Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 10:37:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867847.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_SRR9867847 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867847.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 10:37:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867847.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,347,145
Mapped reads	2,166,709 / 92.31%
Unmapped reads	180,436 / 7.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,305 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	112,961 / 4.81%
Duplication rate	3.89%
Clipped reads	2,170,380 / 92.47%

2.2. ACGT Content

Number/percentage of A's	32,959,623 / 25.83%
Number/percentage of C's	24,941,538 / 19.55%
Number/percentage of T's	39,844,686 / 31.23%
Number/percentage of G's	29,822,333 / 23.37%
Number/percentage of N's	17,851 / 0.01%
GC Percentage	42.92%

2.3. Coverage

Mean	0.0412

Standard Deviation	0.3741

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

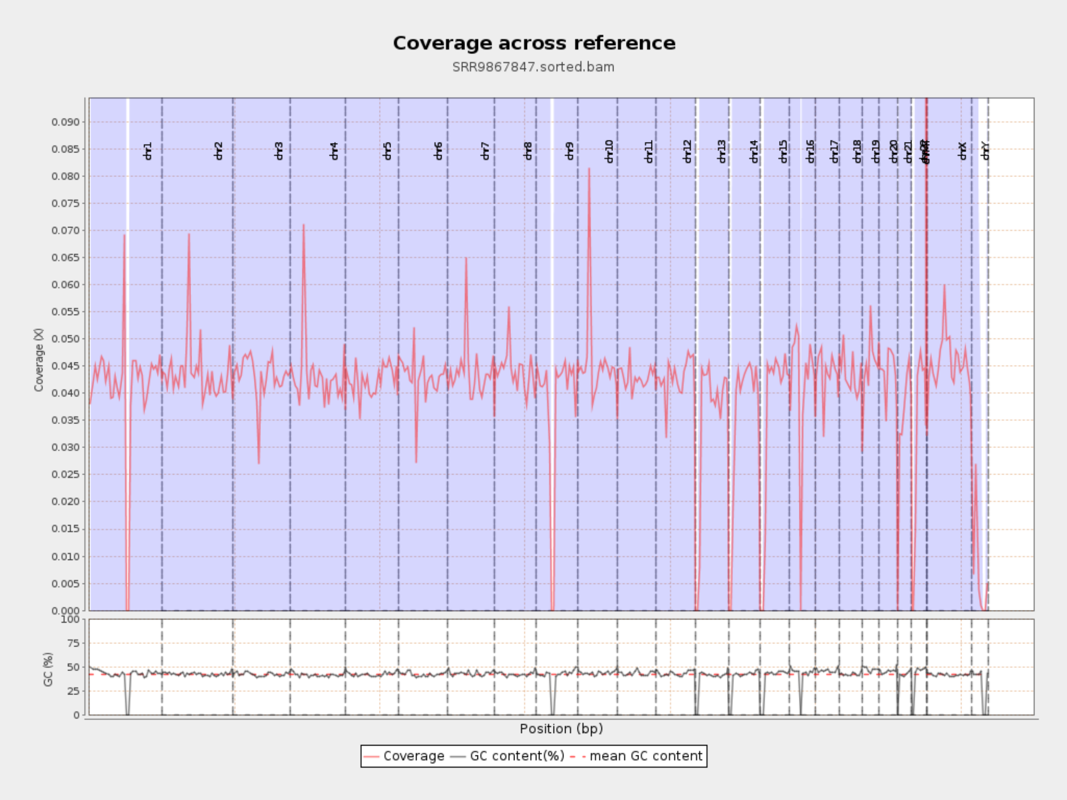
General error rate	0.52%
Mismatches	643,889
Insertions	8,764
Mapped reads with at least one insertion	0.4%
Deletions	24,777
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44.53%

2.6. Chromosome stats

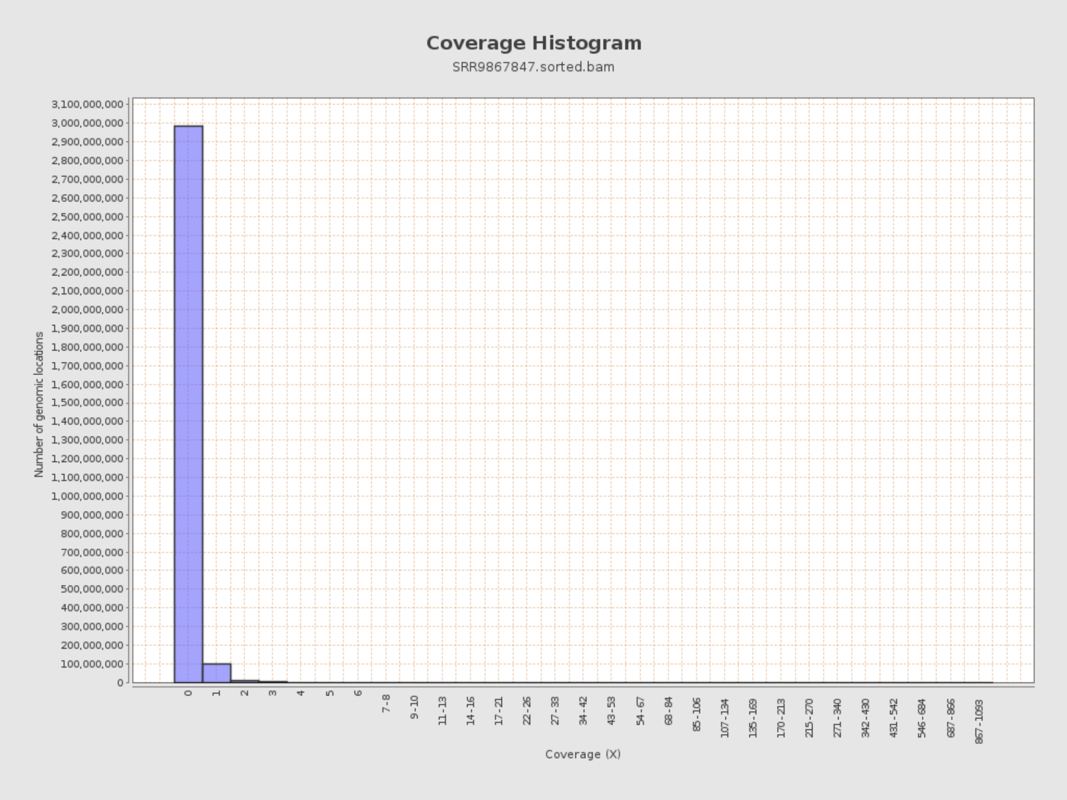
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10211363	0.041	0.6849
chr2	243199373	10689198	0.044	0.5324
chr3	198022430	8536964	0.0431	0.2327
chr4	191154276	8256617	0.0432	0.2764
chr5	180915260	7669924	0.0424	0.2321
chr6	171115067	7366130	0.043	0.2764
chr7	159138663	7002128	0.044	0.4373

chr8	146364022	6452464	0.0441	0.3969
chr9	141213431	5300429	0.0375	0.3103
chr10	135534747	6203617	0.0458	0.3824
chr11	135006516	5781411	0.0428	0.319
chr12	133851895	5748248	0.0429	0.2363
chr13	115169878	3956181	0.0344	0.2096
chr14	107349540	3813225	0.0355	0.2192
chr15	102531392	3672336	0.0358	0.2153
chr16	90354753	3779845	0.0418	0.2546
chr17	81195210	3525127	0.0434	0.2538
chr18	78077248	3397677	0.0435	0.5684
chr19	59128983	2697895	0.0456	0.5044
chr20	63025520	2769308	0.0439	0.2433
chr21	48129895	1677407	0.0349	0.2502
chr22	51304566	1572315	0.0306	0.197
chrMT	16571	26993	1.6289	1.5838
chrX	155270560	7094377	0.0457	0.2711
chrY	59373566	424414	0.0071	0.2732

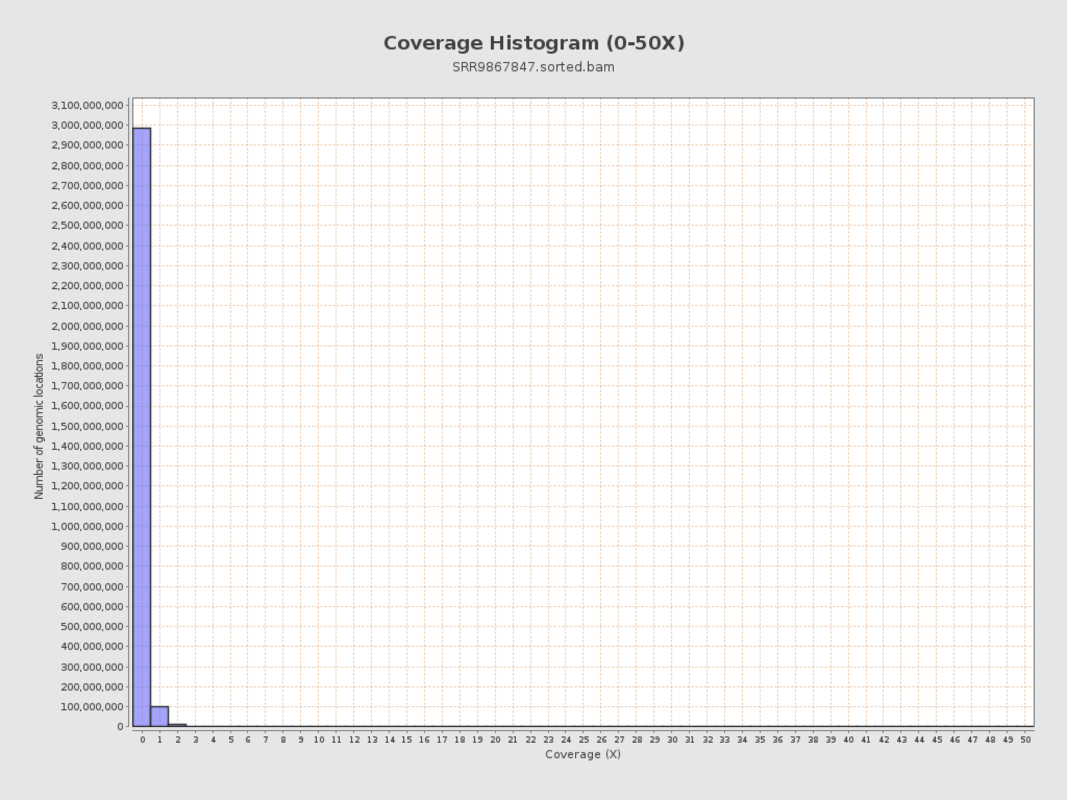
3. Results : Coverage across reference



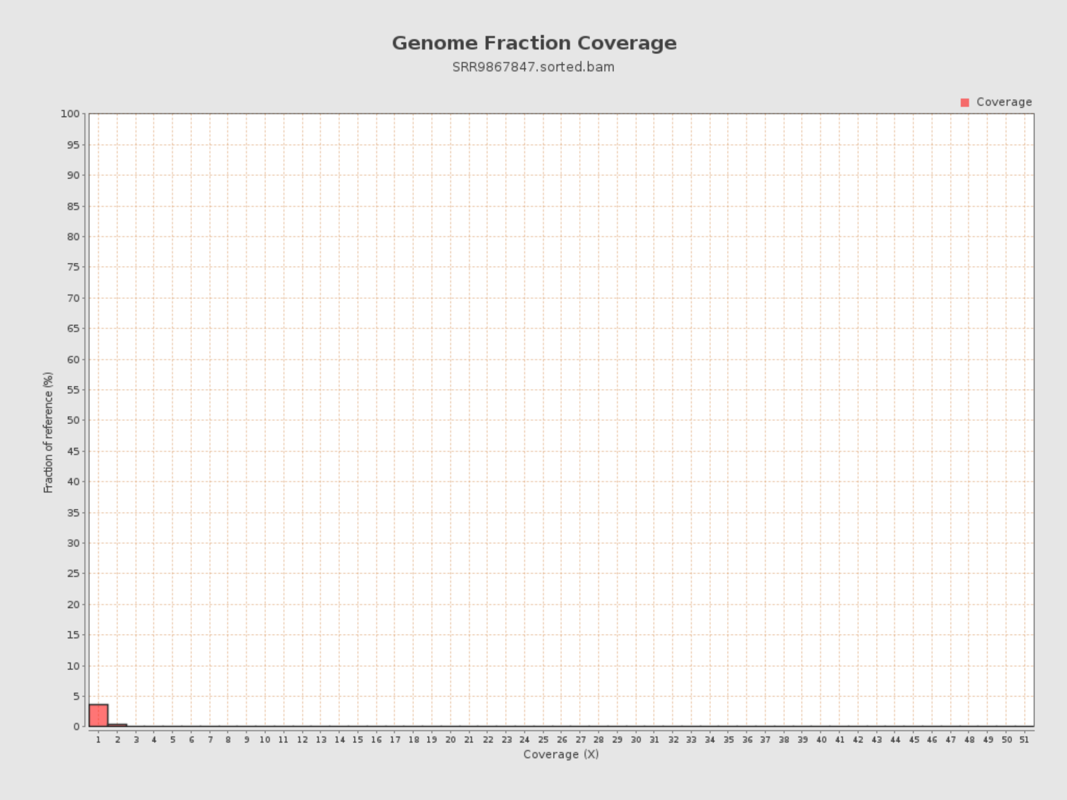
4. Results : Coverage Histogram



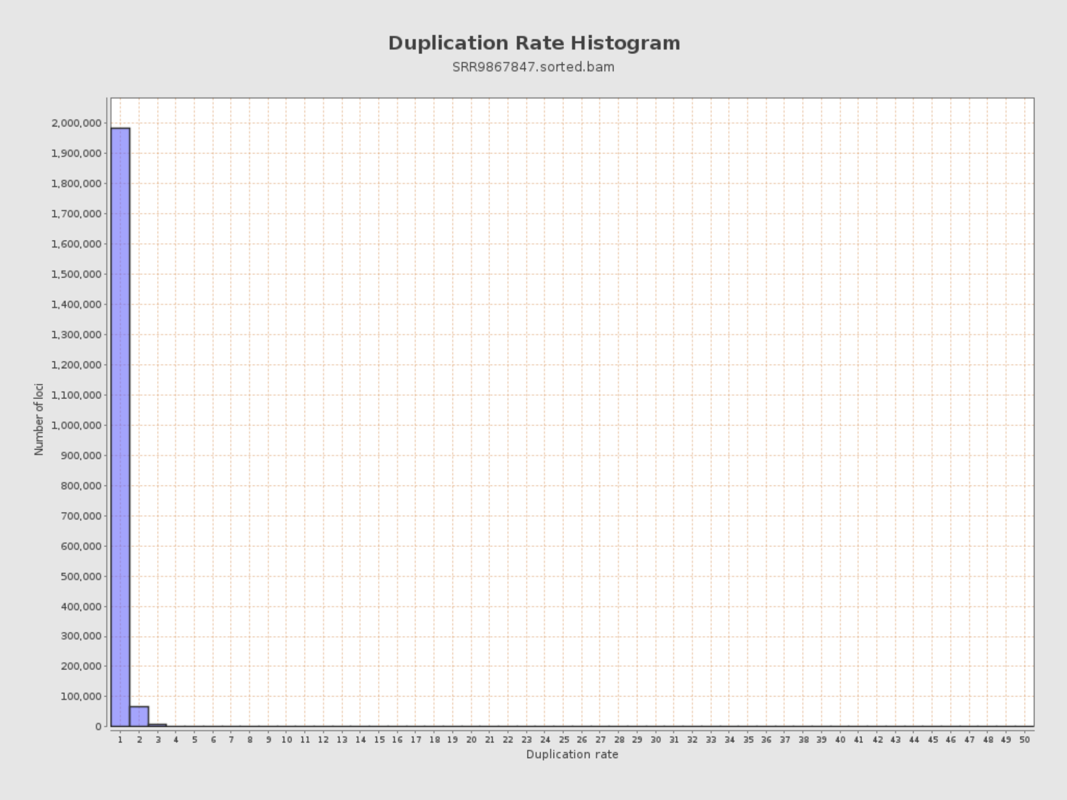
5. Results : Coverage Histogram (0-50X)



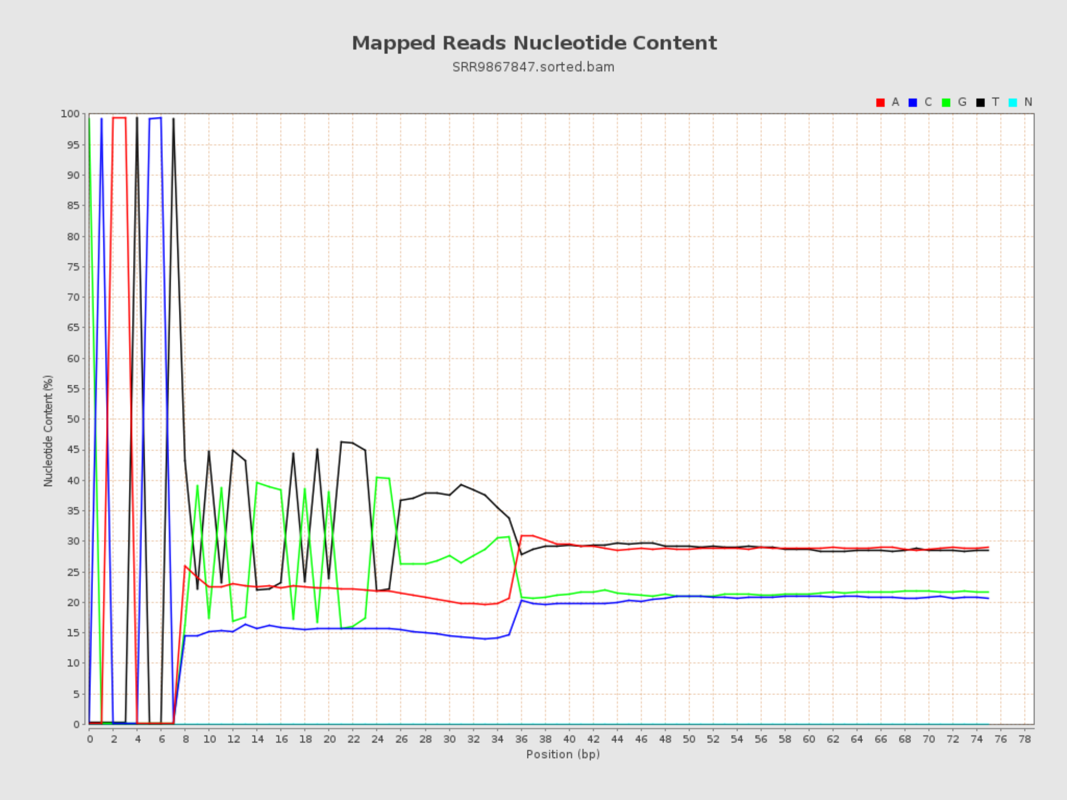
6. Results : Genome Fraction Coverage



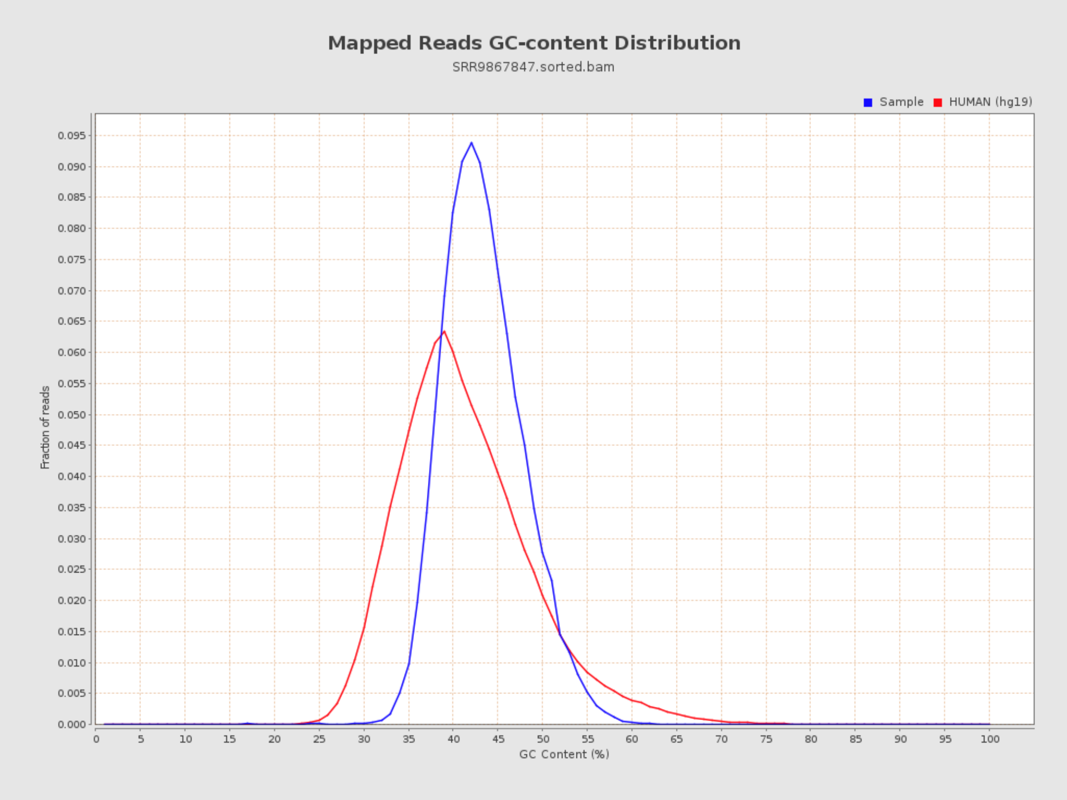
7. Results : Duplication Rate Histogram



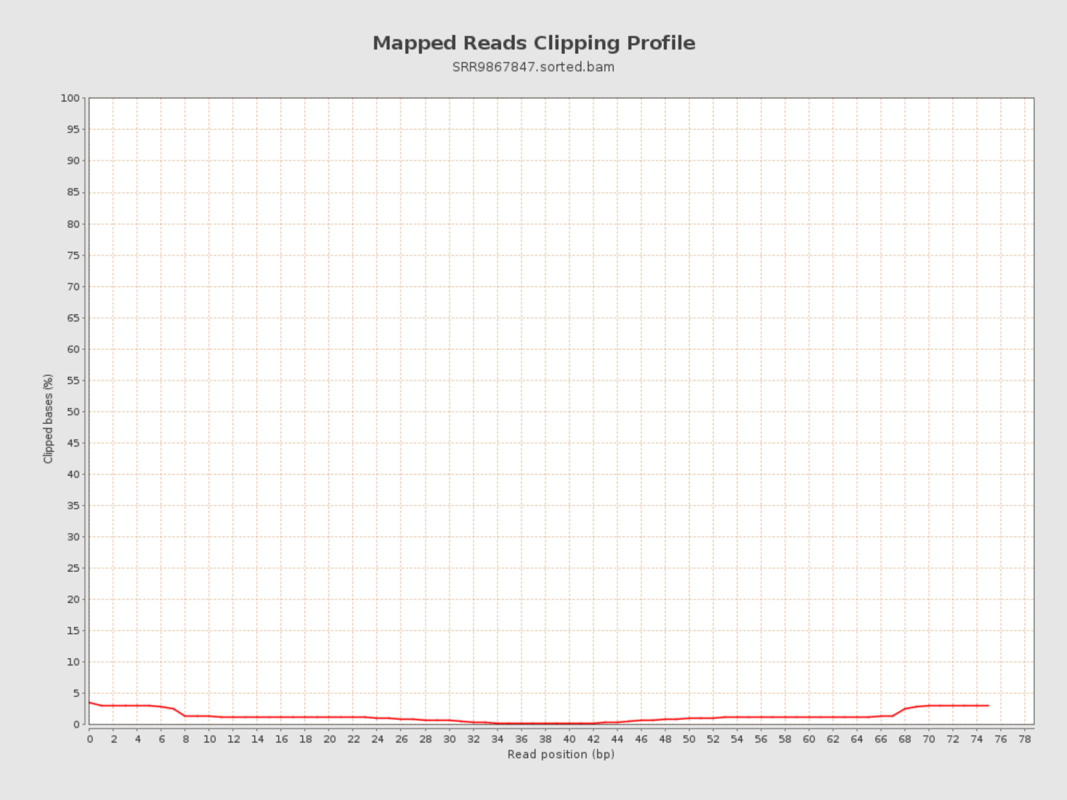
8. Results : Mapped Reads Nucleotide Content



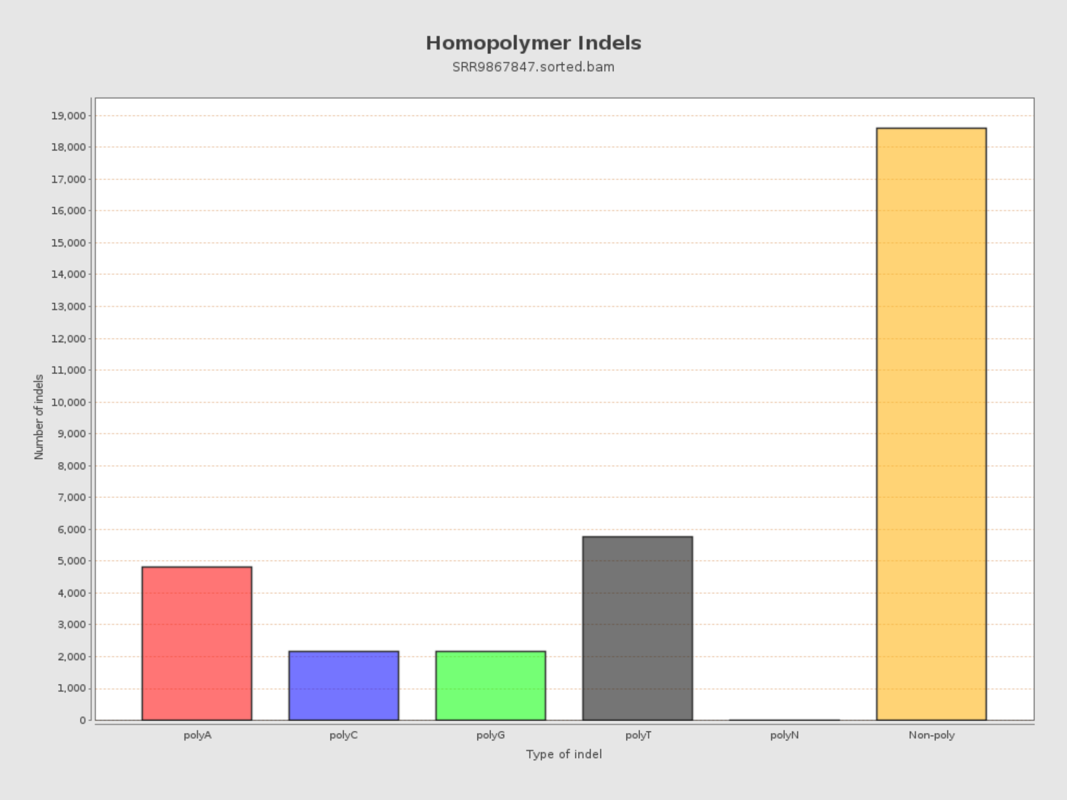
9. Results : Mapped Reads GC-content Distribution



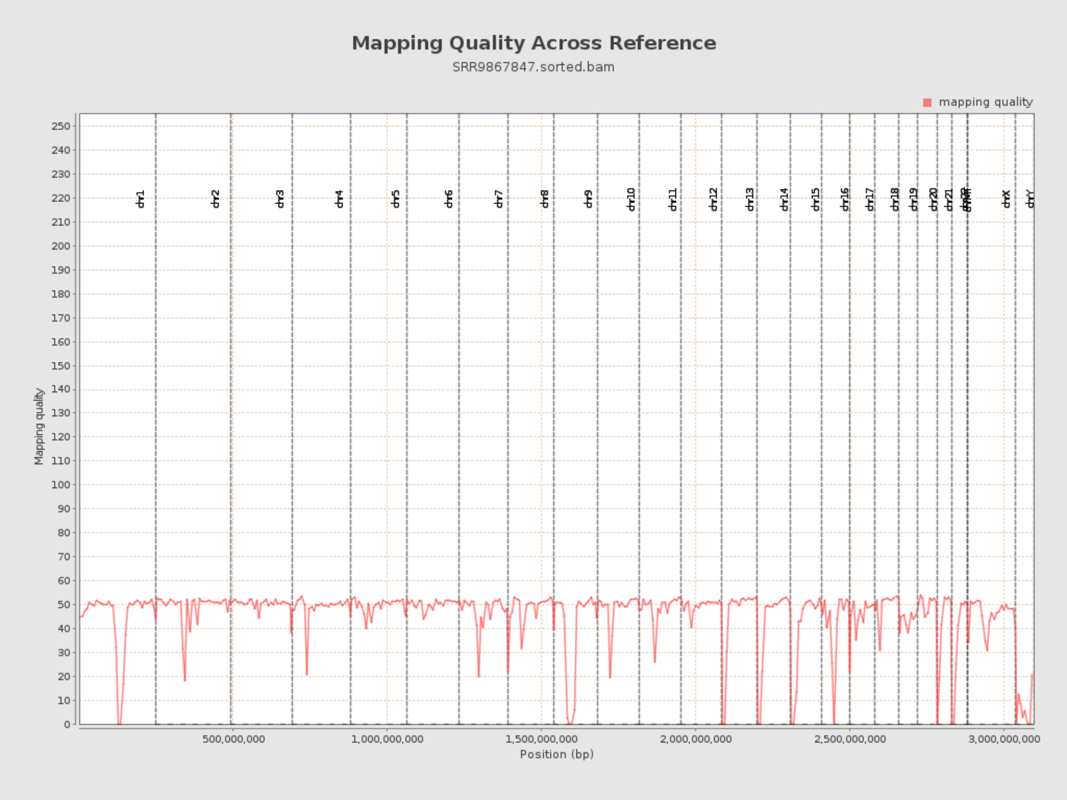
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram