Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:42:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867871.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_SRR9867871 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867871.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:42:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867871.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,100,975
Mapped reads	1,936,607 / 92.18%
Unmapped reads	164,368 / 7.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,857 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	94,632 / 4.5%
Duplication rate	3.64%
Clipped reads	1,943,397 / 92.5%

2.2. ACGT Content

Number/percentage of A's	29,736,103 / 25.92%
Number/percentage of C's	23,563,414 / 20.54%
Number/percentage of T's	34,659,892 / 30.22%
Number/percentage of G's	26,732,218 / 23.3%
Number/percentage of N's	15,754 / 0.01%
GC Percentage	43.85%

2.3. Coverage

Mean	0.0371

Standard Deviation	0.3481

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

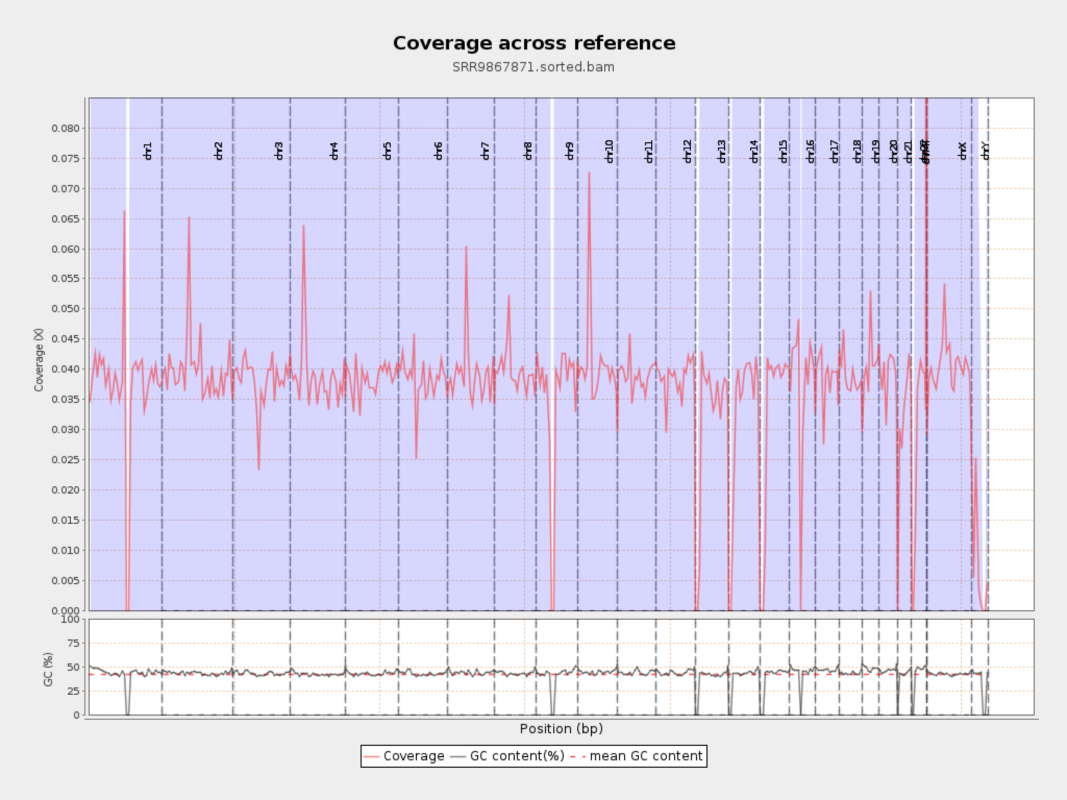
General error rate	0.51%
Mismatches	571,601
Insertions	6,938
Mapped reads with at least one insertion	0.36%
Deletions	21,501
Mapped reads with at least one deletion	1.1%
Homopolymer indels	45.35%

2.6. Chromosome stats

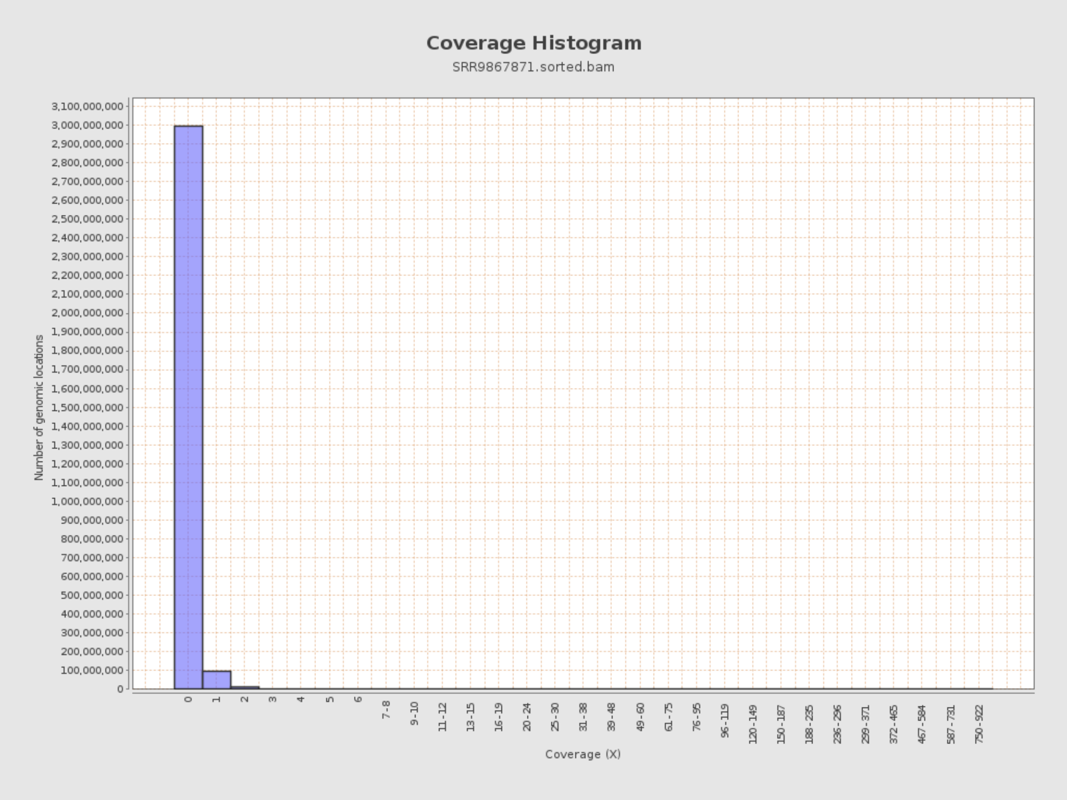
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9218397	0.037	0.6552
chr2	243199373	9754047	0.0401	0.473
chr3	198022430	7552241	0.0381	0.2162
chr4	191154276	7407022	0.0387	0.2565
chr5	180915260	6960127	0.0385	0.2196
chr6	171115067	6589624	0.0385	0.2497
chr7	159138663	6274894	0.0394	0.4079

chr8	146364022	5817697	0.0397	0.3876
chr9	141213431	4858381	0.0344	0.2814
chr10	135534747	5540470	0.0409	0.3502
chr11	135006516	5251415	0.0389	0.2996
chr12	133851895	5167804	0.0386	0.2201
chr13	115169878	3571080	0.031	0.1971
chr14	107349540	3422964	0.0319	0.2032
chr15	102531392	3307908	0.0323	0.2
chr16	90354753	3399789	0.0376	0.2356
chr17	81195210	3129877	0.0385	0.2334
chr18	78077248	3046958	0.039	0.5139
chr19	59128983	2433942	0.0412	0.4829
chr20	63025520	2459125	0.039	0.2251
chr21	48129895	1513357	0.0314	0.2328
chr22	51304566	1382701	0.027	0.182
chrMT	16571	9912	0.5982	0.8514
chrX	155270560	6282783	0.0405	0.2462
chrY	59373566	389651	0.0066	0.2486

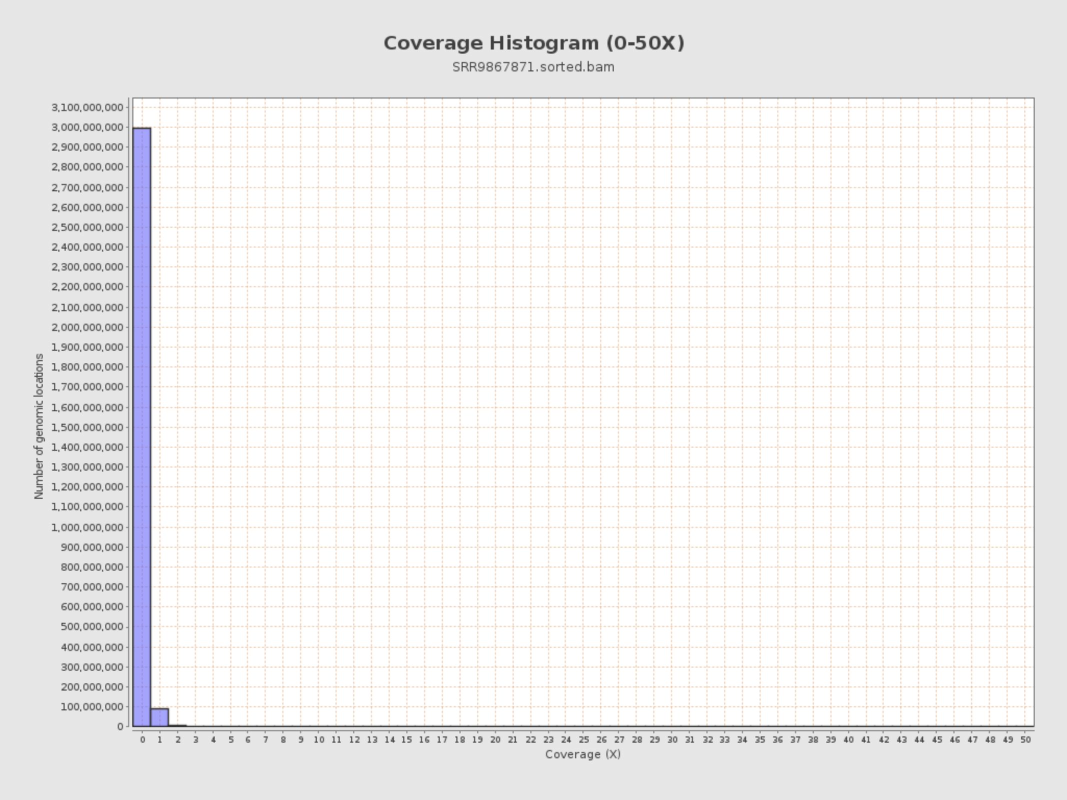
3. Results : Coverage across reference



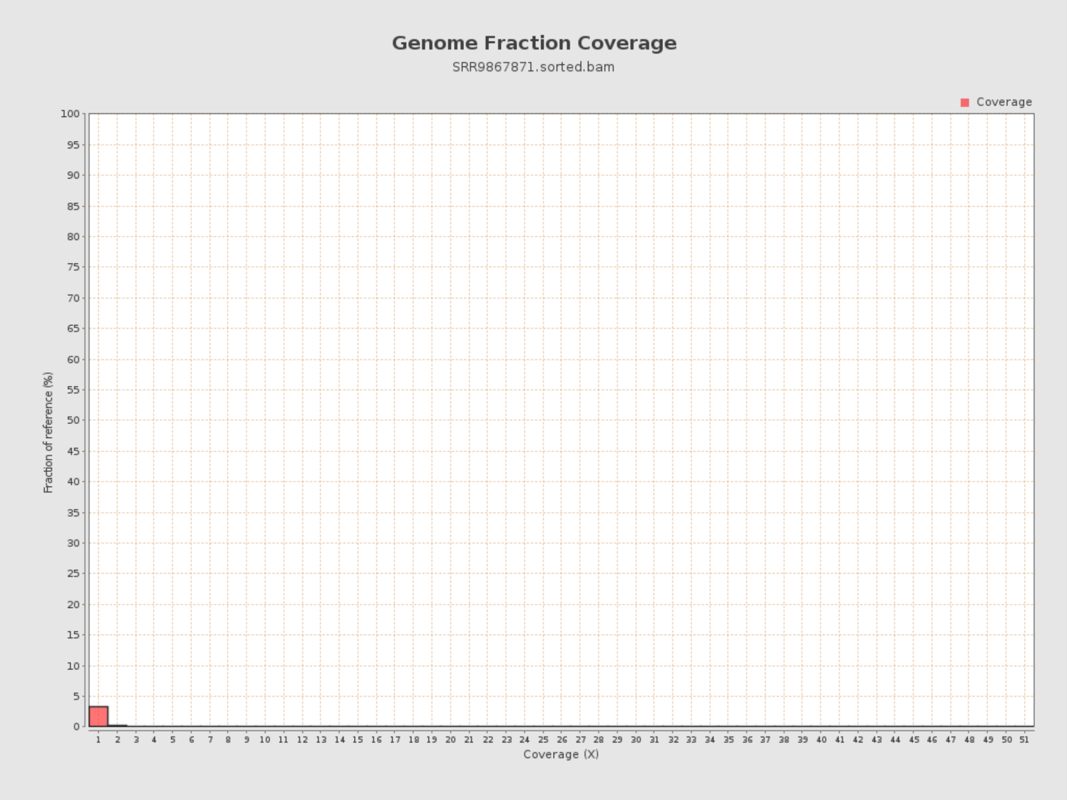
4. Results : Coverage Histogram



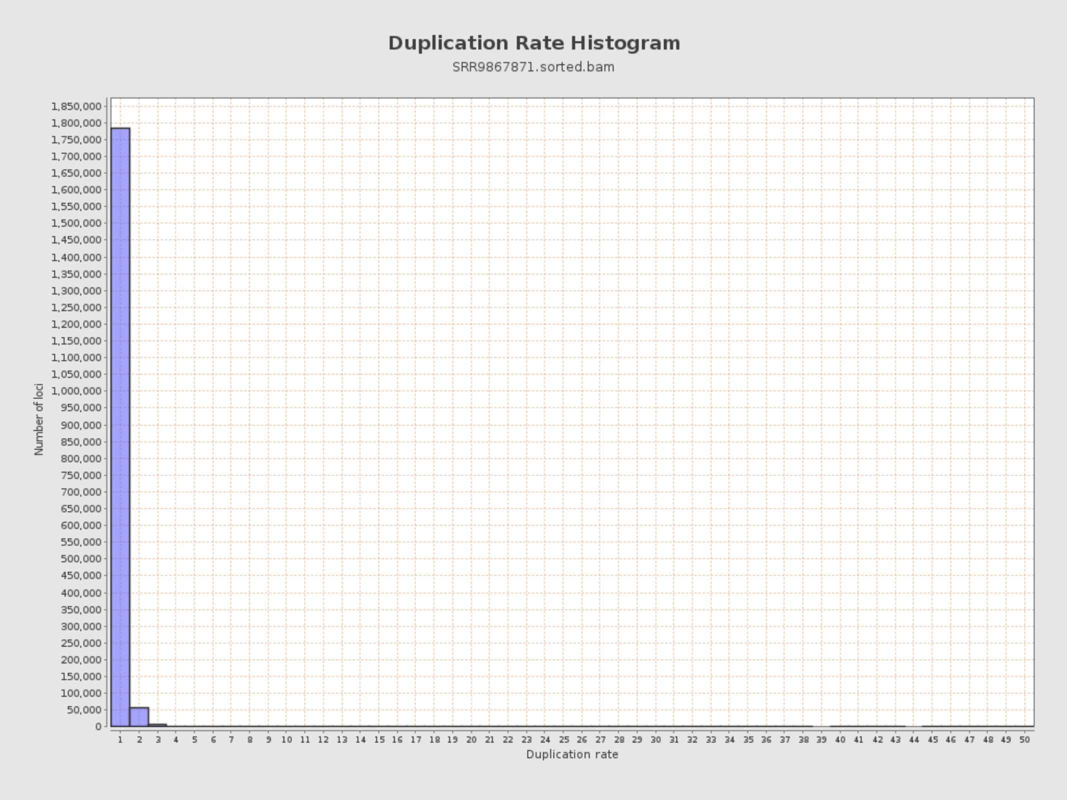
5. Results : Coverage Histogram (0-50X)



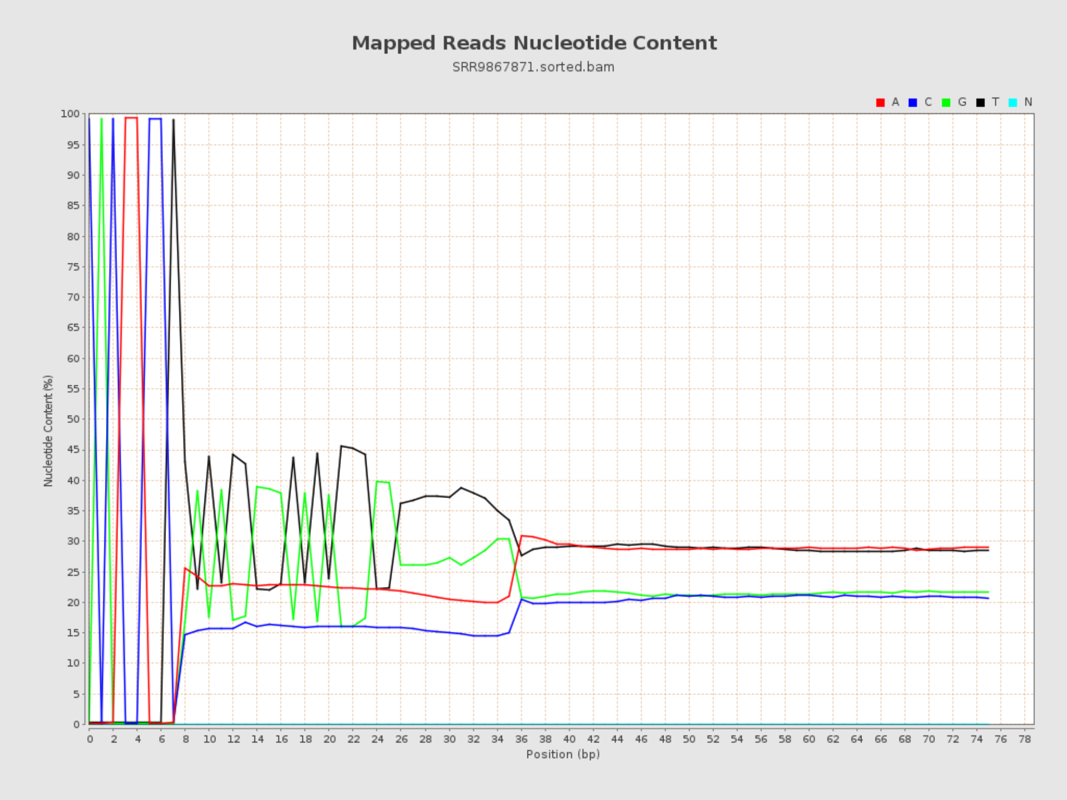
6. Results : Genome Fraction Coverage



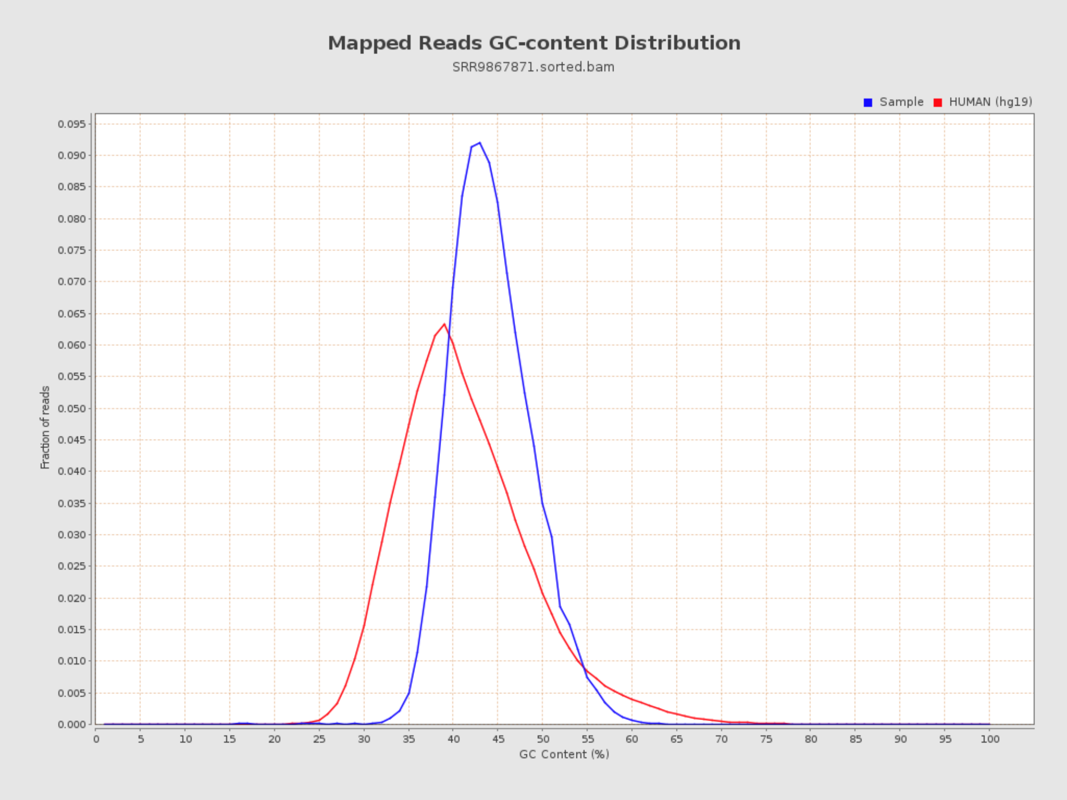
7. Results : Duplication Rate Histogram



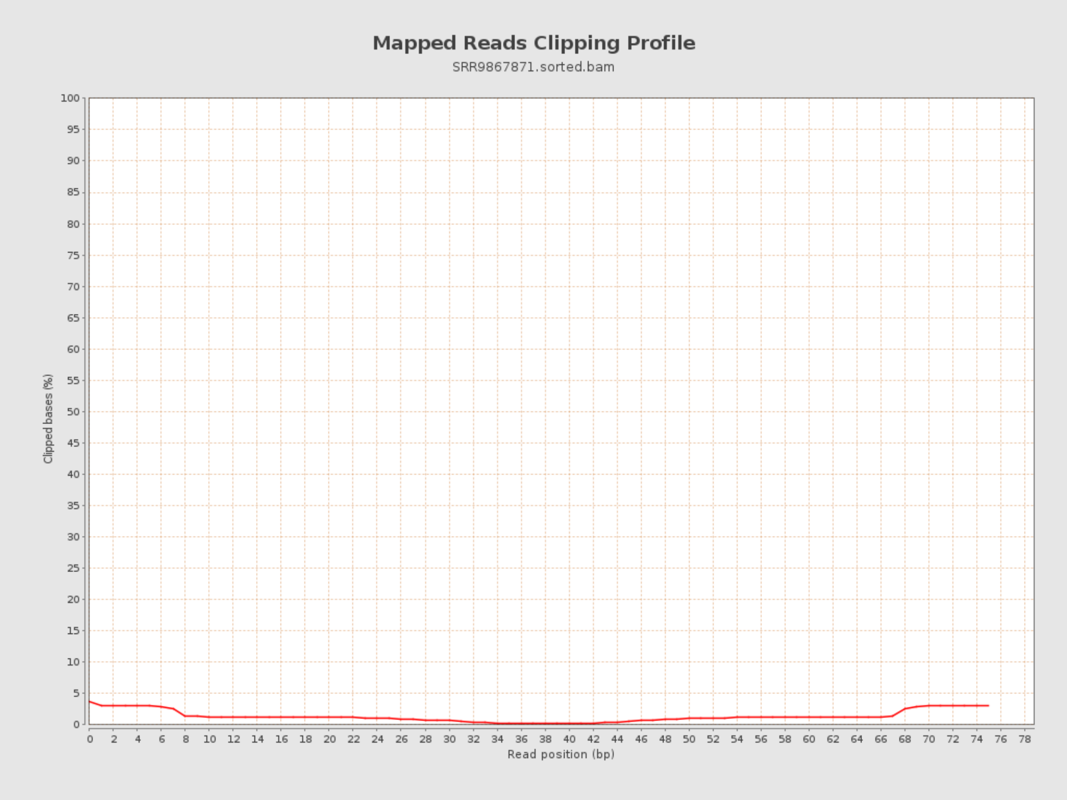
8. Results : Mapped Reads Nucleotide Content



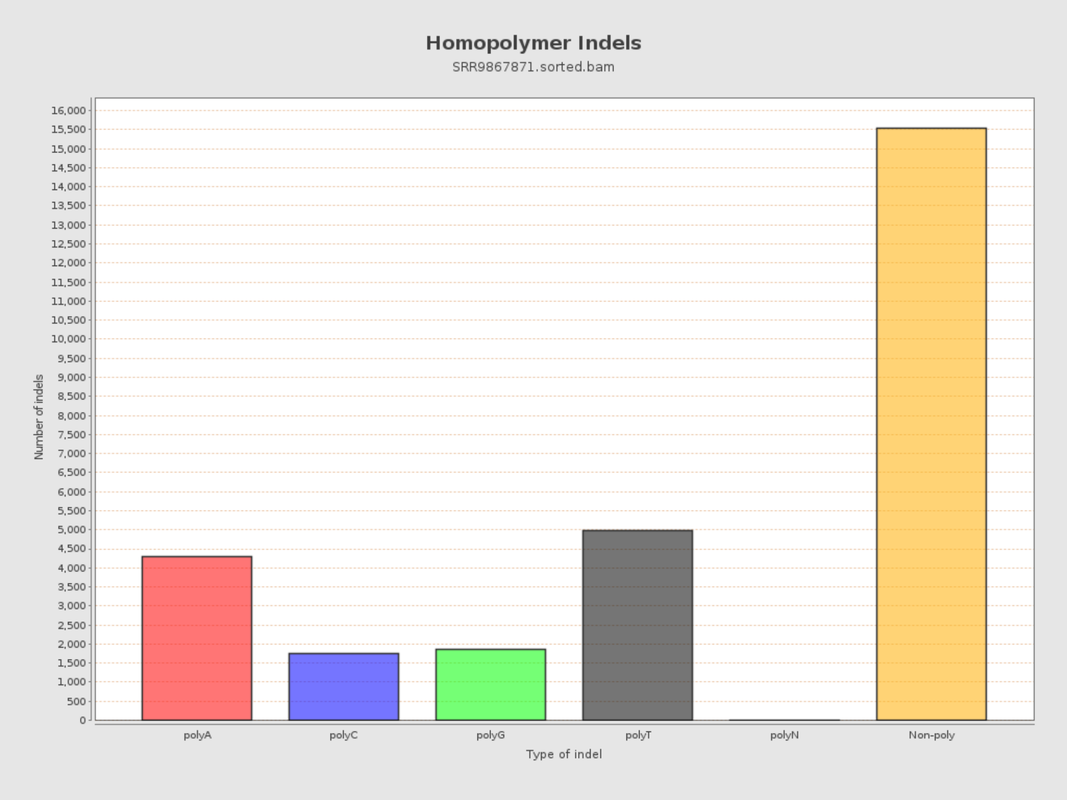
9. Results : Mapped Reads GC-content Distribution



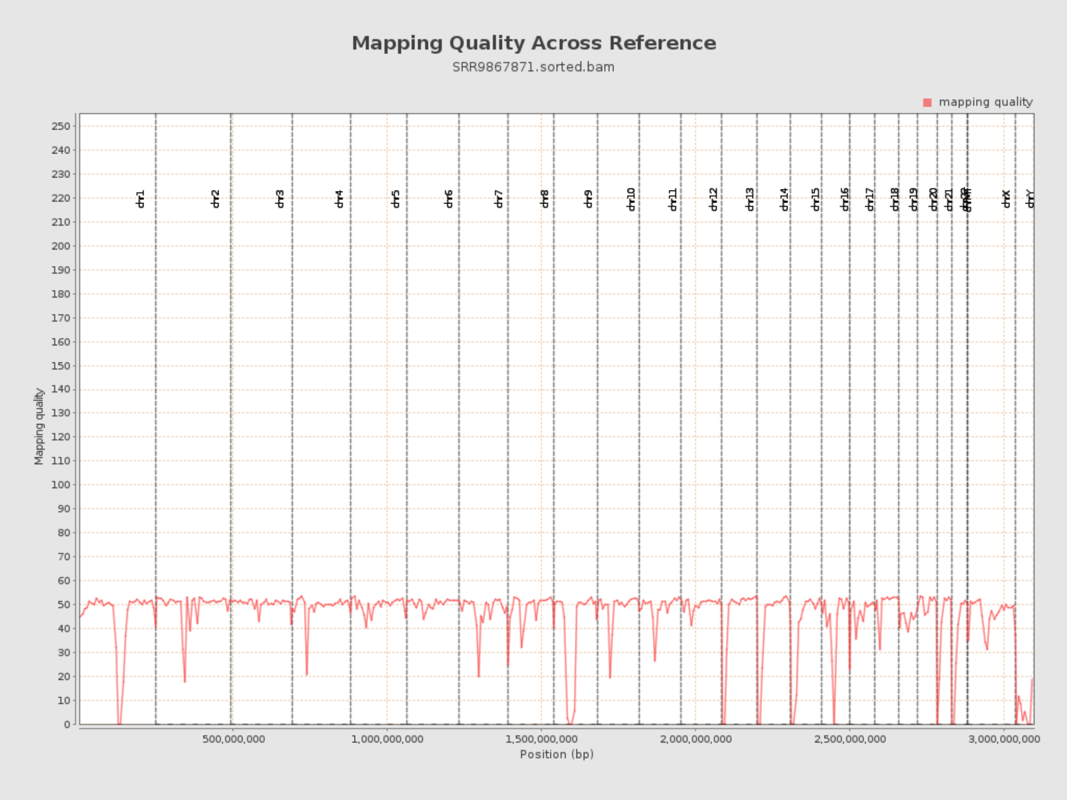
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram