Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 14:08:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867854.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_SRR9867854 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867854.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 14:07:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867854.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,800,314
Mapped reads	1,667,599 / 92.63%
Unmapped reads	132,715 / 7.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,524 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	73,529 / 4.08%
Duplication rate	3.26%
Clipped reads	1,670,151 / 92.77%

2.2. ACGT Content

Number/percentage of A's	24,197,215 / 24.44%
Number/percentage of C's	18,667,720 / 18.85%
Number/percentage of T's	31,474,338 / 31.78%
Number/percentage of G's	24,670,149 / 24.91%
Number/percentage of N's	13,278 / 0.01%
GC Percentage	43.77%

2.3. Coverage

Mean	0.032

Standard Deviation	0.3038

2.4. Mapping Quality

Mean Mapping Quality	45.95

2.5. Mismatches and indels

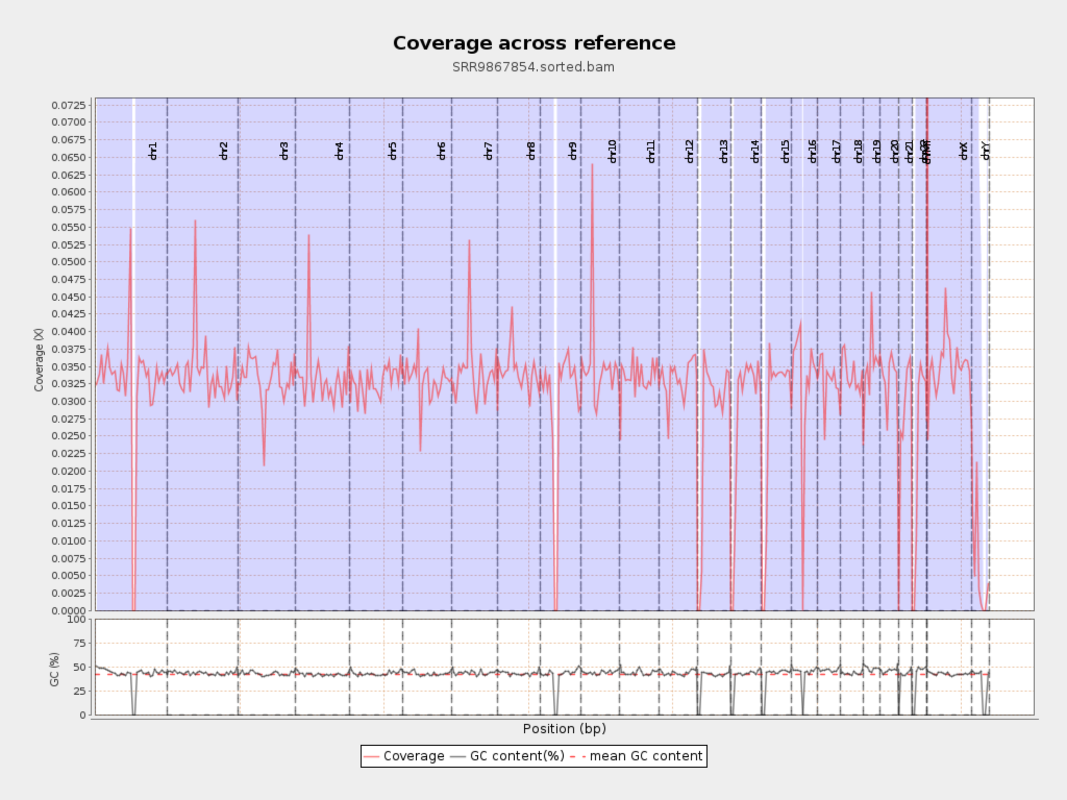
General error rate	0.51%
Mismatches	495,601
Insertions	6,805
Mapped reads with at least one insertion	0.41%
Deletions	19,017
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.27%

2.6. Chromosome stats

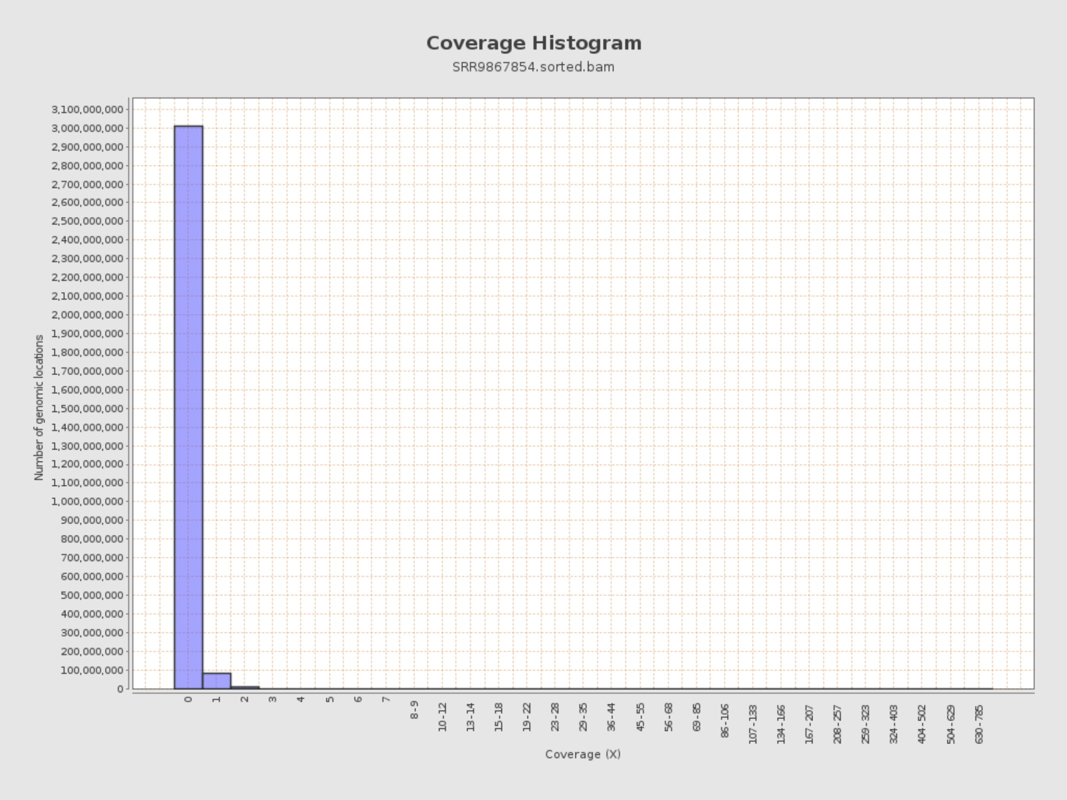
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8032420	0.0322	0.5323
chr2	243199373	8342822	0.0343	0.4108
chr3	198022430	6561372	0.0331	0.1988
chr4	191154276	6392398	0.0334	0.2303
chr5	180915260	5966991	0.033	0.2007
chr6	171115067	5645293	0.033	0.2321
chr7	159138663	5473266	0.0344	0.3513

chr8	146364022	5044336	0.0345	0.3434
chr9	141213431	4160083	0.0295	0.2558
chr10	135534747	4787443	0.0353	0.3128
chr11	135006516	4550623	0.0337	0.2695
chr12	133851895	4443437	0.0332	0.2016
chr13	115169878	3106562	0.027	0.1856
chr14	107349540	2989921	0.0279	0.1888
chr15	102531392	2830394	0.0276	0.1818
chr16	90354753	2900679	0.0321	0.2173
chr17	81195210	2668571	0.0329	0.2152
chr18	78077248	2646091	0.0339	0.4753
chr19	59128983	2096119	0.0354	0.4327
chr20	63025520	2093264	0.0332	0.2053
chr21	48129895	1334983	0.0277	0.2195
chr22	51304566	1178123	0.023	0.1654
chrMT	16571	15510	0.936	1.107
chrX	155270560	5454154	0.0351	0.2265
chrY	59373566	338085	0.0057	0.211

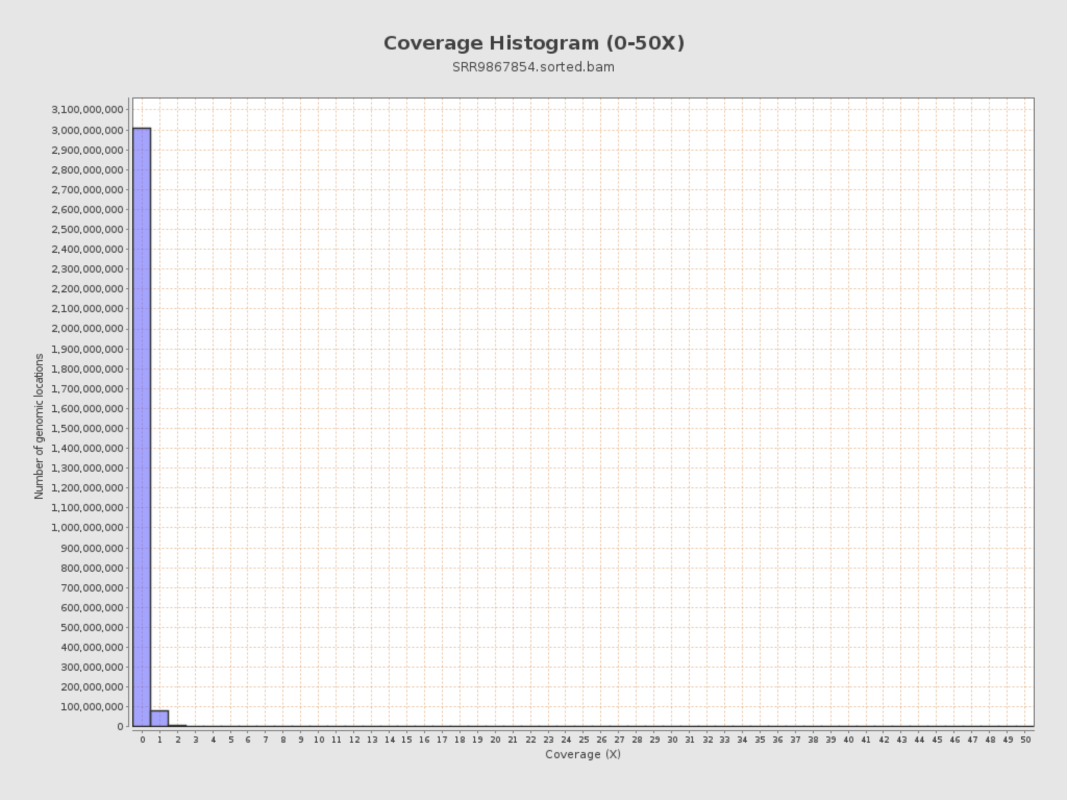
3. Results : Coverage across reference



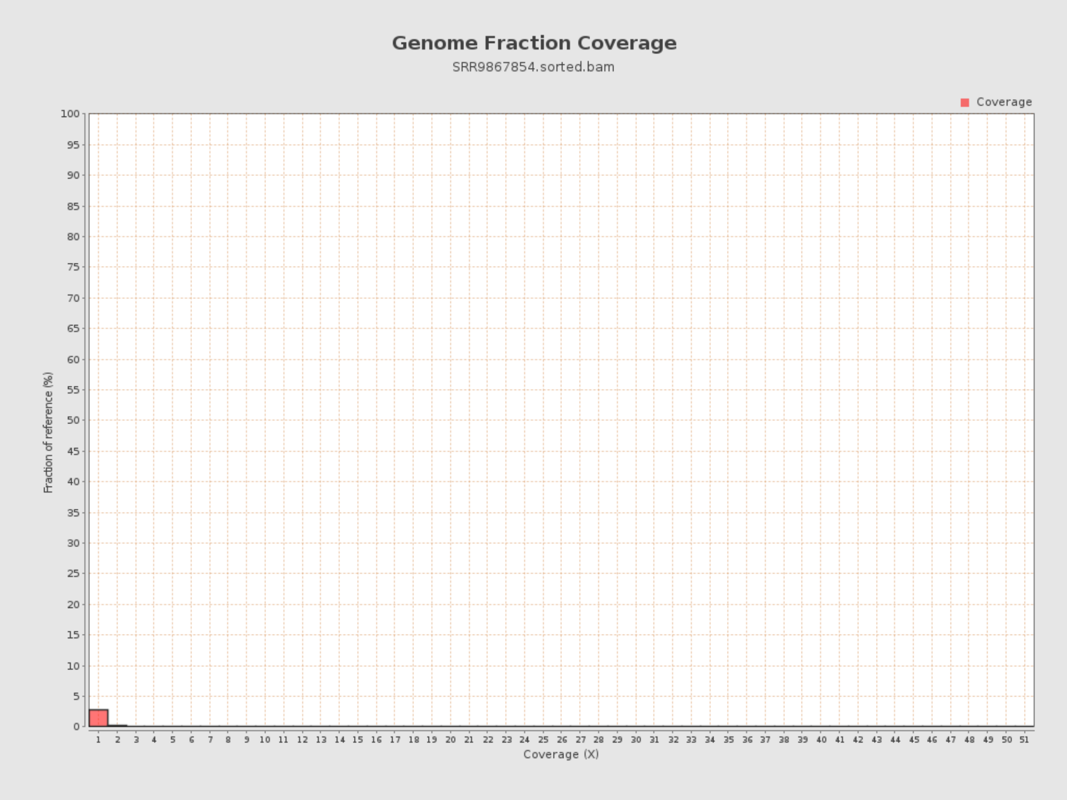
4. Results : Coverage Histogram



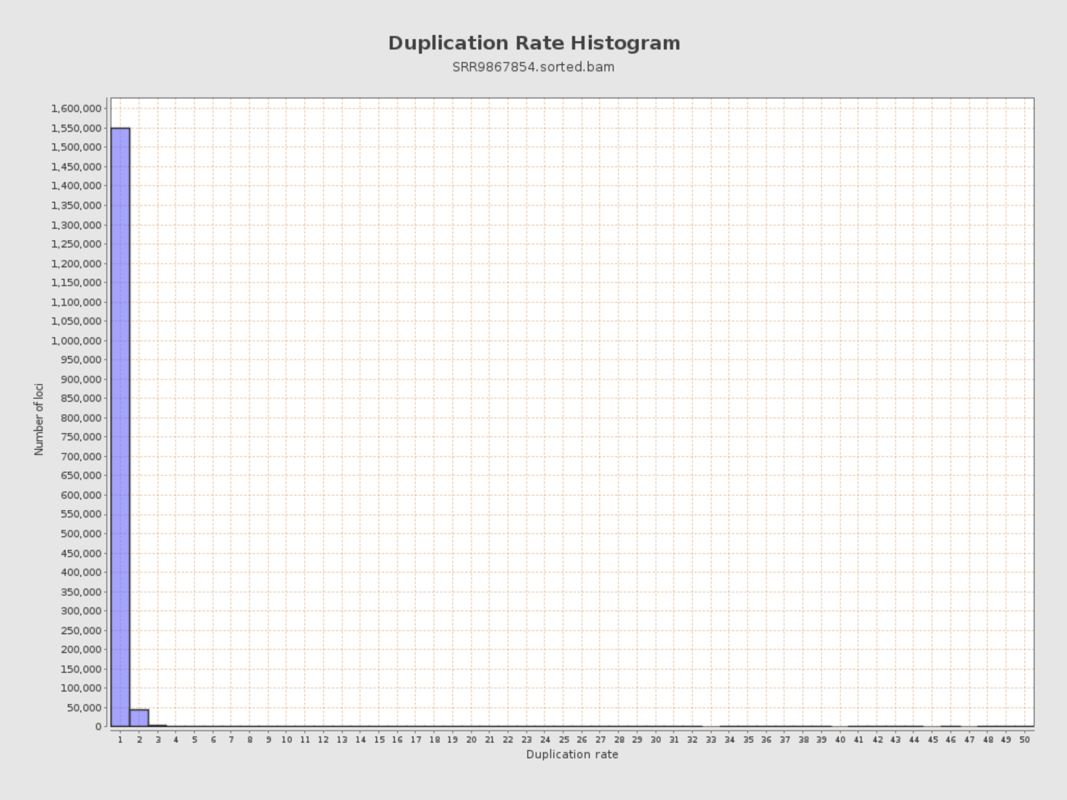
5. Results : Coverage Histogram (0-50X)



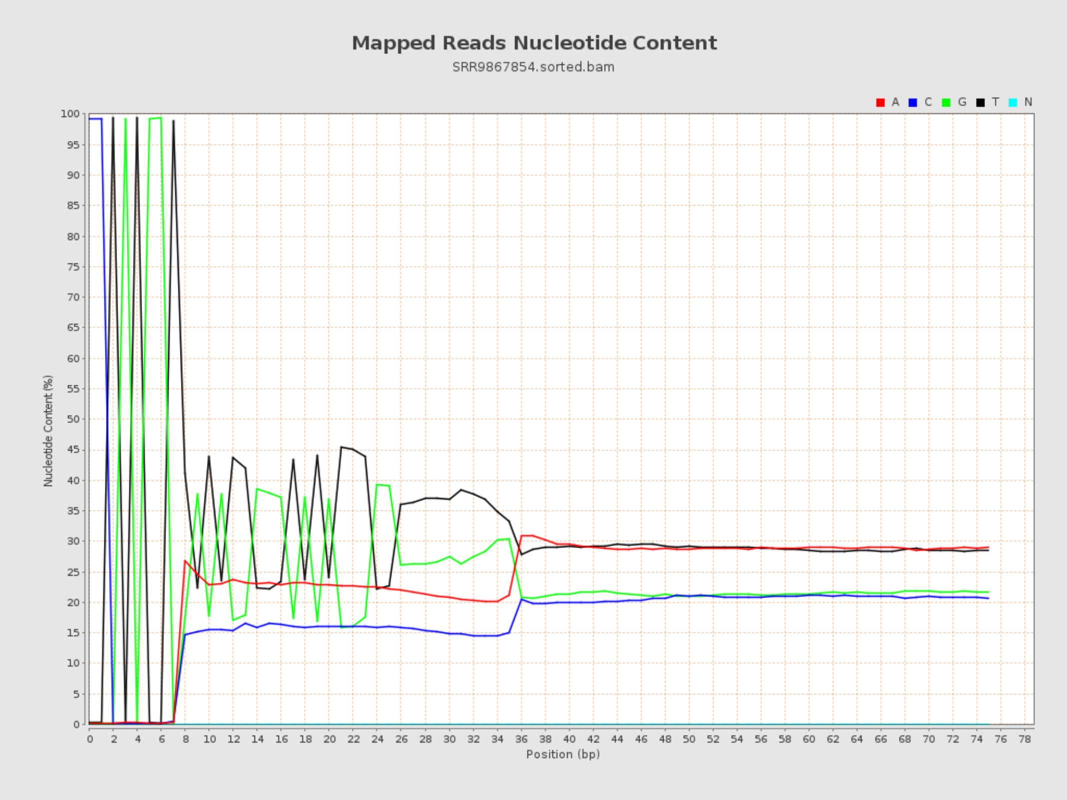
6. Results : Genome Fraction Coverage



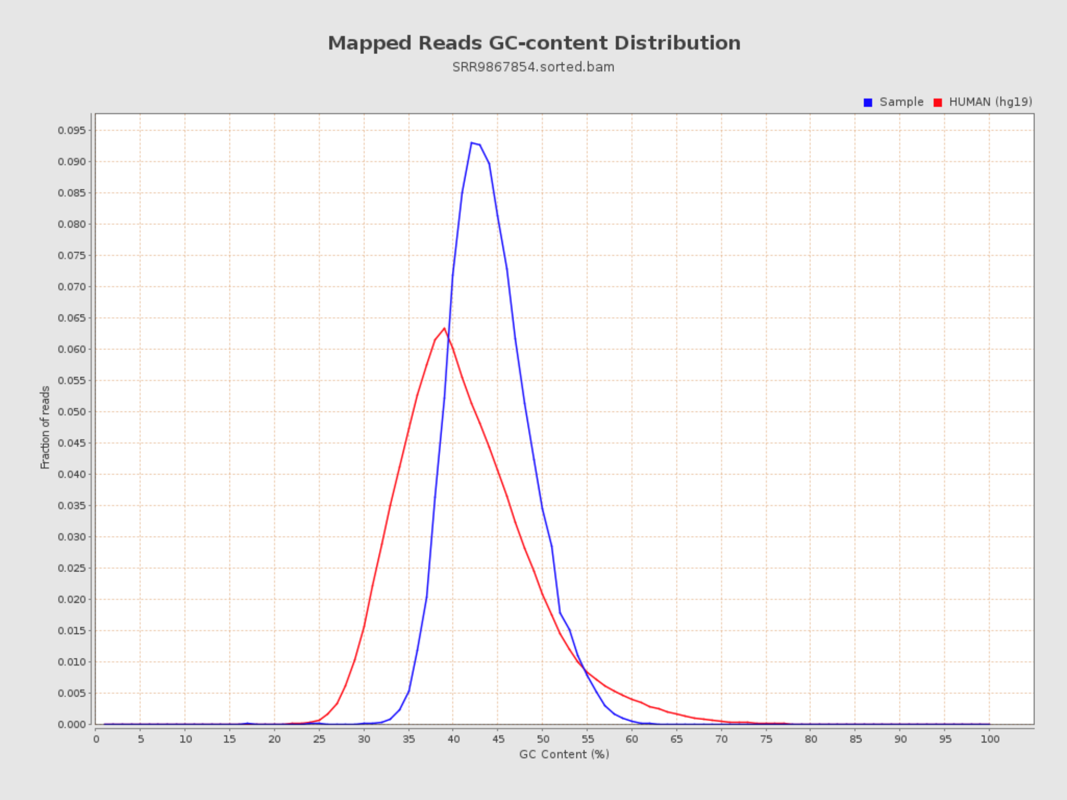
7. Results : Duplication Rate Histogram



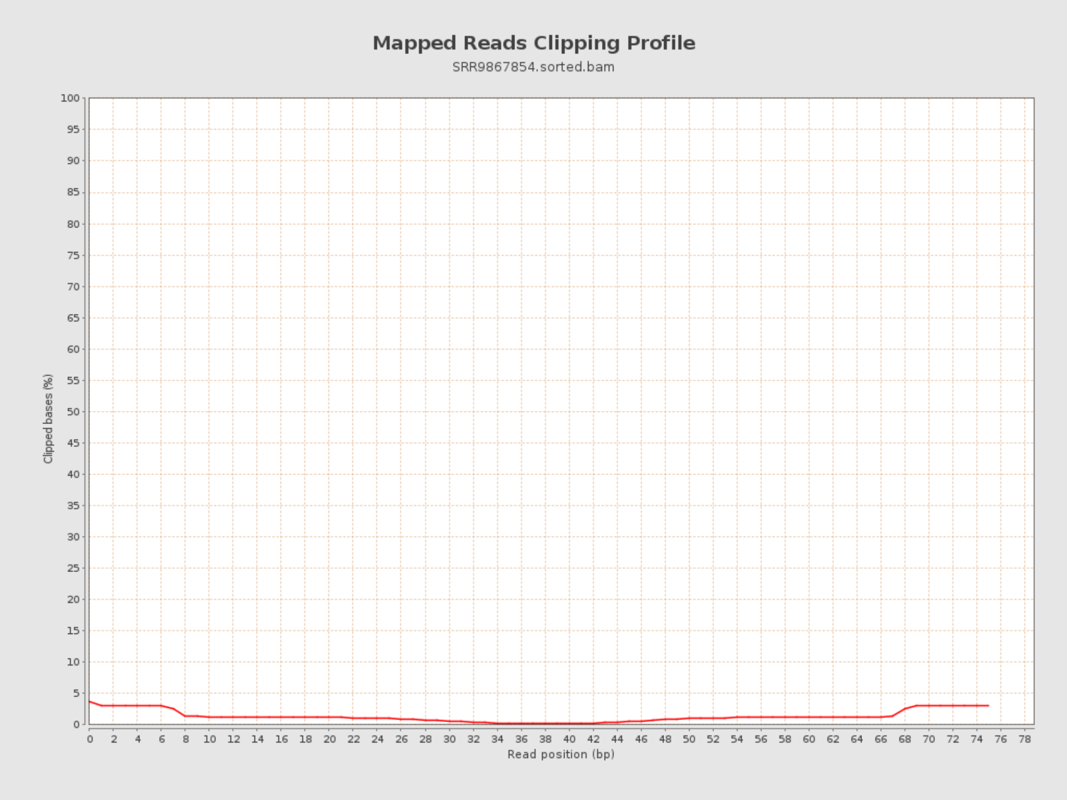
8. Results : Mapped Reads Nucleotide Content



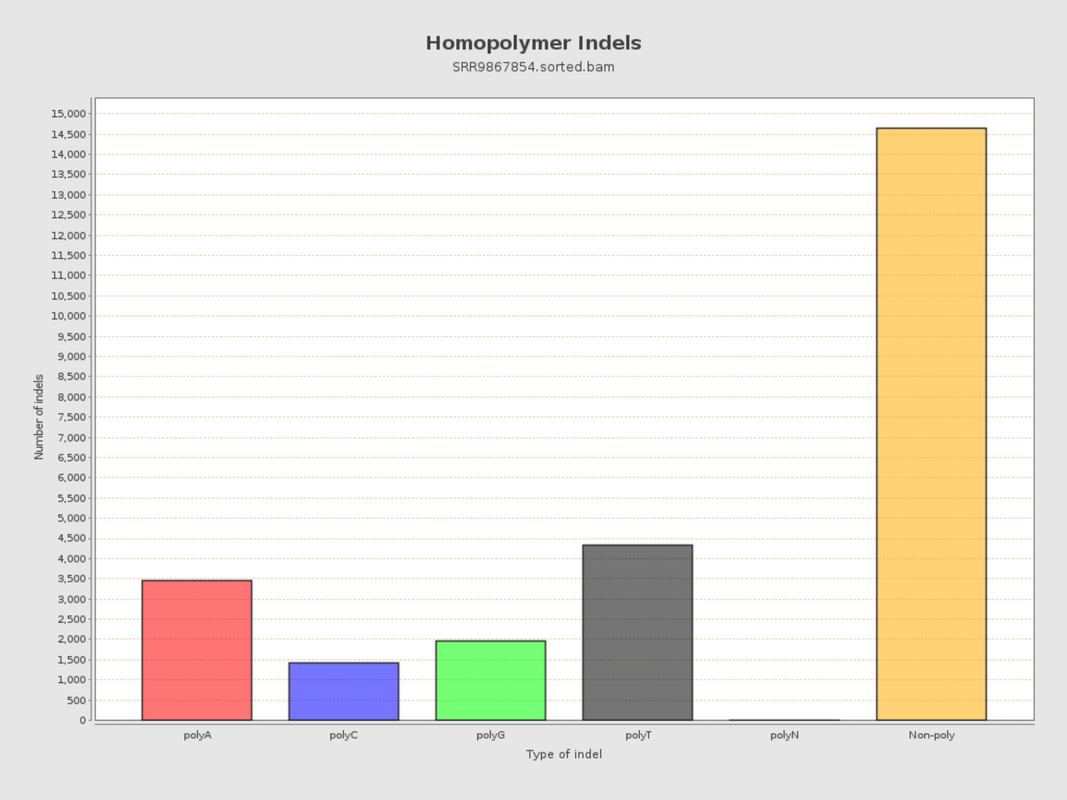
9. Results : Mapped Reads GC-content Distribution



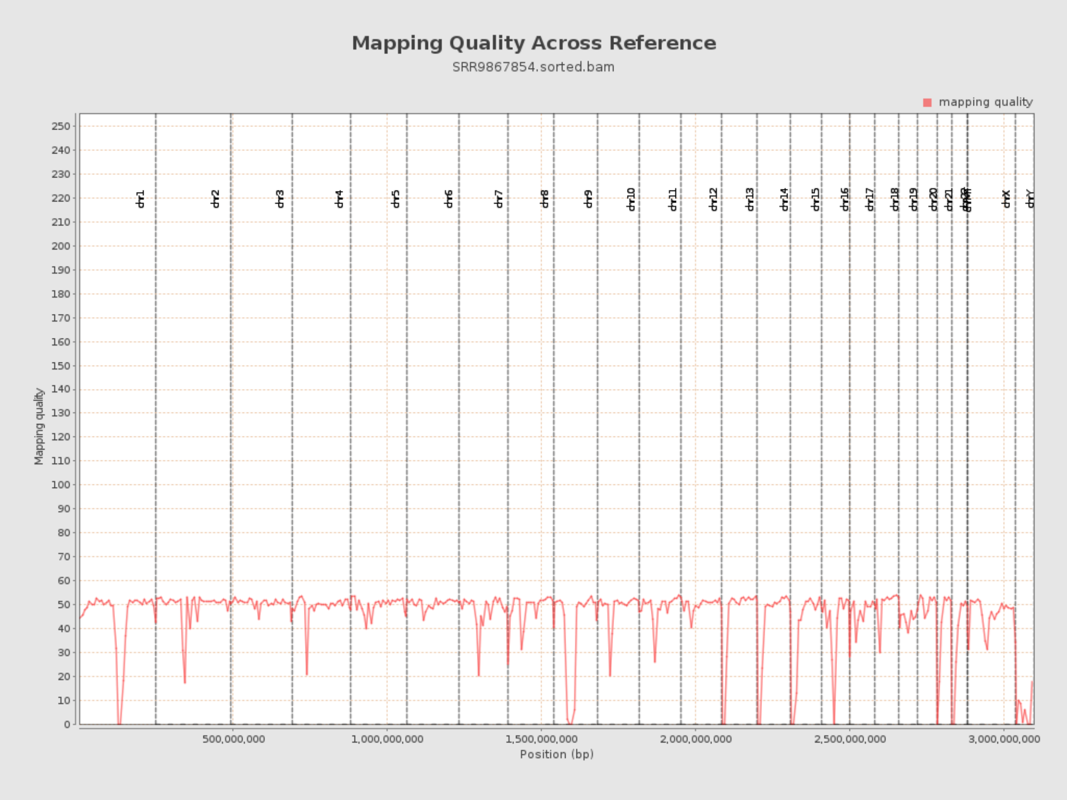
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram