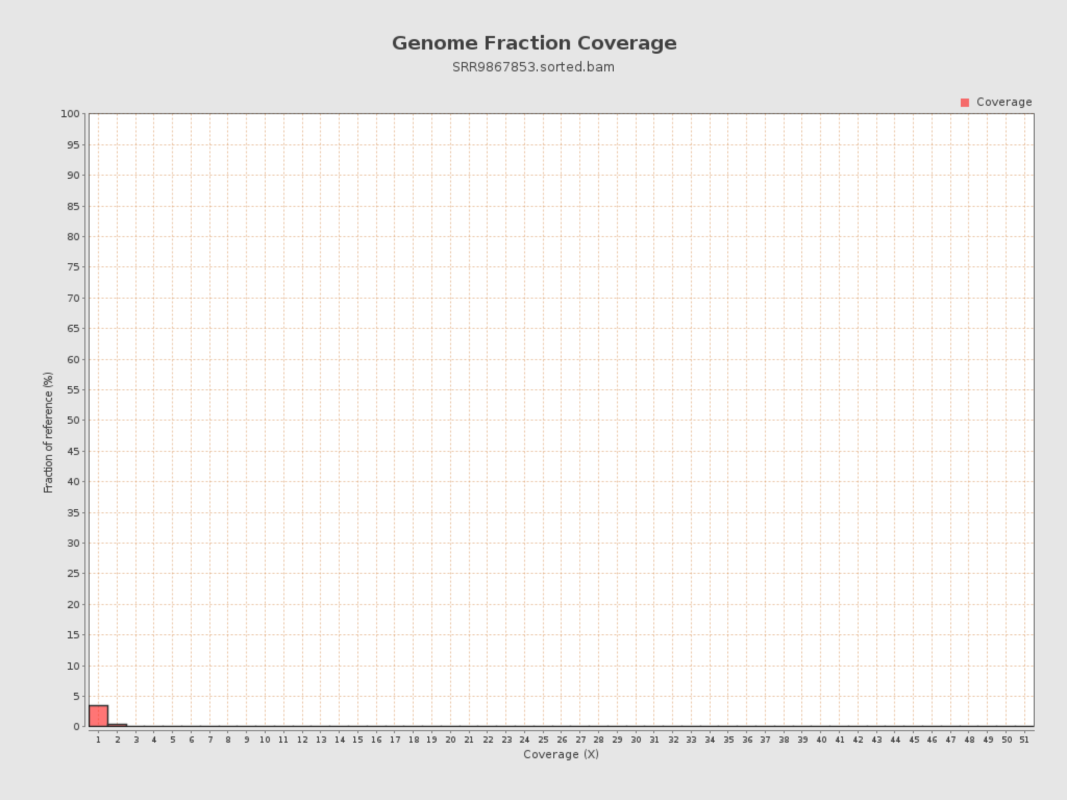
4. Results : Coverage Histogram



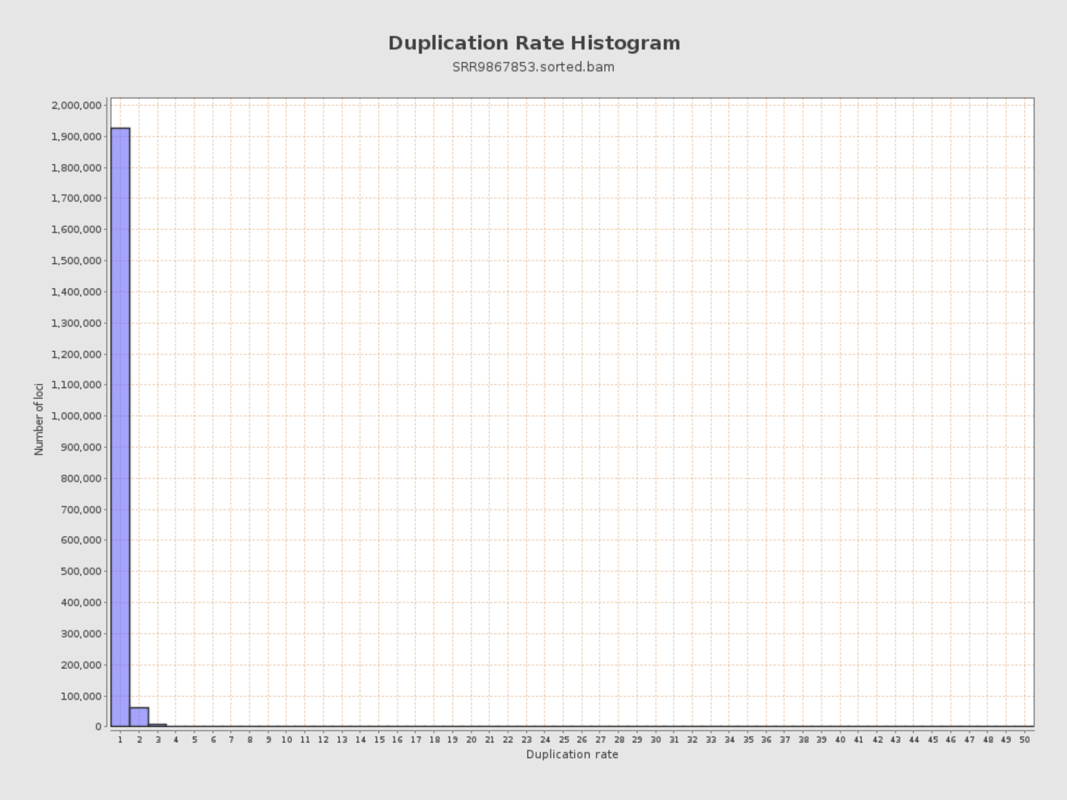
5. Results : Coverage Histogram (0-50X)



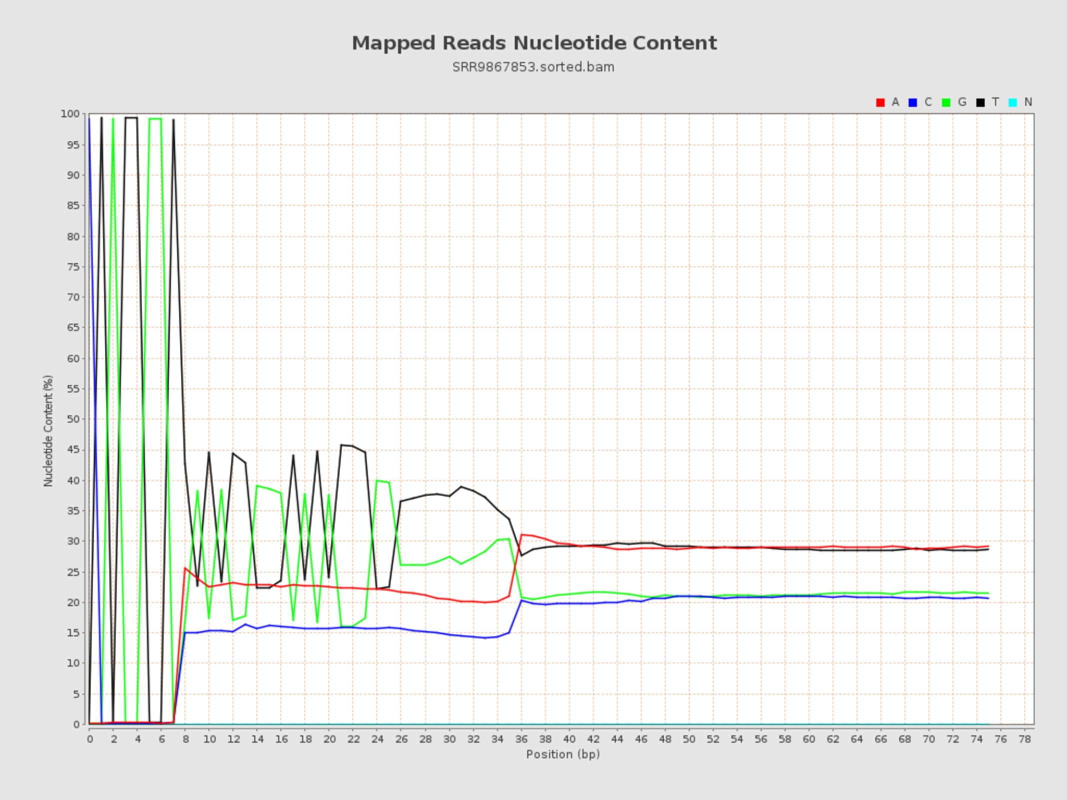
6. Results : Genome Fraction Coverage



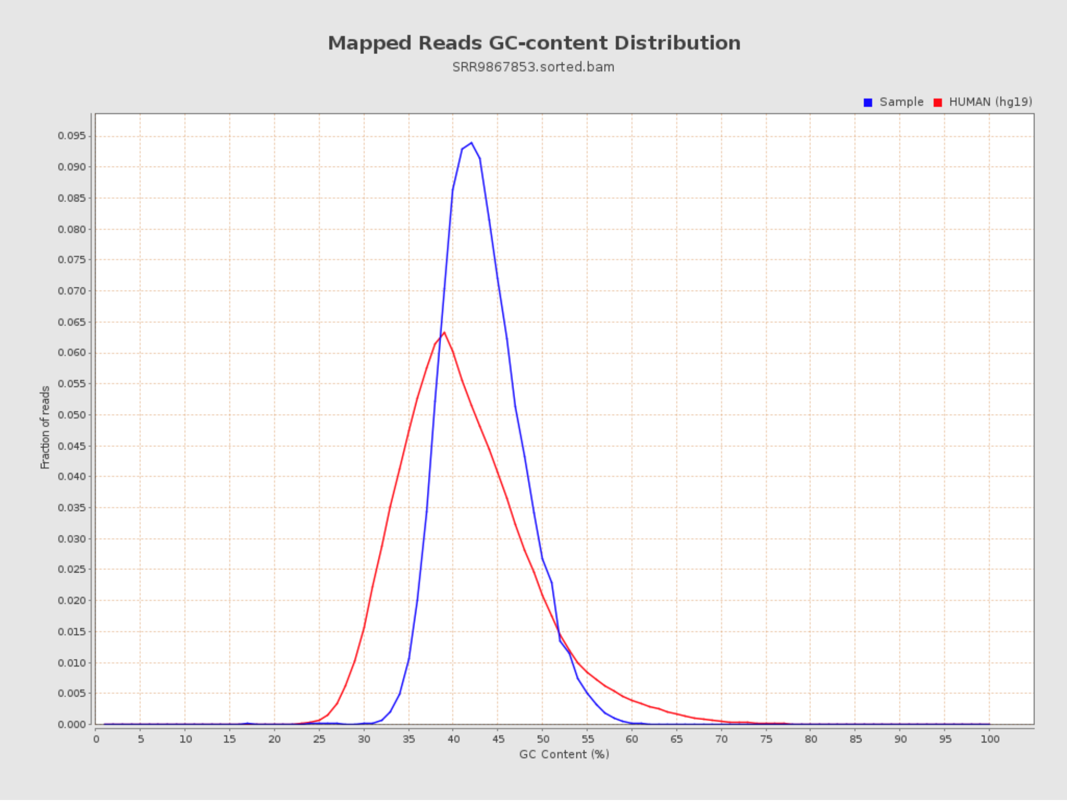
7. Results : Duplication Rate Histogram



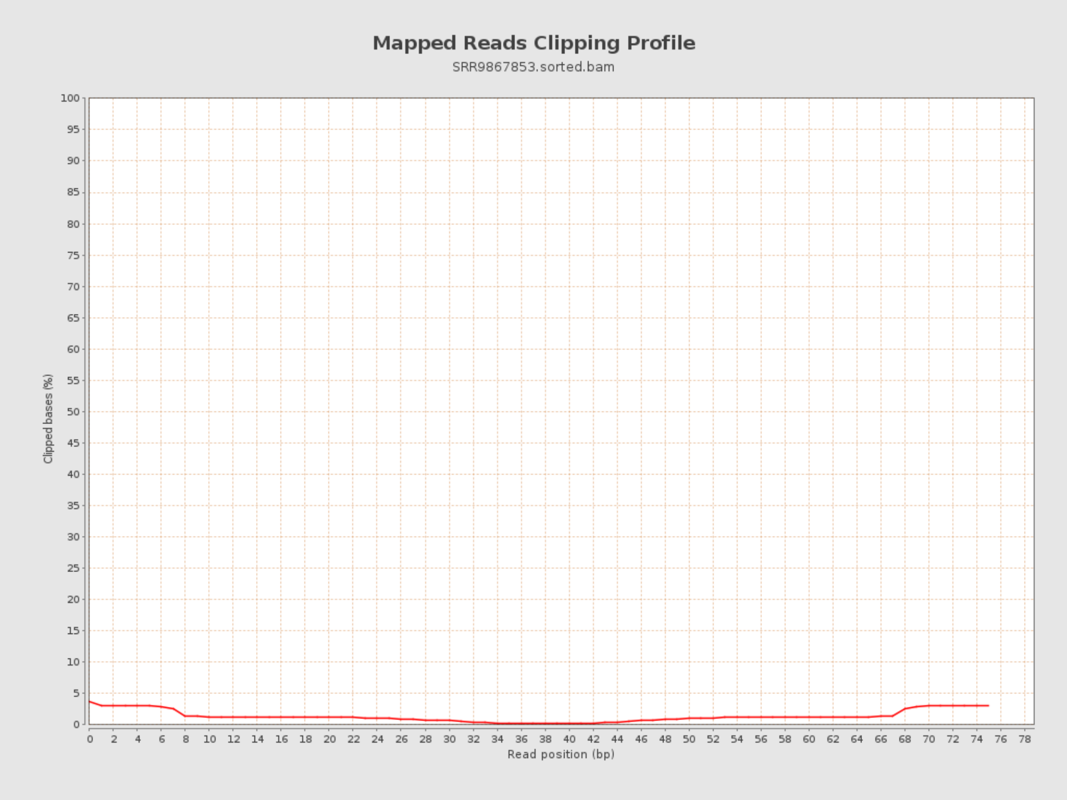
8. Results : Mapped Reads Nucleotide Content



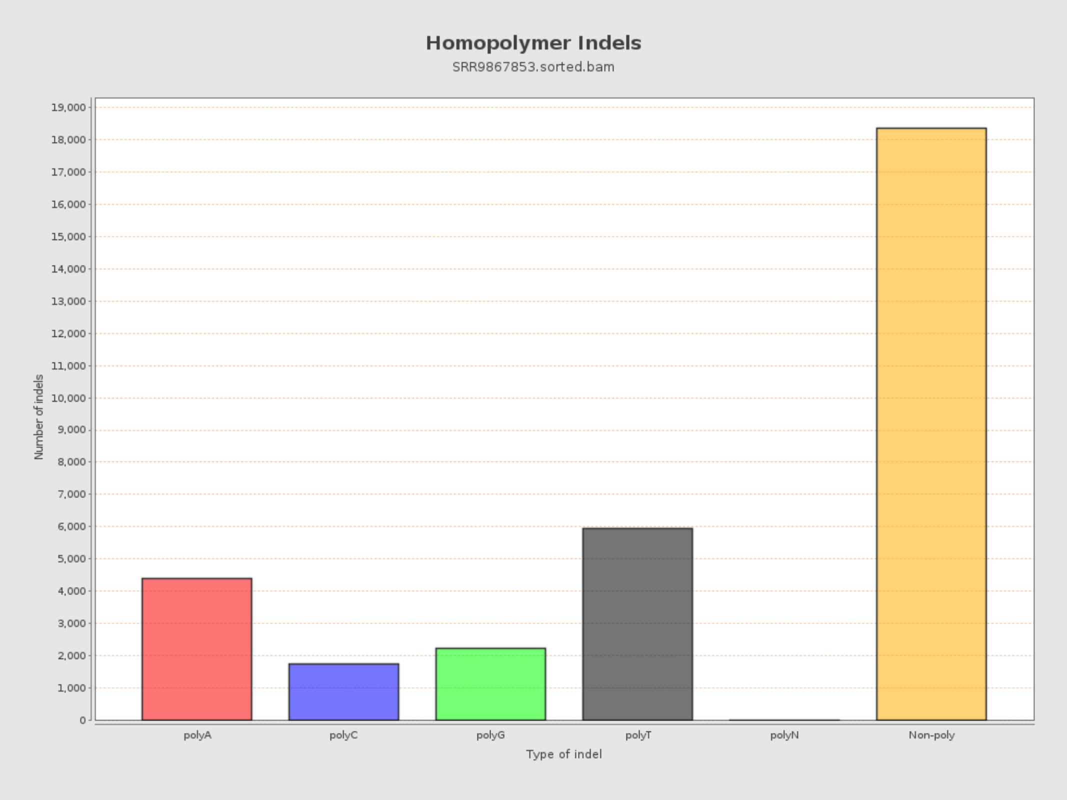
9. Results : Mapped Reads GC-content Distribution



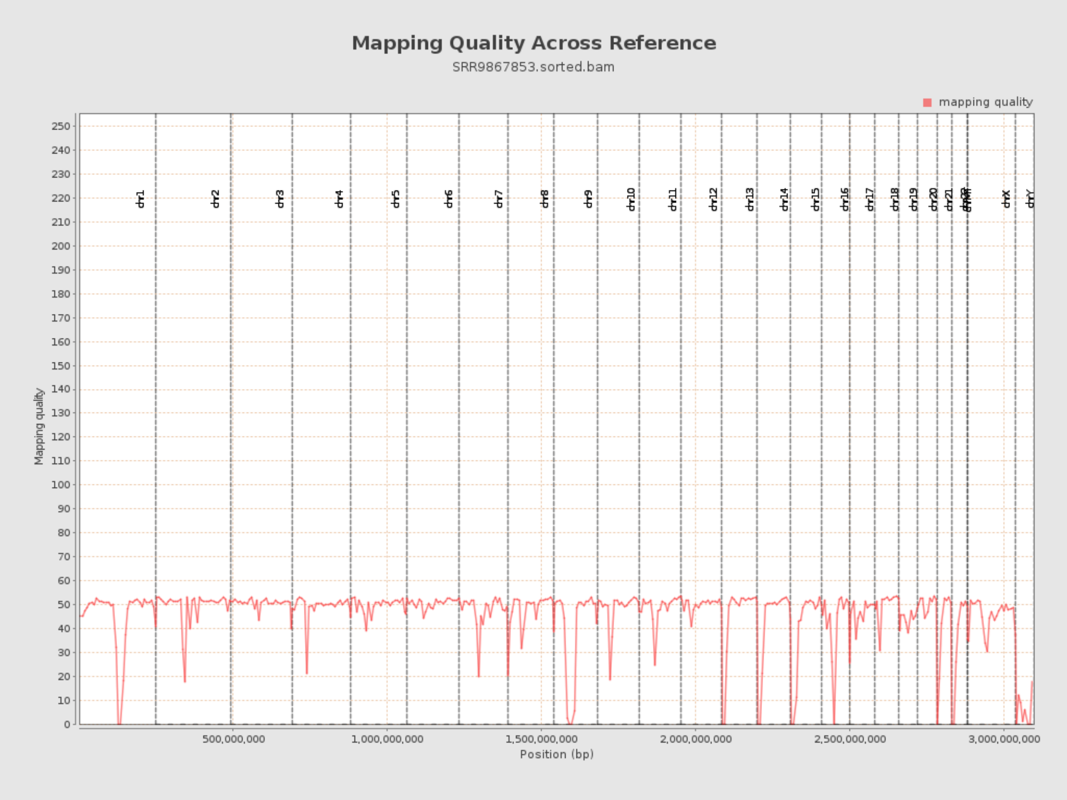
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram